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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 14:40:05 ; Search time 23.3165 Seconds  
(without alignments)  
113.581 Million cell updates/sec

Title: US-09-540-843-11  
Perfect score: 6  
Sequence: 1 ttaggg 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 547746

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
1: /cgn2\_6/ptodata/1/ina/5A COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PTUS COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	100.0	6	1	US-08-381-097A-3
2	6	100.0	6	1	US-08-381-097A-5
3	6	100.0	6	1	US-08-153-051B-4
4	6	100.0	6	1	US-08-337-684-2
5	6	100.0	6	2	US-08-151-477A-4
6	6	100.0	6	2	US-08-151-477A-4
7	6	100.0	6	2	US-08-729-598-4
8	6	100.0	6	3	US-08-819-867-9
9	6	100.0	6	3	US-08-819-867-9
10	6	100.0	6	3	US-08-630-019A-1
11	6	100.0	6	3	US-09-018-545-3
12	6	100.0	6	3	US-09-114-399-3
13	6	100.0	6	4	US-09-608-636A-1
14	6	100.0	6	4	US-09-378-535-9
15	6	100.0	6	4	US-09-378-535-9
16	6	100.0	6	5	PCT-US96-01205-1
17	6	100.0	7	3	US-08-729-598-8
18	6	100.0	8	3	US-08-838-545-15
19	6	100.0	8	3	US-08-838-545-30
20	6	100.0	8	3	US-08-838-545-34
21	6	100.0	8	3	US-09-349-532-15
22	6	100.0	8	3	US-09-349-532-30
23	6	100.0	8	3	US-09-349-532-34
24	6	100.0	9	1	US-08-337-684-3
25	6	100.0	9	3	US-08-630-019A-27
26	6	100.0	9	3	US-09-069-434-14
27	6	100.0	9	3	US-08-838-545-16

28	6	100.0	9	3	US-09-349-532-16	Sequence 16, Appl
29	6	100.0	10	1	US-08-192-300-18	Sequence 18, Appl
30	6	100.0	10	2	US-08-531-743-10	Sequence 10, Appl
31	6	100.0	10	3	US-08-630-019A-8	Sequence 8, Appl
32	6	100.0	10	3	US-08-838-545-7	Sequence 7, Appl
33	6	100.0	10	3	US-08-838-545-11	Sequence 11, Appl
34	6	100.0	10	3	US-08-838-545-17	Sequence 17, Appl
35	6	100.0	10	3	US-08-838-545-21	Sequence 21, Appl
36	6	100.0	10	3	US-08-838-545-29	Sequence 29, Appl
37	6	100.0	10	3	US-08-974-549A-527	Sequence 527, App
38	6	100.0	10	3	US-09-349-532-7	Sequence 7, Appl
39	6	100.0	10	3	US-09-349-532-11	Sequence 11, Appl
40	6	100.0	10	3	US-09-349-532-17	Sequence 17, Appl
41	6	100.0	10	3	US-09-349-532-21	Sequence 21, Appl
42	6	100.0	10	3	US-09-349-532-29	Sequence 29, Appl
43	6	100.0	10	4	US-08-912-951-294	Sequence 294, App
44	6	100.0	10	4	US-09-769-482-41	Sequence 41, Appl
45	6	100.0	11	1	US-08-330-123A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-08-381-097A-3  
; Sequence 3, Application US/08381097A  
; Patent No. 5643890  
; GENERAL INFORMATION:  
; APPLICANT: Iverson, Patrick L.  
; TITLE OF INVENTION: Synthetic Oligodeoxyribonucleotides  
; TITLE OF INVENTION: Which Mimic Telomeric Sequences for Use in the Treatment  
; TITLE OF INVENTION: of Cancer and Other Diseases  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Zarely, McKee, Thomte, Voorhees, & Sease  
; STREET: 801 Grand Suite 3200  
; CITY: Des Moines  
; STATE: Iowa  
; COUNTRY: United States  
; ZIP: 50309  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/381,097A  
; FILING DATE: 31-JAN-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Nebel, Heidi S  
; REGISTRATION NUMBER: 37,719  
; REFERENCE/DOCKET NUMBER: unmc 63092  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 515-288-3667  
; TELEFAX: 515-288-1338  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-381-097A-3

Query Match 100.0%; Score 6; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6.8e+07;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6

Db 1 TTAGGG 6  
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## RESULT 2

US-08-381-097A-5/c  
; Sequence 5, Application US/08381097A  
; Patent No. 5643890  
; GENERAL INFORMATION:  
; APPLICANT: Iverson, Patrick L.  
; APPLICANT: Mata, John E.  
; TITLE OF INVENTION: Synthetic Oligodeoxyribonucleotides  
; TITLE OF INVENTION: Which Mimic Telomeric Sequences for Use in the Treatment  
; TITLE OF INVENTION: of Cancer and Other Diseases  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Zarely, McKee, Thomte, Voorhees, & Sease  
; STREET: 801 Grand Suite 3200  
; CITY: Des Moines  
; STATE: Iowa  
; COUNTRY: United States  
; ZIP: 50309  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/381,097A  
; FILING DATE: 31-JAN-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Nebel, Heidi S  
; REGISTRATION NUMBER: 37,719  
; REFERENCE/DOCKET NUMBER: ummc 63092  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 515-288-3667  
; TELEFAX: 515-288-1338  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; US-08-381-097A-5

Query Match 100.0%; Score 6; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6.8e+07;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TTAGGG 6  
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6 TTAGGG 1

## RESULT 3

US-08-153-051B-4/c  
; Sequence 4, Application US/08153051B  
; Patent No. 5645986  
; GENERAL INFORMATION:  
; APPLICANT: Michael D. West  
; APPLICANT: Jerry W. Shay  
; APPLICANT: Woodring E. Wright  
; APPLICANT: Elizabeth Blackburn  
; APPLICANT: Nam Woo Kim  
; APPLICANT: Calvin B. Harley  
; APPLICANT: Scott L. Weinrich  
; APPLICANT: Catherine Strahl  
; APPLICANT: Michael J. McEachern  
; APPLICANT: Homayoun Vaziri

; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
; TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE  
; TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/153,051B  
; FILING DATE: No. 5645986member 12, 1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/038,766  
; FILING DATE: March 24, 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 204/195  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-153-051B-4

Query Match 100.0%; Score 6; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6.8e+07;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6  
|||||  
Db 6 TTAGGG 1

## RESULT 4

US-08-337-684-2  
; Sequence 2, Application US/08337684  
; Patent No. 5686306  
; GENERAL INFORMATION:  
; APPLICANT: West, Michael David  
; APPLICANT: Shay, Jerry  
; APPLICANT: Wright, Woodring E.  
; TITLE OF INVENTION: METHODS AND REAGENTS FOR  
; TITLE OF INVENTION: MEASURING TELOMERES  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0



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; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/337,684
; FILING DATE: No. 5686306ember 10, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/151,477
; FILING DATE: No. 5686306ember 12, 1993
; APPLICATION NUMBER: 08/153,051
; FILING DATE: No. 5686306ember 12, 1993
; APPLICATION NUMBER: 08/060,952
; FILING DATE: May 13, 1993
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; APPLICATION NUMBER: 07/882,438
; FILING DATE: May 13, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/085
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-337-684-2

Query Match 100.0%; Score 6; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTAGGG 6
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1 TTAGGG 6

RESULT 5
US-08-151-477A-4/c
Sequence 4, Application US/08151477A
Patent No. 5830644
GENERAL INFORMATION:
APPLICANT: Michael D. West
APPLICANT: Jerry W. Shay
APPLICANT: Woodring E. Wright
APPLICANT: Elizabeth Blackburn
APPLICANT: Nam Woo Kim
APPLICANT: Calvin B. Harley
APPLICANT: Scott L. Weinrich
APPLICANT: Catherine Strahl
APPLICANT: Michael J. McEachern
APPLICANT: Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: CONDITIONS RELATED TO TELEOMERE
TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESS: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0

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; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,477A
; FILING DATE: No. 5830644ember 12, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 202/189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-151-477A-4

Query Match 100.0%; Score 6; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTAGGG 6
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6 TTAGGG 1

RESULT 6
US-08-670-999-3
Sequence 3, Application US/08670999
Patent No. 5849727
GENERAL INFORMATION:
APPLICANT: Porter, Thomas R.
APPLICANT: Iverson, Patrick L.
TITLE OF INVENTION: Compositions and Methods for Altering
TITLE OF INVENTION: the Biodistribution of Biological Agents
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: Zarley, McKee, Thomte, Voorhees & Sease
STREET: 801 Grand Suite 3200
CITY: Des Moines
STATE: Iowa
COUNTRY: United States
ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,999
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heidi S.
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: ummc 107A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-288-3667
TELEFAX: 515-288-1338
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO

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ANTI-SENSE: YES  
US-08-670-999-3

Query Match 100.0%; Score 6; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6.8e+07;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTAGGG 6  
|||||  
Db 1 TTAGGG 6

## RESULT 7

US-08-729-598-4  
; Sequence 4, Application US/08729598  
; Patent No. 6001657

## GENERAL INFORMATION:

APPLICANT: Hardin, Charles C.  
APPLICANT: Brown II, Bernard A.  
APPLICANT: Roberts, John J.

APPLICANT: Peluse, Stephen A.

TITLE OF INVENTION: Antibodies That Selectively Bind

TITLE OF INVENTION: Quadruplex Nucleic Acids

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sorojini J. Biswas

STREET: P.O. Box 37428

CITY: Raleigh

STATE: No. 6001657th Carolina

COUNTRY: USA

ZIP: 27627

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/729,598

FILING DATE: 11-OCT-1996

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Biswas, Sorojini J.

REGISTRATION NUMBER: 39,111

REFERENCE/DOCKET NUMBER: 5051-301A

TELEPHONE: (919) 854-1400

TELEFAX: (919) 854-1401

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: not relevant

MOLECULE TYPE: DNA (genomic)

US-08-729-598-4

Query Match 100.0%; Score 6; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6.8e+07;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTAGGG 6  
|||||  
Db 1 TTAGGG 6

## RESULT 8

US-08-819-867-9  
; Sequence 9, Application US/08819867  
; Patent No. 6007989

## GENERAL INFORMATION:

APPLICANT: Michael D. West

APPLICANT: Calvin B. Harley

APPLICANT: Scott L. Weinrich

APPLICANT: Catherine M. Strahl  
APPLICANT: Michael J. Mceachern  
APPLICANT: Jerry Shay  
APPLICANT: Woodring E. Wright  
APPLICANT: Elizabeth H. Blackburn  
APPLICANT: Nam Woo Kim  
APPLICANT: Homayoun Vaziri  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
TITLE OF INVENTION: CONDITIONS RELATED TO  
TITLE OF INVENTION: TELOMERE LENGTH AND/OR  
TITLE OF INVENTION: TELOMERASE ACTIVITY  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSeq for Windows 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/819,867

FILING DATE: March 14, 1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/153,051

FILING DATE: No. 6007989ember 12, 1993

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Chambers, Daniel M.

REGISTRATION NUMBER: 34,561

REFERENCE/DOCKET NUMBER: 224/232

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-819-867-9

Query Match 100.0%; Score 6; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6.8e+07;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTAGGG 6  
|||||  
Db 1 TTAGGG 6

## RESULT 9

US-08-819-867-27/c  
; Sequence 27, Application US/08819867  
; Patent No. 6007989

## GENERAL INFORMATION:

APPLICANT: Michael D. West

APPLICANT: Calvin B. Harley

APPLICANT: Scott L. Weinrich

APPLICANT: Catherine M. Strahl

APPLICANT: Michael J. Mceachern

APPLICANT: Jerry Shay

APPLICANT: Woodring E. Wright

APPLICANT: Elizabeth H. Blackburn

APPLICANT: Nam Woo Kim  
 APPLICANT: Homsyoun Vaziri  
 TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
 CONDITIONS RELATED TO  
 TITLE OF INVENTION: TELOMERE LENGTH AND/OR  
 TITLE OF INVENTION: TELOMERASE ACTIVITY  
 NUMBER OF SEQUENCES: 80  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071-2066  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FastSeq for Windows 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/819,867  
 FILING DATE: March 14, 1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/153,051  
 FILING DATE: No. 6007989ember 12, 1993  
 APPLICATION NUMBER:  
 FILING DATE:

ATTORNEY/AGENT INFORMATION:  
 NAME: Chambers, Daniel M.  
 REGISTRATION NUMBER: 34,561  
 REFERENCE/DOCKET NUMBER: 224/232  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 27:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-819-867-27

Query Match 100.0%; Score 6; DB 3; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 6.8e+07;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTAGGG 6  
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 6 TTAGGG 1

RESULT 10  
 US-08-630-019A-1  
 Sequence 1, Application US/08630019A  
 Patent No. 6015710  
 GENERAL INFORMATION:  
 APPLICANT: Shay, Jerry W.  
 APPLICANT: Wright, Woodring E.  
 APPLICANT: Piatyszek, Mieczyslaw A.  
 APPLICANT: Corey, David  
 APPLICANT: No. 6015710ton, James C.  
 TITLE OF INVENTION: Modulation of Mammalian Telomerase by  
 TITLE OF INVENTION: Peptide Nucleic Acids  
 NUMBER OF SEQUENCES: 46  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California

COUNTRY: USA  
 ZIP: 94111-3834  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/630,019A  
 FILING DATE: 09-JUN-1996  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Storella, John R.  
 REGISTRATION NUMBER: 32,944  
 REFERENCE/DOCKET NUMBER: 015389-001600US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 DESCRIPTION: /desc = "peptide nucleic acid (PNA),  
 DESCRIPTION: where (deoxy)ribose-phosphate linkages are replaced by  
 DESCRIPTION: N-(2-aminoethyl)glycine units linked to nucleotide bases via  
 DESCRIPTION: glycine amino nitrogen through a methylenecarbonyl linker"

US-08-630-019A-1

Query Match 100.0%; Score 6; DB 3; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 6.8e+07;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6  
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 Db 1 TTAGGG 6

RESULT 11  
 US-09-018-545-3  
 Sequence 3, Application US/09018545  
 Patent No. 6087493  
 GENERAL INFORMATION:  
 APPLICANT: Wheelhouse, Richard T.  
 APPLICANT: Hurley, Laurence H.  
 TITLE OF INVENTION: PORPHYRIN COMPOUNDS AS TELOMERASE  
 TITLE OF INVENTION: INHIBITORS  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Arnold, White & Durkee  
 STREET: P.O. Box 4433  
 CITY: Houston  
 STATE: Texas  
 COUNTRY: U.S.  
 ZIP: 77210

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/018,545  
 FILING DATE: Concurrently Herewith  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/037,295  
 FILING DATE: 05-FEB-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kitchell, Barbara S.  
 REGISTRATION NUMBER: 33,928  
 REFERENCE/DOCKET NUMBER: UTSB:654

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-018-545-3

Query Match 100.0%; Score 6; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6.8e+07;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 TTAGGG 6

RESULT 12  
US-09-114-399-3  
Sequence 3, Application US/09114399  
Patent No. 6245747  
GENERAL INFORMATION:  
APPLICANT: Porter, Thomas R.  
APPLICANT: Iversen, Patrick L.  
APPLICANT: Meyer, Gary D.  
TITLE OF INVENTION: Targeted Site Specific Drug Delivery  
FILE OF INVENTION: Compositions and Method of Use  
CURRENT APPLICATION NUMBER: US/09/114,399  
CURRENT FILING DATE: 1998-07-13  
PRIOR APPLICATION NUMBER: US 08/615,495  
PRIOR FILING DATE: 1996-03-12  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 6  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: PS-ODN  
US-09-114-399-3

Query Match 100.0%; Score 6; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6.8e+07;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13  
US-09-608-636A-1  
Sequence 1, Application US/09608636A  
Patent No. 6518268  
GENERAL INFORMATION:  
APPLICANT: Geron Corporation  
APPLICANT: Kyowa Hakko Kogyo Co., Ltd.  
APPLICANT: Chin, Allison C.  
APPLICANT: Holcomb, Ryan C.  
APPLICANT: Piatyszek, Mieczyslaw A  
APPLICANT: Singh, Upinder  
APPLICANT: Tolman, Richard L.  
APPLICANT: Akama, Tsutomu  
APPLICANT: Kanda, Yutaka  
APPLICANT: Asai, Akira  
APPLICANT: Yamashita, Yoshinori  
APPLICANT: Endo, Kaori  
APPLICANT: Yamaguchi, Hiroyuki  
TITLE OF INVENTION: Telomerase Inhibitors and Methods of Their Use

FILE REFERENCE: 055/003  
CURRENT APPLICATION NUMBER: US/09/608,636A  
CURRENT FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 60/142,173  
PRIOR FILING DATE: 1999-07-10  
PRIOR APPLICATION NUMBER: JP 11-187616  
PRIOR FILING DATE: 1999-07-01  
PRIOR APPLICATION NUMBER: JP 11-307576  
PRIOR FILING DATE: 1999-10-28  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 6  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: oligonucleotide  
US-09-608-636A-1

Query Match 100.0%; Score 6; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6.8e+07;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6  
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Db 1 TTAGGG 6

RESULT 14  
US-09-378-535-9  
Sequence 9, Application US/09378535  
Patent No. 6551774  
GENERAL INFORMATION:  
APPLICANT: Michael D. West  
Calvin B. Harley  
Scott L. Weinrich  
Catherine M. Strahl  
Michael J. Mceachern  
Jerry Shay  
Woodring E. Wright  
Elizabeth H. Blackburn  
Nam Woo Kim  
Homayoun Vaziri  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
CONDITIONS RELATED TO  
TELOMERE LENGTH AND/OR  
TELOMERASE ACTIVITY  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,535  
FILING DATE: 20-Aug-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/819,867  
FILING DATE: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Chambers, Daniel M.  
REGISTRATION NUMBER: 34,561  
REFERENCE/DOCKET NUMBER: 224/232

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-378-535-9

Query Match 100.0%; Score 6; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTAGGG 6

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Job time : 23.4276 secs

; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-378-535-27

Query Match 100.0%; Score 6; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
Db 6 TTAGGG 1

Search completed: January 1, 2004, 00:32:19
Job time : 23.4276 secs

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-378-535-9

Query Match 100.0%; Score 6; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.8e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
Db 1 TTAGGG 6

RESULT 15
US-09-378-535-27/c
Sequence 27, Application US/09378535
Patent No. 6551774
GENERAL INFORMATION:
APPLICANT: Michael D. West
Calvin B. Hatley
Scott L. Weinrich
Catherine M. Strahl
Michael J. McEachern
Jerry Shay
Woodring E. Wright
Elizabeth H. Blackburn
Nam Woo Kim
Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
CONDITIONS RELATED TO
TELOMERE LENGTH AND/OR
TELOMERASE ACTIVITY

NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,535
FILING DATE: 20-Aug-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/819,867
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 17:10:00 ; Search time 69.9494 Seconds  
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Title: US-09-540-843-11  
Perfect score: 6  
Sequence: 1 ttaggg 6

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2263443 seqs, 1730637950 residues  
Total number of hits satisfying chosen parameters: 998502

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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16: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	100.0	6	9	US-09-817-387-29
2	6	100.0	6	9	US-09-735-363A-49
3	6	100.0	6	10	US-09-730-893-1
4	6	100.0	6	11	US-09-940-173A-1
5	6	100.0	6	13	US-10-255-535-8
6	6	100.0	6	13	US-10-336-265-1
7	6	100.0	6	13	US-10-336-265-3
8	6	100.0	6	13	US-10-336-265-4
9	6	100.0	6	13	US-10-336-265-63
10	6	100.0	6	13	US-10-336-265-64
11	6	100.0	6	13	US-10-232-927A-9
12	6	100.0	6	13	US-10-232-927A-27
13	6	100.0	6	15	US-10-122-630-11
14	6	100.0	6	15	US-10-122-630-12
15	6	100.0	6	15	US-10-122-633-11

c	16	6	100.0	6	15	US-10-122-633-12	Sequence 12, Appl
	17	6	100.0	7	10	US-09-730-893-6	Sequence 6, Appl
	18	6	100.0	7	11	US-09-940-173A-6	Sequence 6, Appl
	19	6	100.0	8	10	US-09-730-893-4	Sequence 4, Appl
	20	6	100.0	8	11	US-09-940-173A-4	Sequence 4, Appl
	21	6	100.0	8	13	US-10-336-265-58	Sequence 58, Appl
c	22	6	100.0	9	10	US-09-728-574-19	Sequence 19, Appl
	23	6	100.0	10	13	US-10-330-627-92	Sequence 41, Appl
	24	6	100.0	10	13	US-10-330-627-92	Sequence 92, Appl
c	25	6	100.0	10	13	US-10-330-627-1296	Sequence 1296, Ap
	26	6	100.0	10	13	US-10-330-627-1297	Sequence 1297, Ap
c	27	6	100.0	10	13	US-10-330-627-1298	Sequence 1298, Ap
	28	6	100.0	10	13	US-10-330-627-1439	Sequence 1439, Ap
	29	6	100.0	10	14	US-10-033-145-56	Sequence 56, Appl
	30	6	100.0	10	14	US-10-033-145-358	Sequence 358, App
	31	6	100.0	10	14	US-10-033-145-613	Sequence 613, App
	32	6	100.0	10	14	US-10-033-145-1694	Sequence 1694, Ap
	33	6	100.0	10	15	US-10-044-692-294	Sequence 294, App
	34	6	100.0	10	15	US-10-044-539-294	Sequence 294, App
c	35	6	100.0	11	9	US-09-057-351-2	Sequence 2, Appl
	36	6	100.0	11	11	US-09-835-370-63	Sequence 63, Appl
	37	6	100.0	11	11	US-09-249-155-57	Sequence 57, Appl
c	38	6	100.0	11	11	US-09-942-310-7	Sequence 7, Appl
	39	6	100.0	11	11	US-09-942-310-44	Sequence 44, Appl
c	40	6	100.0	11	12	US-10-314-322-57	Sequence 57, Appl
	41	6	100.0	11	12	US-10-314-322-271	Sequence 271, App
c	42	6	100.0	11	13	US-10-255-535-4	Sequence 4, Appl
	43	6	100.0	11	13	US-10-255-535-14	Sequence 14, Appl
c	44	6	100.0	11	13	US-10-359-935-2	Sequence 2, Appl
	45	6	100.0	11	15	US-10-122-630-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1  
US-09-817-387-29  
; Sequence 29, Application US/09817387  
; Patent No. US20010039263A1  
; GENERAL INFORMATION:  
; APPLICANT: Max-Delbruck-Centrum fur Molekulare Medizin  
; TITLE OF INVENTION: Chimeric Oligonucleotides and the Use Thereof  
; FILE REFERENCE: 101195-24  
; CURRENT APPLICATION NUMBER: US/09/817,387  
; CURRENT FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: DE 197 20 151.2  
; PRIOR FILING DATE: 1997-05-02  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 29  
; LENGTH: 6  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: telomeric  
; OTHER INFORMATION: DNA of man  
US-09-817-387-29

Query Match 100.0%; Score 6; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.6e+08;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6  
Db 1 TTAGGG 6

RESULT 2  
US-09-735-363A-49  
; Sequence 49, Application US/09735363A  
; Patent No. US20010041681A1  
; GENERAL INFORMATION:  
; APPLICANT: Filion, Mario

; APPLICANT: Phillip, Nigel  
 ; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
 ; FILE REFERENCE: 02811-0181  
 ; CURRENT APPLICATION NUMBER: US/09/735,363A  
 ; CURRENT FILING DATE: 2000-12-12  
 ; PRIOR APPLICATION NUMBER: 60/170,325  
 ; PRIOR FILING DATE: 1999-12-13  
 ; PRIOR APPLICATION NUMBER: 60/228,925  
 ; PRIOR FILING DATE: 2000-08-29  
 ; NUMBER OF SEQ ID NOS: 87  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 49  
 ; LENGTH: 6  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic Oligonucleotide  
 ; US-09-735-363A-49

Query Match 100.0%; Score 6; DB 9; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+08;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3  
 US-09-730-893-1  
 ; Sequence 1, Application US/09730893  
 ; Publication No. US20020107258A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KERWIN, SEAN M.  
 ; APPLICANT: FEDOROFF, OLEG Y.  
 ; APPLICANT: SALAZAR, MIGUEL  
 ; APPLICANT: HURLEY, LAURENCE H.  
 ; TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A  
 ; FILE REFERENCE: G-QUADRUPLIX-INTERACTION COMPOUND  
 ; FILE REFERENCE: UTSS:679USC1  
 ; CURRENT APPLICATION NUMBER: US/09/730,893  
 ; CURRENT FILING DATE: 2000-12-05  
 ; PRIOR APPLICATION NUMBER: 09/244,675  
 ; PRIOR FILING DATE: 1999-04-02  
 ; PRIOR APPLICATION NUMBER: 60/073,629  
 ; PRIOR FILING DATE: 1998-04-02  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1  
 ; LENGTH: 6  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: Primer  
 ; US-09-730-893-1

Query Match 100.0%; Score 6; DB 10; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+08;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 1 TTAGGG 6

RESULT 4  
 US-09-940-173A-1  
 ; Sequence 1, Application US/09940173A  
 ; Publication No. US20030040525A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KERWIN, SEAN M.  
 ; APPLICANT: FEDOROFF, OLEG Y.

; APPLICANT: SALAZAR, MIGUEL  
 ; APPLICANT: HURLEY, LAURENCE H.  
 ; TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A  
 ; TITLE OF INVENTION: G-QUADRUPLIX-INTERACTION COMPOUND  
 ; FILE REFERENCE: UTSS:679USC2  
 ; CURRENT APPLICATION NUMBER: US/09/940,173A  
 ; CURRENT FILING DATE: 2002-06-24  
 ; PRIOR APPLICATION NUMBER: 09/730,893  
 ; PRIOR FILING DATE: 2000-12-05  
 ; PRIOR APPLICATION NUMBER: 09/244,675  
 ; PRIOR FILING DATE: 1999-04-02  
 ; PRIOR APPLICATION NUMBER: 60/073,629  
 ; PRIOR FILING DATE: 1998-04-02  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1  
 ; LENGTH: 6  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: Primer  
 ; US-09-940-173A-1

Query Match 100.0%; Score 6; DB 11; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+08;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5  
 US-10-255-535-8  
 ; Sequence 8, Application US/10255535  
 ; Publication No. US20030138814A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Geron Corporation  
 ; APPLICANT: Gryaznov, Sergei  
 ; APPLICANT: Pongracz, Krisztina  
 ; APPLICANT: Tolman, Richard L.  
 ; APPLICANT: Morin, Gregg B.  
 ; TITLE OF INVENTION: Oligonucleotide Conjugates  
 ; FILE REFERENCE: 072/002P  
 ; CURRENT APPLICATION NUMBER: US/10/255,535  
 ; CURRENT FILING DATE: 2002-09-25  
 ; PRIOR APPLICATION NUMBER: PCT/US02/09138  
 ; PRIOR FILING DATE: 2002-03-21  
 ; PRIOR APPLICATION NUMBER: US 60/278,322  
 ; PRIOR FILING DATE: 2001-03-23  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 8  
 ; LENGTH: 6  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: oligonucleotide  
 ; US-10-255-535-8

Query Match 100.0%; Score 6; DB 13; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+08;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6  
 US-10-336-265-1  
 ; Sequence 1, Application US/10336265



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Publication No. US20030148988A1
; GENERAL INFORMATION:
; APPLICANT: Kool, Eric T.
; TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for
; FILE REFERENCE: 12665.0021.NPUS01
; CURRENT APPLICATION NUMBER: US/10/336,265
; PRIOR FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 60/345,056
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-336-265-1
Query Match 100.0%; Score 6; DB 13; Length 6;
Best Local Similarity 100.0%; Pred. No. 5.6e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTAGGG 6
Db 1 TTAGGG 6
RESULT 7
US-10-336-265-3/c
Sequence 3, Application US/10336265
Publication No. US20030148988A1
; GENERAL INFORMATION:
; APPLICANT: Kool, Eric T.
; TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for
; FILE REFERENCE: 12665.0021.NPUS01
; CURRENT APPLICATION NUMBER: US/10/336,265
; PRIOR FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 60/345,056
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-336-265-3
Query Match 100.0%; Score 6; DB 13; Length 6;
Best Local Similarity 100.0%; Pred. No. 5.6e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTAGGG 6
Db 6 TTAGGG 1
RESULT 8
US-10-336-265-4/c
Sequence 4, Application US/10336265
Publication No. US20030148988A1
; GENERAL INFORMATION:
; APPLICANT: Kool, Eric T.
; TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for
; FILE REFERENCE: 12665.0021.NPUS01
; CURRENT APPLICATION NUMBER: US/10/336,265
; PRIOR FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 60/345,056
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
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Publication No. US20030148988A1
; GENERAL INFORMATION:
; APPLICANT: Kool, Eric T.
; TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for
; FILE REFERENCE: 12665.0021.NPUS01
; CURRENT APPLICATION NUMBER: US/10/336,265
; PRIOR FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 60/345,056
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 6
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-336-265-4
Query Match 100.0%; Score 6; DB 13; Length 6;
Best Local Similarity 100.0%; Pred. No. 5.6e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTAGGG 6
Db 6 TTAGGG 1
RESULT 9
US-10-336-265-63
Sequence 63, Application US/10336265
Publication No. US20030148988A1
; GENERAL INFORMATION:
; APPLICANT: Kool, Eric T.
; TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for
; FILE REFERENCE: 12665.0021.NPUS01
; CURRENT APPLICATION NUMBER: US/10/336,265
; PRIOR FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 60/345,056
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-336-265-63
Query Match 100.0%; Score 6; DB 13; Length 6;
Best Local Similarity 100.0%; Pred. No. 5.6e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTAGGG 6
Db 1 TTAGGG 6
RESULT 10
US-10-336-265-64
Sequence 64, Application US/10336265
Publication No. US20030148988A1
; GENERAL INFORMATION:
; APPLICANT: Kool, Eric T.
; TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for
; FILE REFERENCE: 12665.0021.NPUS01
; CURRENT APPLICATION NUMBER: US/10/336,265
; PRIOR FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 60/345,056
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
; LENGTH: 6
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-336-265-64
Query Match 100.0%; Score 6; DB 13; Length 6;
Best Local Similarity 66.7%; Pred. No. 5.6e+08;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTAGGG 6
Db 1 UUAGGG 6
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RESULT 11  
 US-10-232-927A-9  
 ; Sequence 9, Application US/10232927A  
 ; Publication No. US20030190638A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Michael D. West  
 ; Calvin B. Harley  
 ; Scott L. Weinrich  
 ; Catherine M. Strahl  
 ; Michael J. Mceachern  
 ; Jerry Shay  
 ; Woodring E. Wright  
 ; Elizabeth H. Blackburn  
 ; Nam Woo Kim  
 ; Homayoun Vaziri  
 TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
 CONDITIONS RELATED TO  
 TELOMERE LENGTH AND/OR  
 TELOMERASE ACTIVITY  
 NUMBER OF SEQUENCES: 80  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071-2066  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FastSEQ for Windows 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/232,927A  
 FILING DATE: 29-Aug-2002  
 CLASSIFICATION: <unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/378,535  
 FILING DATE: 20-Aug-1999  
 APPLICATION NUMBER: 08/819,867  
 FILING DATE: <unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Chambers, Daniel M.  
 REGISTRATION NUMBER: 34,561  
 REFERENCE/DOCKET NUMBER: 224/232  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
 US-10-232-927A-9

Query Match 100.0%; Score 6; DB 13; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+08;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6  
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 Db 1 TTAGGG 6

RESULT 12  
 US-10-232-927A-27/c  
 ; Sequence 27, Application US/10232927A

; Publication No. US20030190638A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Michael D. West  
 ; Calvin B. Harley  
 ; Scott L. Weinrich  
 ; Catherine M. Strahl  
 ; Michael J. Mceachern  
 ; Jerry Shay  
 ; Woodring E. Wright  
 ; Elizabeth H. Blackburn  
 ; Nam Woo Kim  
 ; Homayoun Vaziri  
 TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
 CONDITIONS RELATED TO  
 TELOMERE LENGTH AND/OR  
 TELOMERASE ACTIVITY  
 NUMBER OF SEQUENCES: 80  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071-2066  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FastSEQ for Windows 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/232,927A  
 FILING DATE: 29-Aug-2002  
 CLASSIFICATION: <unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/378,535  
 FILING DATE: 20-Aug-1999  
 APPLICATION NUMBER: 08/819,867  
 FILING DATE: <unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Chambers, Daniel M.  
 REGISTRATION NUMBER: 34,561  
 REFERENCE/DOCKET NUMBER: 224/232  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 27:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
 US-10-232-927A-27

Query Match 100.0%; Score 6; DB 13; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+08;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6  
 |||||  
 Db 6 TTAGGG 1

RESULT 13  
 US-10-122-630-11  
 ; Sequence 11, Application US/10122630  
 ; Publication No. US20030032610A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gilcrest, Barbara A.  
 ; APPLICANT: Eller, Mark S.

APPLICANT: Yaar, Mina  
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
; FILE REFERENCE: 0054.1088-018  
; CURRENT APPLICATION NUMBER: US/10/122,630  
; PRIOR FILING DATE: 2002-04-12  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR FILING DATE: 1996-06-03  
; PRIOR FILING DATE: 1996-06-03  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11  
LENGTH: 6  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
; OTHER INFORMATION: Synthetic DNA Fragment  
US-10-122-630-11

Query Match 100.0%; Score 6; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.6e+08;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTAGGG 6  
|||||  
1 TTAGGG 6

RESULT 14  
US-10-122-630-12/c  
Sequence 12, Application US/10122630  
Publication No. US20030032610A1  
GENERAL INFORMATION:  
APPLICANT: Gilchrest, Barbara A.  
APPLICANT: Eller, Mark S.  
APPLICANT: Yaar, Mina  
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
; FILE REFERENCE: 0054.1088-018  
; CURRENT APPLICATION NUMBER: US/10/122,630  
; PRIOR FILING DATE: 2002-04-12  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR FILING DATE: 1996-06-03  
; PRIOR FILING DATE: 1996-06-03  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 6  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
; OTHER INFORMATION: Synthetic DNA Fragment  
US-10-122-630-12

Query Match 100.0%; Score 6; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.6e+08;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6

Db |||||  
6 TTAGGG 1  
RESULT 15  
US-10-122-633-11  
Sequence 11, Application US/10122633  
Publication No. US20030032611A1  
GENERAL INFORMATION:  
APPLICANT: Gilchrest, Barbara A.  
APPLICANT: Eller, Mark S.  
APPLICANT: Yaar, Mina  
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
; FILE REFERENCE: 0054.1088-019  
; CURRENT APPLICATION NUMBER: US/10/122,633  
; PRIOR FILING DATE: 2002-04-12  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11  
LENGTH: 6  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
; OTHER INFORMATION: Synthetic DNA Fragment  
US-10-122-633-11

Query Match 100.0%; Score 6; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 5.6e+08;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6  
|||||  
Db 1 TTAGGG 6

Search completed: January 1, 2004, 01:10:39  
Job time : 69.9494 secs



LOCUS  
DEFINITION 2821056.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821056 3', linear mRNA EST 07-JAN-2000  
ACCESSION AW248826  
VERSION AW248826.1 GI:6591819  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 21)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Other ESTs: 2821056.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: c9apbs-remail.nih.gov  
Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling  
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.lnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 21  
contiguous PHRED high quality bases following vector sequence. Very  
Low Quality Sequence: Trace file contained 21 contiguous distinct  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was  
polyadenylated.  
Plate: LLCMS row: N column: 1  
High quality sequence stop: 21.  
Location/Qualifiers

Copied from 09980559 on 05/19/2004

## FEATURES

1..21  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821056"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dt priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."  
4 a 3 c 3 g 11 t

## BASE COUNT

Query Match 100.0%; Score 6; DB 9; Length 21;  
Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6

Db 20 TTAGGG 15

## RESULT 15

AW248836/c  
LOCUS  
DEFINITION 2821108.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821108 3', linear mRNA EST 07-JAN-2000  
ACCESSION AW248836  
VERSION AW248836.1 GI:6591829

KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 21)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Other ESTs: 2821108.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: c9apbs-remail.nih.gov  
Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling  
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.lnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 10  
contiguous PHRED high quality bases following vector sequence. Very  
Low Quality Sequence: Trace file contained 21 contiguous distinct  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was  
polyadenylated.  
Plate: LLCMS row: P column: 5  
High quality sequence stop: 10.  
Location/Qualifiers

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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821108"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dt priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."  
4 a 6 c 0 g 11 t

## FEATURES

1..21  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821108"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dt priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."  
4 a 6 c 0 g 11 t

## BASE COUNT

Query Match 100.0%; Score 6; DB 9; Length 21;  
Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6

Db 20 TTAGGG 15

Search completed: December 31, 2003, 19:41:30  
Job time : 692.392 secs

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1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0227G21"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
8 a 5 c 2 g 5 t
BASE COUNT
ORIGIN

Query Match 100.0%; Score 6; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTAGGG 6
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18 TTAGGG 13

RESULT 12
TA158A03P/c
LOCUS
DEFINITION
T. brucei sheared genomic DNA clone 158A03, forward sequence,
genomic survey sequence.
ACCESSION
AL472050.1 GI:11837404
VERSION
GSS.
KEYWORDS
Trypanosoma brucei
SOURCE
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 20)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1. .20
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="158A03"
6 a 11 c 0 g 3 t
BASE COUNT
ORIGIN

Query Match 100.0%; Score 6; DB 29; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTAGGG 6
|||||
19 TTAGGG 14

RESULT 13
TA199G02Q/c
LOCUS
DEFINITION
T. brucei sheared genomic DNA clone 199G02, reverse sequence,
genomic survey sequence.
ACCESSION
AL476798.1 GI:11843362
VERSION
GSS.
KEYWORDS
Trypanosoma brucei
SOURCE
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 20)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1. .20
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="199G02"
5 a 4 c 3 g 8 t
BASE COUNT
ORIGIN

Query Match 100.0%; Score 6; DB 29; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTAGGG 6
|||||
20 TTAGGG 15

RESULT 14
AW248826/c

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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0542G17"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_libs="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 2 c 11 g 5 t

ORIGIN

Query Match 100.0%; Score 6; DB 28; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.6e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTAGGG 6  
|||||  
7 TTAGGG 12

RESULT 10

AZ808291

LOCUS

DEFINITION 2M0071D09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0071D09 R, genomic survey sequence.

ACCESSION

AZ808291

VERSION

AZ808291.1

KEYWORDS

GSS

SOURCE

Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0071 row: D column: 09  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
1. .20

FEATURES

source

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0071D09"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_libs="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 2 c 10 g 6 t

ORIGIN

Query Match 100.0%; Score 6; DB 28; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.6e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAGGG 6  
|||||  
Db 6 TTAGGG 11

RESULT 11

AZ960008/c

LOCUS

DEFINITION 2M0227G21R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0227G21 R, genomic survey sequence.

ACCESSION

AZ960008

VERSION

AZ960008.1

KEYWORDS

GSS

SOURCE

Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0227 row: G column: 21  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers

FEATURES

Location/Qualifiers

/db\_xref="taxon:10090"  
 /clone="UUGCLM0080J04"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGCLM library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (G1/4732114[gb]|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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3 a      13 c      0 g      4 t.
ch      100.0%;      Score 6;      DB 28;      Length 20;
1 Similarity 100.0%;      Pred. No. 6.6e+05;
6;      Conservative      0;      Mismatches      0;      Indels      0;      Gaps      0;

1 TTATGG 6
16 TTAGGG 11
|||||
|||||

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RESULT 8  
 AZ627174 linear GSS 13-DEC-2000  
 1M0467010R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0467010 R, genomic survey sequence.  
 AZ627174  
 AZ627174.1 GI:11749364  
 GSS.  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 20)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
 and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunne@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0467 row: 0 column: 10  
 Seq primer: CACACAGGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 20.  
 Location/Qualifiers  
 1..20  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0467010"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
5 a 2 c 7 g 6 t
BASE COUNT
ORIGIN
Query Match 100.0%; Score 6; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTAGGG 6
|||||
Db 13 TTAGGG 18
RESULT 9
AZ662909
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112 USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0542 row: G column: 17
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid end
High quality sequence stop: 20.
Location/Qualifiers
1 .20
/orcnam="Mus musculus"

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**FEATURES**  
**source**



Plate: 0102 row: N column: 07  
 Seq primer: CACACAGGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.

# FEATURES

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 Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUC2M0102N07"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 8 a 6 c 2 g 3 t  
 ORIGIN  
 Query Match 100.0%; Score 6; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 TTAGGG 6  
 |||||  
 17 TTAGGG 12

RESULT 6  
 AZ345513/c  
 LOCUS  
 DEFINITION  
 S015529-024-026-P04-SP6 MP12-ADIS-024-developing root Beta vulgaris  
 CDNA clone 024-026-P04 5-PRIME, mRNA sequence.  
 ACCESSION  
 BQ593485  
 VERSION  
 BQ593485.1 GI:26123068  
 KEYWORDS  
 EST.  
 ORGANISM  
 Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
 1 (bases 1 to 20)  
 Herwig,R., Schulz,B., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. Drungowski,M., and Radelof,U.  
 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)  
 Contact: Weisshaar B  
 ADIS DNA core facility at MPIZ  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weisshaar@mpiz-koeln.mpg.de  
 Insert Length: 20 Std Error: 0.00  
 Plate: 26 row: P column: 04

FEATURES  
 source  
 1..20  
 Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"

Seq primer: SP6; CATACGATTAGGTGACACTATAG.

FEATURES  
 source  
 1..20  
 Location/Qualifiers  
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 /cultivar="KWS2320 (double haploid, monogerm breeding line)"  
 /db\_xref="GABI:193369"  
 /db\_xref="taxon:161934"  
 /clone="024-026-P04"  
 /tissue\_type="developing root"  
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 /clone\_lib="MP12-ADIS-024-developing root"  
 /note="Vector: PCWSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schwanz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
 SP6-SalI-CCACGCGCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

BASE COUNT 7 a 6 c 2 g 5 t  
 ORIGIN  
 Query Match 100.0%; Score 6; DB 13; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 6.6e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 TTAGGG 6  
 |||||  
 18 TTAGGG 13

RESULT 7  
 AZ345513/c  
 LOCUS  
 DEFINITION  
 1M0080J04F Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0080J04 F, genomic survey sequence.  
 ACCESSION  
 AZ345513  
 VERSION  
 AZ345513.1 GI:10424750  
 KEYWORDS  
 GSS.  
 SOURCE  
 Mus musculus (house mouse)  
 ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 20)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0080 row: J column: 04  
 Seq primer: CGTTGTAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 20.

FEATURES  
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 /mol\_type="genomic DNA"  
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Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1. .19  
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/db\_xref="taxon:10090"  
/clone="UUGC1M0200F10"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 7 a 5 c 2 g 5 t  
ORIGIN

Query Match 100.0%; Score 6; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.5e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTAGGG 6  
|||||  
8 TTAGGG 3

RESULT 4  
LOCUS AZ614760 19 bp DNA linear GSS 13-DEC-2000  
DEFINITION IM0443A17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0443A17 R, genomic survey sequence.  
ACCESSION AZ614760  
VERSION AZ614760.1 GI:11736950  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0443 row: A column: 17

Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1. .19  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0443A17"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 3 a 0 c 10 g 6 t  
ORIGIN

Query Match 100.0%; Score 6; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.5e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTAGGG 6  
|||||  
4 TTAGGG 9

RESULT 5  
LOCUS AZ826736/c 19 bp DNA linear GSS 20-FEB-2001  
DEFINITION 2M0102N07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0102N07 R, genomic survey sequence.  
ACCESSION AZ826736  
VERSION AZ826736.1 GI:12996644  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00

PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu/LowQualitySequence>: 15 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: trace file contained 16 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: L1C01 row: K column: 7  
High quality sequence stop: 15.

#### FEATURES

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/mol\_type="mRNA"  
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/clone="IMAGE:2819454"  
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/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NH MGC 7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 3 a 0 c 3 g 10 t

#### ORIGIN

Query Match 100.0%; Score 6; DB 9; Length 16;  
Best Local Similarity 100.0%; Pred. No. 6.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTAGGG 6  
|||||  
9 TTAGGG 14

RESULT 2  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AZ392246 19 bp DNA linear GSS 03-OCT-2000  
1M0154G12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0154G12 R, genomic survey sequence.

AZ392246.1 GI:10507234  
GSS.  
Mus musculus (house mouse)  
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,  
and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: [ddunne@genetics.utah.edu](mailto:ddunne@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00  
Plate: 0154 row: G column: 12

Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends

High quality sequence stop: 19.

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/db\_xref="taxon:10090"  
/clone="UUGC1M0154G12"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi14732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 3 a 5 c 5 g 6 t

#### ORIGIN

Query Match 100.0%; Score 6; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.5e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTAGGG 6  
|||||  
14 TTAGGG 19

RESULT 3  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AZ422271 19 bp DNA linear GSS 03-OCT-2000  
1M0200F10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0200F10 R, genomic survey sequence.

AZ422271.1 GI:10546284  
GSS.  
Mus musculus (house mouse)  
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,  
and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: [ddunne@genetics.utah.edu](mailto:ddunne@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00  
Plate: 0200 row: F column: 10

Seq primer: CACACAGGAACAGCTATGACC

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 13:58:09 ; Search time 689.392 Seconds  
(without alignments)  
211.530 Million cell updates/sec

Title: US-09-540-843-11  
Perfect score: 6  
Sequence: 1 ttaggg 6

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 33330

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpi:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_pbg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	100.0	16	9	AW248958
2	6	100.0	19	28	AZ392246
3	6	100.0	19	28	AZ422271
4	6	100.0	19	28	AZ614760

C	5	6	100.0	19	28	AZ826736
C	6	6	100.0	20	13	BQ593485
C	7	6	100.0	20	28	AZ345513
	8	6	100.0	20	28	AZ621714
	9	6	100.0	20	28	AZ662909
	10	6	100.0	20	28	AZ862917
C	11	6	100.0	20	28	AZ960008
C	12	6	100.0	20	29	TA158A03P
C	13	6	100.0	20	29	TA199G02Q
C	14	6	100.0	21	9	AW248826
C	15	6	100.0	21	9	AW248836
C	16	6	100.0	21	28	AZ331625
C	17	6	100.0	21	28	AZ399400
C	18	6	100.0	21	28	AZ445481
C	19	6	100.0	21	28	AZ626594
C	20	6	100.0	21	28	AZ760907
C	21	6	100.0	21	28	AZ766315
C	22	6	100.0	21	28	AZ828389
C	23	6	100.0	21	28	AZ833919
C	24	6	100.0	21	28	AZ877328
C	25	6	100.0	22	9	AA954126
C	26	6	100.0	22	9	AA954126
C	27	6	100.0	22	14	DI8745
C	28	6	100.0	22	28	AZ324747
C	29	6	100.0	22	28	AZ464647
C	30	6	100.0	22	28	AZ483833
C	31	6	100.0	22	28	AZ500414
C	32	6	100.0	22	28	AZ598320
C	33	6	100.0	22	28	AZ629501
C	34	6	100.0	22	28	AZ666649
C	35	6	100.0	22	28	AZ836104
C	36	6	100.0	22	28	AZ855118
C	37	6	100.0	23	9	AU258772
C	38	6	100.0	23	14	CA794240
C	39	6	100.0	23	28	AZ423815
C	40	6	100.0	23	28	AZ465280
C	41	6	100.0	23	28	AZ623979
C	42	6	100.0	23	28	AZ817008
C	43	6	100.0	23	28	AZ979817
C	44	6	100.0	23	28	BH857265
C	45	6	100.0	24	28	AZ309633

ALIGNMENTS

RESULT 1  
AW248958  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AW248958  
2819454.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2819454 3',  
mRNA sequence.  
AW248958  
2819454.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2819454 3',  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 16)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Other ESTs: 2819454.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: DCTD/DP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LNL at:  
[www-bio.lnl.gov/bbrp/image/image.html](http://www-bio.lnl.gov/bbrp/image/image.html) Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross\_match from University of Washington Genome Center

```
XX SQ Sequence 8 BP; 1 A; 0 C; 3 G; 2 T; 2 other;
Query Match 100.0%; Score 6; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.2e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTAGGG 6
Db 2 TTAGGG 7

RESULT 14
AAT05735
ID AAT05735 standard; DNA; 9 BP.
XX AAT05735;
01-FEB-1996 (first entry)
Telomerase oligonucleotide substrate #2.
Telomerase; proliferation; telomere; hybrid; immortalised cell; anaemia;
transplantation; cell therapy; treatment; AIDS; leukaemia; lymphoma; ss.
Synthetic.
WO9513383-A1.
18-MAY-1995.
10-NOV-1994; 94WO-US13130.
12-NOV-1993; 93US-0153051.
12-NOV-1993; 93US-0151477.
(GERO-) GERON CORP.
(TEXA) UNIV TEXAS SYSTEM.
Shay J, West MD, Wright WE;
WPI; 1995-224051/29.
Increasing telomere length in cells - to increase proliferative
capacity and therefore delay cellular senescence, useful in cell
therapy and transplantation
Claim 12; Page 29; 38pp; English.
Oligonucleotides AAT05734-7 are examples of telomerase substrates used
to increase the proliferative capacity of normal cells that express
telomerase activity. The oligonucleotides allow an increase in
length of telomeres in normal cells and in hybrids of normal and
immortalised cells. The increase in telomere length extends the
capacity of cells to replicate, esp. those treated ex vivo and used
for transplantation techniques e.g. cell therapy, for the treatment
of AIDS, anaemia, leukaemia or lymphoma.
XX SQ Sequence 9 BP; 2 A; 0 C; 3 G; 4 T; 0 other;
Query Match 100.0%; Score 6; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.9e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTAGGG 6
Db 1 TTAGGG 6

RESULT 15
AAT89240
ID AAT89240 standard; DNA; 9 BP.
XX
```

```
AC AAT89240;
XX 12-MAY-1998 (first entry)
XX Peptide nucleic acid 15, targeted to mammalian telomerase.
DE Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;
XX inhibitor; ss.
KW Synthetic.
XX Key Location/Qualifiers
FH modified_base 1..9
FT /*tag= a
FT /note= "Sugar-phosphate backbone has been replaced by
FT a peptide backbone"
XX WO9738013-A1.
XX 16-OCT-1997.
XX 09-APR-1997; 97WO-US05931.
XX 09-APR-1996; 96US-0630019.
XX (GERO-) GERON CORP.
XX Corey D, Norton JC, Piatyszek MA, Shay JW, Wright WE;
XX WPI; 1997-512647/47.
XX New peptide nucleic acids hybridising to mammalian telomerase RNA -
XX used to inhibit telomerase, for treating tumours and other
XX proliferative diseases, also for diagnosis
XX Claim 9; Page 59; 76pp; English.
XX This sequence is a novel peptide nucleic acid (PNA), which acts as
XX an inhibitor of mammalian, preferably human, telomerase. The PNAs
XX hybridise specifically to an RNA component of mammalian telomerase,
XX and include the sequence GGG for specific hybridisation to the template
XX region of this component. PNAs can be used as probes to detect the
XX RNA component of mammalian telomerase and as inhibitors of telomerase
XX activity, especially in the treatment of cancer.
XX SQ Sequence 9 BP; 2 A; 0 C; 4 G; 3 T; 0 other;
Query Match 100.0%; Score 6; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.9e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTAGGG 6
Db 3 TTAGGG 8
Search completed: December 31, 2003, 15:08:16
Job time : 173.392 secs
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inflammation; lymphoproliferative disease; autoimmune disease; neurodegenerative disease; neoplasia; hyperplasia; HIV; AIDS; human immunodeficiency virus; acquired immunodeficiency syndrome; telomere metabolism; mutant; cytostatic; anti-inflammatory; immunosuppressive; polyamide backbone; ss.

Homo sapiens.

Synthetic.

Key Location/Qualifiers

modified\_base 1..8

/\*tag= a

/note= "This sequence is a peptide nucleic acid, i.e. it contains a polyamide backbone instead of a deoxyribose backbone"

US6294650-B1.

25-SEP-2001.

08-JUL-1999; 99US-0349532.

09-APR-1997; 97US-0838545.

09-APR-1996; 96US-0630019.

(TEXA ) UNIV TEXAS SYSTEM.

Shay JW, Wright WE, Piatyszek MA, Corey DR, Norton JC; WPI; 2001-638024/73.

New peptide nucleic acids that hybridises to the RNA component of mammalian telomerase, useful for treating or preventing cancer, inflammation, lymphoproliferative diseases, autoimmune disease, or neurodegenerative diseases -

Claim 7; Column 73; 46pp; English.

The present invention relates to peptide nucleic acids (PNAs), comprising a sequence of 6-25 nucleobases, that inhibit telomerase activity in mammalian cells by hybridising to the RNA component of mammalian telomerase. The PNAs are useful as probes to detect the RNA component of mammalian telomerase and as inhibitors of telomerase activity, or to detect and/or quantitate polynucleotide having the human telomerase RNA component (hTR) sequence, as well as in forensic identification of individuals, such as paternity testing or identification of criminal suspects or unknown descendants based on the hTR gene RFLP pattern. The PNA can be further used for treating or preventing cancer, inflammation, lymphoproliferative diseases, autoimmune disease, or neurodegenerative diseases. The PNAs in combination with other pharmaceuticals (such as antineoplastic or cytostatic agents) can be used for treating neoplasia, hyperplasia, human immunodeficiency virus (HIV) infections, acquired immunodeficiency syndrome (AIDS) and associated pathologies, and other diseases characterised by abnormal telomere metabolism or telomerase activity. The present sequence represents one of the PNA sequences of the invention.

Sequence 8 BP; 1 A; 0 C; 4 G; 3 T; 0 other;

Query Match 100.0%; Score 6; DB 23; Length 8;

Best Local Similarity 100.0%; Pred. No. 3.2e+08;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTAGGG 6

2 TTAGGG 7

RESULT 13

AAS15474

ID AAS15474 standard; DNA; 8 BP.

XX AC AAS15474;

14-FEB-2002 (first entry)

PNA 34 inhibiting human and mammalian telomerase activity.

Mammalian; peptide nucleic acid; probe; forensic; paternity testing; human telomerase RNA component; hTR gene RFLP pattern; cancer; inflammation; lymphoproliferative disease; autoimmune disease; neurodegenerative disease; neoplasia; hyperplasia; HIV; AIDS; human immunodeficiency virus; acquired immunodeficiency syndrome; telomere metabolism; mutant; cytostatic; anti-inflammatory; immunosuppressive; polyamide backbone; ss.

Homo sapiens.

Synthetic.

Key Location/Qualifiers

modified\_base 1..8

/\*tag= a

/note= "This sequence is a peptide nucleic acid, i.e. it contains a polyamide backbone instead of a deoxyribose backbone"

modified\_base 1

/\*tag= b

/note= "N= 1-50 peptide nucleic acid nucleobases, selected from U, T, A, G, C or i"

modified\_base 8

/\*tag= c

/note= "N= 1-50 peptide nucleic acid nucleobases, selected from U, T, A, G, C or i"

US6294650-B1.

25-SEP-2001.

08-JUL-1999; 99US-0349532.

09-APR-1997; 97US-0838545.

09-APR-1996; 96US-0630019.

(TEXA ) UNIV TEXAS SYSTEM.

Shay JW, Wright WE, Piatyszek MA, Corey DR, Norton JC; WPI; 2001-638024/73.

New peptide nucleic acids that hybridises to the RNA component of mammalian telomerase, useful for treating or preventing cancer, inflammation, lymphoproliferative diseases, autoimmune disease, or neurodegenerative diseases -

Disclosure; Column 59; 46pp; English.

The present invention relates to peptide nucleic acids (PNAs), comprising a sequence of 6-25 nucleobases, that inhibit telomerase activity in mammalian cells by hybridising to the RNA component of mammalian telomerase. The PNAs are useful as probes to detect the RNA component of mammalian telomerase and as inhibitors of telomerase activity, or to detect and/or quantitate polynucleotide having the human telomerase RNA component (hTR) sequence, as well as in forensic identification of individuals, such as paternity testing or identification of criminal suspects or unknown descendants based on the hTR gene RFLP pattern. The PNA can be further used for treating or preventing cancer, inflammation, lymphoproliferative diseases, autoimmune disease, or neurodegenerative diseases. The PNAs in combination with other pharmaceuticals (such as antineoplastic or cytostatic agents) can be used for treating neoplasia, hyperplasia, human immunodeficiency virus (HIV) infections, acquired immunodeficiency syndrome (AIDS) and associated pathologies, and other diseases characterised by abnormal telomere metabolism or telomerase activity. The present sequence represents one of the PNA sequences of the invention.

Note: The present sequence is given in the SEQ ID listing but is not mentioned elsewhere in the patent.

PT activity in mammalian cells is useful as probes to detect the RNA  
 component of a mammalian telomerase  
 Claim 6; Column 71; 45pp; English.  
 The present sequence represents a peptide nucleic acid molecule which  
 hybridises to the mRNA component of mammalian telomerase, and inhibits  
 telomerase activity. Telomerase is a ribonucleoprotein enzyme that  
 synthesizes one strand of the telomeric DNA, using as a template an 11  
 nucleotide sequence contained within the RNA component of the enzyme. The  
 invention relates to PNA molecules having a sequence of no more than 25  
 bases, which include the sequence GTTAGG. The uncharged nature of the PNA  
 backbone increases the melting temperature of associating strands,  
 increases the rate of association with targeted nucleic acids, and  
 affords greater resistance of degradation by proteases or nucleases. The  
 therapeutic PNAs may be used for treating disease conditions such as  
 cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human  
 immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency  
 syndrome) and associated pathologies, fungal infections, and other  
 diseases characterized by abnormal telomere metabolism or telomerase  
 activity, in combination with antineoplastic and other cytotoxic or  
 cytostatic agents, antifungal agents, and other nucleotides. PNAs may be  
 used for molecular diagnostics, labelled PNAs are used as hybridization  
 probes to detect or quantitate polynucleotides having a human telomerase  
 RNA (hTR) sequence. PNA probes are also used for forensic identification  
 of individuals, e.g. paternity testing, based on hTR gene restriction  
 fragment length polymorphism (RFLP) pattern. PNAs are also useful as  
 probes to detect the RNA component of a mammalian telomerase and as  
 inhibitors of telomerase activity. The method of the present invention  
 allows cancerous conditions to be detected with increased confidence and  
 possibly at an earlier stage, before cells are detected as cancerous  
 based on pathological characteristics. The diagnostic and prognostic  
 methods of the present invention can be used to detect an immortal or  
 neoplastic cell or tumour tissue or cancer of any origin, provided the  
 cell expresses telomerase activity and its RNA component.

Sequence 8 BP; 1 A; 0 C; 4 G; 3 T; 0 other;

Query Match 100.0%; Score 6; DB 21; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+08;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTAGGG 6  
 |||||  
 2 TTAGGG 7

RESULT 11  
 AAS15436/c  
 AAS15436 standard; DNA; 8 BP.

AAS15436;

15-AUG-2000 (first entry)

PNA sequence #30 used to inhibit telomerase activity.

Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;  
 inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;  
 AIDS; HIV; fungal infection; forensic identification; detect; tumour;  
 paternity testing; ss.

Synthetic.

Key Location/Qualifiers  
 misc\_feature 1..8

/tag= a  
 /note= "Peptide nucleic acid molecule, where  
 N-(2-aminoethyl)glycine units are linked to  
 nucleotide bases via glycine amino N through a  
 methylenecarbonyl linker"

US6046307-A.

XX 04-APR-2000.  
 XX 09-APR-1997; 97US-0838545.  
 XX 09-APR-1996; 96US-0630019.  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 XX Wright WE, Piatyszek MA, Shay JW, Norton JC, Corey DR;  
 XX WPI; 2000-292432/25.  
 XX New peptide nucleic acid (PNA) compounds that inhibit telomerase  
 XX activity in mammalian cells is useful as probes to detect the RNA  
 XX component of a mammalian telomerase  
 XX Example 2; Column 33; 45pp; English.  
 XX The present sequence represents a peptide nucleic acid molecule which  
 XX hybridises to the mRNA component of mammalian telomerase, and inhibits  
 XX telomerase activity. Telomerase is a ribonucleoprotein enzyme that  
 XX synthesizes one strand of the telomeric DNA, using as a template an 11  
 XX nucleotide sequence contained within the RNA component of the enzyme. The  
 XX invention relates to PNA molecules having a sequence of no more than 25  
 XX bases, which include the sequence GTTAGG. The uncharged nature of the PNA  
 XX backbone increases the melting temperature of associating strands,  
 XX increases the rate of association with targeted nucleic acids, and  
 XX affords greater resistance of degradation by proteases or nucleases. The  
 XX therapeutic PNAs may be used for treating disease conditions such as  
 XX cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human  
 XX immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency  
 XX syndrome) and associated pathologies, fungal infections, and other  
 XX diseases characterized by abnormal telomere metabolism or telomerase  
 XX activity, in combination with antineoplastic and other cytotoxic or  
 XX cytostatic agents, antifungal agents, and other nucleotides. PNAs may be  
 XX used for molecular diagnostics, labelled PNAs are used as hybridization  
 XX probes to detect or quantitate polynucleotides having a human telomerase  
 XX RNA (hTR) sequence. PNA probes are also used for forensic identification  
 XX of individuals, e.g. paternity testing, based on hTR gene restriction  
 XX fragment length polymorphism (RFLP) pattern. PNAs are also useful as  
 XX probes to detect the RNA component of a mammalian telomerase and as  
 XX inhibitors of telomerase activity. The method of the present invention  
 XX allows cancerous conditions to be detected with increased confidence and  
 XX possibly at an earlier stage, before cells are detected as cancerous  
 XX based on pathological characteristics. The diagnostic and prognostic  
 XX methods of the present invention can be used to detect an immortal or  
 XX neoplastic cell or tumour tissue or cancer of any origin, provided the  
 XX cell expresses telomerase activity and its RNA component.

Sequence 8 BP; 3 A; 4 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 6; DB 21; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+08;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTAGGG 6  
 |||||  
 7 TTAGGG 2

RESULT 12  
 AAS15436  
 AAS15436 standard; DNA; 8 BP.

AAS15436;

14-FEB-2002 (first entry)

PNA 28 inhibiting human and mammalian telomerase activity.

Mammalian; peptide nucleic acid; probe; forensic; paternity testing;  
 human telomerase RNA component; hTR gene RFLP pattern; cancer;

XX (ISIS-) ISIS PHARM INC.  
 PA Ecker DJ;  
 PI WPI; 1995-082179/11.  
 DR  
 XX Oligomer hybridisable to HIV sequence and contg. peptide nucleic  
 PT acid subunit - binds in complementary manner to DNA and RNA, and  
 PT useful for modulating HIV viral activity, e.g. in treating AIDS  
 XX  
 PS Claim 2; Page 176; 186pp; English.  
 XX  
 CC New peptide nucleic acid (PNA) oligomers are provided which (a) consist  
 CC of naturally occurring nucleobases covalently bound to a polyamide  
 CC backbone and (b) hybridise to the translation initiation AUG region,  
 CC 5' untranslated region (5' UTR), 3' untranslated region (3' UTR),  
 CC splice junctions or coding sequence of a human immunodeficiency virus  
 CC gene chosen from env, gag, pol, rev and tat.  
 CC The PNAs can be used to target RNA and single stranded DNA (ssDNA) to  
 CC produce antisense-type gene regulation moieties. They have utility  
 CC as gene-targeted drugs for modulating HIV processes. Hence they  
 CC can be used to treat AIDS and other viral infections. They are also  
 CC useful in diagnostic applications and as research tools.  
 CC PNA oligomers have high affinity for complementary single stranded DNA.  
 CC They are also able to form triple helices in which a first PNA strand  
 CC binds with RNA or ssDNA and a second PNA strand binds with the resulting  
 CC double helix or with the first PNA strand. The PNAs possess no  
 CC significant charge and are water soluble, which facilitates cellular  
 CC uptake. Further, since they contain amides of non-biological amino acids,  
 CC they are biostable and resistant to enzymatic degradation by proteases.  
 CC The present sequence is a specifically claimed PNA sequence  
 CC (represented by the sequence of nucleobases) targetting HIV genes.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX Sequence 8 BP; 1 A; 0 C; 3 G; 4 T; 0 other;  
 XX  
 Query Match 100.0%; Score 6; DB 16; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+08;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1 TTAGGG 6  
 DB |||||  
 2 TTAGGG 7  
 XX  
 RESULT 9  
 AAT89239  
 ID AAT89239 standard; DNA; 8 BP.  
 AC AAT89239;  
 XX  
 DT 12-MAY-1998 (first entry)  
 XX  
 DE Peptide nucleic acid 14, targeted to mammalian telomerase.  
 XX  
 KW Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;  
 KW inhibitor; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 1..8  
 FT /\*tag= a  
 FT /note= "Sugar-phosphate backbone has been replaced by  
 FT a peptide backbone"  
 XX  
 PN WO9738013-A1.  
 XX  
 PD 16-OCT-1997.  
 XX  
 PF 09-APR-1997; 97WO-US05931.  
 XX

PR 09-APR-1996; 96US-0630019.  
 XX (GERO-) GERON CORP.  
 PA  
 XX Corey D, Norton JC, Piatyszek MA, Shay JW, Wright WE;  
 PI WPI; 1997-512647/47.  
 DR  
 XX New peptide nucleic acids hybridising to mammalian telomerase RNA -  
 PT used to inhibit telomerase, for treating tumours and other  
 PT proliferative diseases, also for diagnosis  
 XX  
 PS Claim 9; Page 59; 76pp; English.  
 XX  
 CC This sequence is a novel peptide nucleic acid (PNA), which acts as  
 CC an inhibitor of mammalian, preferably human, telomerase. The PNAs  
 CC hybridise specifically to an RNA component of mammalian telomerase,  
 CC and include the sequence GGG for specific hybridisation to the template  
 CC region of this component. PNAs can be used as probes to detect the  
 CC RNA component of mammalian telomerase and as inhibitors of telomerase  
 CC activity, especially in the treatment of cancer.  
 XX  
 SQ Sequence 8 BP; 1 A; 0 C; 4 G; 3 T; 0 other;  
 XX  
 Query Match 100.0%; Score 6; DB 18; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+08;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1 TTAGGG 6  
 DB |||||  
 2 TTAGGG 7  
 XX  
 RESULT 10  
 AAA37558  
 ID AAA37558 standard; DNA; 8 BP.  
 AC AAA37558;  
 XX  
 DT 15-AUG-2000 (first entry)  
 XX  
 DE PNA sequence #15 used to inhibit telomerase activity.  
 XX  
 KW Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;  
 KW inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;  
 KW AIDS; HIV; fungal infection; forensic identification; detect; tumour;  
 KW paternity testing; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 1..8  
 FT /\*tag= a  
 FT /note= "Peptide nucleic acid molecule, where  
 FT N-(2-aminoethyl)glycine units are linked to  
 FT nucleotide bases via glycine amino N through a  
 FT methylenecarbonyl linker"  
 XX  
 PN US6046307-A.  
 XX  
 PD 04-APR-2000.  
 XX  
 PF 09-APR-1997; 97US-0838545.  
 XX  
 PR 09-APR-1996; 96US-0630019.  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX Wright WE, Piatyszek MA, Shay JW, Norton JC, Corey DR;  
 XX WPI; 2000-292432/25.  
 DR  
 XX New peptide nucleic acid (PNA) compounds that inhibit telomerase  
 PT



Db 1 TTAGGG 6

RESULT 6  
AA091439/c  
ID AA091439 standard; DNA; 7 BP.

XX AC AA091439;  
XX DT 25-MAR-2003 (updated)  
XX DT 22-FEB-1990 (first entry)

XX Telomere of Arabidopsis thaliana.

XX Telomere; Arabidopsis thaliana; vector; artificial chromosomes;  
XX tandem repeat.

XX Arabidopsis thaliana.

XX WO8909219-A.

XX 05-OCT-1989.

XX 27-FEB-1989; 89WO-US00795.

XX 24-MAR-1988; 88US-0172467.

XX (GEO) GEN HOSPITAL CORP.

XX Richards E, Ausubel FM;

XX WPI; 1989-309497/42.

XX New recombinant DNA contg. eukaryotic telomere esp. from higher plant  
XX - useful as vector for specific genes and maintained in nucleus as  
XX independent replicating molecule.

XX Claim 28; page 50; 65pp; English.

XX Tandem repeats (1-1000) of the telomere are used in a vector for  
XX expressing specific genes in plants. They provide 'artificial  
XX chromosomes' which are maintained in the nucleus, so are not subjected to  
XX variable expression due to integration-position effects. They allow the  
XX integration of very foreign DNA without host range limitations.  
XX The telomere opt. contains variant repeats of CTCCTAAA. The telomere is  
XX pref. the pAT4 plasmid (ATCC 67577).  
XX (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 7 BP; 3 A; 3 C; 0 G; 1 T; 0 other;

XX Query Match 100.0%; Score 6; DB 10; Length 7;  
XX Best Local Similarity 100.0%; Pred. No. 3.7e+08;  
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6  
Db 6 TTAGGG 1

RESULT 7  
AA091442/c  
ID AA091442 standard; DNA; 7 BP.

XX AC AA091442;

XX 25-MAR-2003 (updated)

XX 22-FEB-1990 (first entry)

XX Variant of Arabidopsis thaliana telomere.

XX Variant telomere; Arabidopsis thaliana; vector; artificial chromosomes;  
XX tandem repeat.

XX Arabidopsis thaliana.

XX WO8909219-A.

XX 05-OCT-1989.

XX 27-FEB-1989; 89WO-US00795.

XX 24-MAR-1988; 88US-0172467.

XX (GEO) GEN HOSPITAL CORP.

XX Richards E, Ausubel FM;

XX WPI; 1989-309497/42.

XX New recombinant DNA contg. eukaryotic telomere esp. from higher plant  
XX - useful as vector for specific genes and maintained in nucleus as  
XX independent replicating molecule.

XX Claim 35; page 50; 65pp; English.

XX The DNA is a variant of the telomere of the pAT4 plasmid (ATCC 67577).  
XX (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 7 BP; 3 A; 3 C; 0 G; 1 T; 0 other;

XX Query Match 100.0%; Score 6; DB 10; Length 7;  
XX Best Local Similarity 100.0%; Pred. No. 3.7e+08;  
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6  
Db 6 TTAGGG 1

RESULT 8

AA097993

ID AA097993 standard; DNA; 8 BP.

XX AC AA097993;

XX 25-MAR-2003 (updated)

XX 19-OCT-1995 (first entry)

XX Peptide nucleic acid oligomer targeting HIV gene.

XX Peptide nucleic acid; PNA; HIV; human immunodeficiency virus;

XX AIDS; antiviral; antisense; triple helix; ss.

XX Synthetic.

XX Key misc\_feature Location/Qualifiers  
XX 1..8  
XX /\*tag= a  
XX /note= "at least one (and preferably all) of

XX the backbone subunits are composed of N-acetyl  
XX N-(2-aminoethyl)glycine peptide residues, the  
XX nucleobase being attached covalently to the  
XX acetyl group and the peptide linkage being  
XX formed by condensation of the glycine  
XX carboxy group of one residue with the amino  
XX group of the 2-aminoethyl moiety in the next  
XX residue"

XX WO9504068-A1.

XX 09-FEB-1995.

XX 28-JUL-1994; 94WO-US08517.

XX 29-JUL-1993; 93US-0099718.

CC epithelial cell proliferation, described in the method of the invention.

XX Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 other;

SQ Query Match 100.0%; Score 6; DB 23; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.3e+08;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6  
Db 1 TTAGGG 6

RESULT 4  
AAS14916/c  
ID AAS14916 standard; DNA; 6 BP.

XX AAS14916;  
XX 14-FEB-2002 (first entry)  
XX Melanogenesis associated oligonucleotide #12.

XX Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;  
XX anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;  
XX immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;  
XX tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;  
XX carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;  
XX conjunctivitis; allergic rhinitis; vitiligo; ss.

XX Synthetic.  
XX WO200174342-A2.  
XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10162.  
XX 31-MAR-2000; 2000US-0540843.  
XX (UYBO-) UNIV BOSTON.

XX Gilchrist BA, Yaar M, Eller M;  
XX WPI; 2001-626338/72.

XX Inhibiting proliferation of epithelial cells, useful e.g. for treating  
XX carcinoma, using specific oligonucleotides that mimic the effects of  
XX ultra-violet light -

XX Claim 1; Page 37; 74pp; English.

XX The invention describes inhibition of mammalian epithelial cell  
XX proliferation by treating cells with at least one oligonucleotide, or  
XX its fragment. The compounds, which have cytostatic, anti-allergic,  
XX anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and  
XX immunosuppressive activities, function as 'ultra-violet mimics' to induce  
XX DNA repair processes (or a protective response to later exposure to  
XX radiation or chemicals), as a proliferation inhibitor, apoptosis inducer  
XX or a tumour necrosis factor inhibitor. Probably they mimic products of  
XX DNA damage, or processed DNA-damage intermediates, by inducing the p53  
XX pathway, resulting in transient arrest of cell growth, allowing more time  
XX for DNA repair to occur before cell division takes place. The method is  
XX especially used to treat carcinoma but may also be used to: treat other  
XX hyperproliferative states (e.g. psoriasis or precancerous conditions);  
XX reduce photoaging, oxidative stress or damage; prevent skin cancer; treat  
XX allergically mediated inflammation (atopic or contact dermatitis;  
XX allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in  
XX cells caused by radiation or chemicals; increase melanin production  
XX (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to  
XX promote apoptosis in epithelial cells that contain damaged DNA. Also  
XX oligonucleotides that contain non-hydrolyzable backbones are used to  
XX inhibit apoptosis, in response to DNA damage, in epithelial cell. This

CC sequence is melanogenesis associated oligonucleotide #12, the reverse  
CC complementary sequence of AAS149015, a truncated version of the sequence  
CC representing the telomere over-hang sequence (AAS14909), described in the  
CC method of the invention.

XX Sequence 6 BP; 2 A; 3 C; 0 G; 1 T; 0 other;

SQ Query Match 100.0%; Score 6; DB 23; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.3e+08;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6  
Db 6 TTAGGG 1

RESULT 5  
ABN73654  
ID ABN73654 standard; cDNA; 6 BP.

XX ABN73654;  
XX ABN73654;  
XX 03-JUL-2002 (first entry)

XX Bovine embryonic germ (EG) cell cDNA EST 990913a CONTIG 1.  
XX Bovine; Bos taurus; EST; expressed sequence tag; totipotency;  
XX development; gene; ss.  
XX Bos taurus.  
XX WO200194550-A2.  
XX 13-DEC-2001.

XX 07-JUN-2001; 2001WO-US18576.  
XX 06-JUN-2000; 2000US-209874P.  
XX 06-JUN-2001; 2001US-0876143.  
XX (INFI-) INFIGEN INC.  
XX Eilertsen KJ, Pfister-Genskow M, Childs L;  
XX WPI; 2002-351289/38.

XX An expressed sequence tag (EST), the expression of which, or its  
XX complementary sequence, in a cell identifies the cell as a  
XX developmentally competent or incompetent cell -

XX Example 16; Page 210; 584pp; English.

XX The present invention describes an expressed sequence tag (EST), where  
XX the EST is an isolated, enriched, or purified nucleic acid sequence  
XX representing all or part of a gene, the expression of which, or its  
XX complementary sequence, in a cell identifies the cell as a  
XX developmentally competent or incompetent cell. Molecules which induce  
XX developmental competence in a cell line are useful for inducing  
XX totipotency in one or more cells. Molecules which induce developmental  
XX incompetence in a cell line are useful for preventing a full term  
XX pregnancy in an animal and inhibiting totipotency. The molecules are  
XX also useful for treating a disease in an animal by inducing development  
XX of one or more cells of the animal into a specific cell type. The  
XX present sequence represents a bovine EST which is given in the  
XX exemplification of the present invention.

XX Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 other;

SQ Query Match 100.0%; Score 6; DB 24; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.3e+08;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6

PT Increasing telomere length in cells - to increase proliferative  
PT capacity and therefore delay cellular senescence, useful in cell  
PT therapy and transplantation

PS Claim 12; Page 29; 38pp; English.

XX Oligonucleotides AAT05734-7 are examples of telomerase substrates used  
CC to increase the proliferative capacity of normal cells that express  
CC telomerase activity. The oligonucleotides allow an increase in  
CC length of telomeres in normal cells and in hybrids of normal and  
CC immortalised cells. The increase in telomere length extends the  
CC capacity of cells to replicate, esp. those treated ex vivo and used  
CC for transplantation techniques e.g. cell therapy, for the treatment  
CC of AIDS, anaemia, leukaemia or lymphoma.

XX Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 other;

Query Match 100.0%; Score 6; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.3e+08;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTAGGG 6  
|||||  
1 TTAGGG 6

# RESULT 2

AAX80998  
AAX80998 standard; DNA; 6 BP.

AAX80998;

13-SEP-1999 (first entry)

Telomeric repeat sequence.

Telomerase reverse transcriptase; TERT; mouse; telomere length assay;  
immunogen; enzyme; telomerase-mediated DNA replication; human; ss.

Homo sapiens.

WO927113-A1.

03-JUN-1999.

25-NOV-1998; 98WO-US25211.

16-MAR-1998; 98US-0042460.

26-NOV-1997; 97US-0979742.

(GERO-) GERON CORP.

(YESH ) UNIV YESHIVA EINSTEIN COLLEGE.

Allsopp R, Depinho R, Greenberg R, Morin GB;

WPI; 1999-347722/29.

Mouse telomerase reverse transcriptase (mTERT) enzyme proteins and  
nucleic acids

Disclosure; Page 62; 135pp; English.

CC The invention relates to a mouse telomerase reverse transcriptase (mTERT)  
CC enzyme. Compositions containing mTERT can be used in telomere length  
CC assays. Isolated mTERT is useful as an immunogen for the production of  
CC monoclonal or polyclonal antibodies. The method is useful for assessing  
CC the degree of purification and identification of new mTERT species, such  
CC as an mTERT allele, homolog or isoform, or to screen for modulators  
CC (antagonists and agonists) of telomerase-mediated DNA replication.  
CC Other telomerase and agonists of mTERT can be used to modify the activity of  
CC other telomerase enzymes such as human TERT (hTERT).

XX Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 other;

Query Match 100.0%; Score 6; DB 20; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.3e+08;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6  
|||||  
Db 1 TTAGGG 6

# RESULT 3

AAS14915  
ID AAS14915 standard; DNA; 6 BP.

XX AAS14915;

XX 14-FEB-2002 (first entry)

Melanogenesis associated oligonucleotide #11.

KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;  
KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;  
KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;  
KW tumour necrosis factor inhibitor; photodag; hyperproliferative disease;  
KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;  
KW conjunctivitis; allergic rhinitis; vitiligo; ss.

OS Synthetic.

XX WO200174342-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10162.

XX 31-MAR-2000; 2000US-0540843.

XX (UYBO-) UNIV BOSTON.

XX Gilchrest BA, Yaar M, Eller M;

XX WPI; 2001-626338/72.

Inhibiting proliferation of epithelial cells, useful e.g. for treating  
carcinoma, using specific oligonucleotides that mimic the effects of  
ultra-violet light

Claim 1; Page 37; 74pp; English.

CC The invention describes inhibition of mammalian epithelial cell  
CC proliferation by treating cells with at least one oligonucleotide, or  
CC its fragment. The compounds, which have cytostatic, anti-allergic,  
CC anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and  
CC immunosuppressive activities, function as 'ultra-violet mimics' to induce  
CC DNA repair processes (or a protective response to later exposure to  
CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer  
CC or a tumour necrosis factor inhibitor. Probably they mimic products of  
CC DNA damage, or processed DNA-damage intermediates, by inducing the p53  
CC pathway, resulting in transient arrest of cell growth, allowing more time  
CC for DNA repair to occur before cell division takes place. The method is  
CC especially used to treat carcinoma but may also be used to: treat other  
CC hyperproliferative states (e.g. psoriasis or precancerous conditions);  
CC reduce photodag, oxidative stress or damage; prevent skin cancer; treat  
CC allergically mediated inflammation (atopic or contact dermatitis,  
CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in  
CC cells caused by radiation or chemicals; increase melanin production  
CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to  
CC promote apoptosis in epithelial cells that contain damaged DNA. Also  
CC oligonucleotides that contain non-hydrolyzable backbones are used to  
CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This  
CC version of the sequence representing the telomere over-hang sequence  
CC (AAS14909) and one of the oligonucleotides used to inhibit mammalian

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 11:36:21 ; Search time 173.392 Seconds  
(without alignments)  
93.410 Million cell updates/sec

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 2101872

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	100.0	6	16 AAT05734	Telomerase oligonu
2	6	100.0	6	20 AAX80998	Telomeric repeat s
3	6	100.0	6	23 AAS14915	Melanogenesis asso
4	6	100.0	6	23 AAS14916	Melanogenesis asso
5	6	100.0	6	24 AEN73654	Bovine embryonic g
6	6	100.0	7	10 AAN91439	Telomere of Arabid
7	6	100.0	7	10 AAN91442	Variant of Arabido
8	6	100.0	8	16 AAQ97993	Peptide nucleic ac

9	6	100.0	8	18 AAT89239	Peptide nucleic ac
10	6	100.0	8	21 AAA37558	PNA sequence #15 u
11	6	100.0	8	21 AAA37572	PNA sequence #30 u
12	6	100.0	8	23 AAS15436	PNA 28 inhibiting
13	6	100.0	8	23 AAS15474	PNA 34 inhibiting
14	6	100.0	9	16 AAT05735	Telomerase oligonu
15	6	100.0	9	18 AAT89240	Peptide nucleic ac
16	6	100.0	9	18 AAT93240	Telomerase substra
17	6	100.0	9	20 AAT21987	Telomere motif mim
18	6	100.0	9	21 AAA37559	Telomere motif #16 u
19	6	100.0	9	21 AAZ56813	Primer for human t
20	6	100.0	9	22 AAL20082	Human breast cance
21	6	100.0	9	23 AAS15437	PNA 29 inhibiting
22	6	100.0	9	24 ABK87319	Drosophila Bicoid
23	6	100.0	10	18 AAV07770	N3 to P5 oligonucl
24	6	100.0	10	18 AAV07771	N3 to P5 oligonucl
25	6	100.0	10	18 AAT89241	Peptide nucleic ac
26	6	100.0	10	18 AAT89249	DNA oligonucleotid
27	6	100.0	10	18 AAT89231	Peptide nucleic ac
28	6	100.0	10	19 AAV41382	Antisense oligonuc
29	6	100.0	10	20 AAZ28358	Lung cancer indica
30	6	100.0	10	20 AAX22183	Random amplified p
31	6	100.0	10	20 AAX21986	Telomere motif mim
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33	6	100.0	10	21 AAA56520	Human macrophage g
34	6	100.0	10	21 AAA37550	PNA sequence #7 us
35	6	100.0	10	21 AAA37554	Template region of
36	6	100.0	10	21 AAA37560	PNA sequence #17 u
37	6	100.0	10	21 AAA37563	PNA sequence #21 u
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42	6	100.0	10	21 AAZ79266	Human dendritic ce
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ALIGNMENTS

RESULT 1	
AAT05734	
ID AAT05734 standard; DNA; 6 BP.	
AC AAT05734;	
XX	
XX	
DT 01-FEB-1996 (first entry)	
XX	
DE Telomerase oligonucleotide substrate #1.	
XX	
KW Telomerase; proliferation; telomere; hybrid; immortalised cell; anaemia;	
KW transplantation; cell therapy; treatment; AIDS; leukaemia; lymphoma; ss.	
XX	
OS Synthetic.	
XX	
PN WO9513383-A1.	
XX	
PD 18-MAY-1995.	
XX	
PF 10-NOV-1994; 94WO-US13130.	
XX	
PR 12-NOV-1993; 93US-0153051.	
PR 12-NOV-1993; 93US-0151477.	
XX	
PA (GERO-) GERON CORP.	
PA (TEXA ) UNIV TEXAS SYSTEM.	
XX	
PI Shay J, West MD, Wright WB;	
XX WPI; 1995-224051/29.	
DR	
XX	



```

REFERENCE
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE        Velulescu,V.E., Vogelstein,B. and Kinzler,K.W.
JOURNAL      Human transcriptomes
              Patent: WO 0138577-A 92 31-MAY-2001;
              The Johns Hopkins University (US)
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QY          1 TTAGGG 6
DB          8 TTAGGG 3

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LOCUS       AX153383
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ACCESSION  AX153383
VERSION     AX153383.1 GI:14535032
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Velulescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE       Human transcriptomes
JOURNAL     Patent: WO 0138577-A 1296 31-MAY-2001;
              The Johns Hopkins University (US)
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              8 TTAGGG 3

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Best Local Similarity 100.0%; Pred. No. 5.3e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 TTAGGG 6
DB          8 TTAGGG 3

RESULT 14
AX153382/c
LOCUS       AX153382
DEFINITION Sequence 1297 from Patent WO0138577.
ACCESSION  AX153382
VERSION     AX153382.1 GI:14535033
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Velulescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE       Human transcriptomes
JOURNAL     Patent: WO 0138577-A 1297 31-MAY-2001;
              The Johns Hopkins University (US)
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Query Match 100.0%; Score 6; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 TTAGGG 6
DB          8 TTAGGG 3

Search completed: December 31, 2003, 17:09:51
Job time : 553.38 secs

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CC from U, T, A,
CC G, i or C' Location/Qualifiers
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FT modified base 8.
FT Location/Qualifiers
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    /mol_type="genomic DNA"
    /db_xref="taxon:32644"
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Best Local Similarity 100.0%; Pred. No. 5.1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTAGGG 6
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RESULT 9
LOCUS BD071050 9 bp DNA linear PAT 27-AUG-2002
DEFINITION Modulation of mammalian telomerase by peptide nucleic acids.
ACCESSION BD071050.1 GI:22616653
VERSION JP 2001517929-A/16.
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 9)
AUTHORS Shay, J.W., Wright, W.E., Piatyszek, M.A., Corey, D. and Norton, J.C.
TITLE Modulation of mammalian telomerase by peptide nucleic acids
JOURNAL Patent: JP 2001517929-A 16 09-OCT-2001;
Geron Corp
COMMENT
OS Unidentified
PN JP 2001517929-A/16
PD 09-OCT-2001
PF 09-APR-1997 JP 1997536487
PR 09-APR-1996 US 08/630019
PI JERRY W SHAY, WOODRING E WRIGHT, MIECZYSLAW A PIATYSZEK, DAVID
PI COREY,
PI JAMES C NORTON
PC C07K14/00, A61K38/16, C12Q1/68
CC Strandedness: Single;
CC Topology: Linear;
CC /desc = 'peptide nucleic acid (PNA), where (deoxy(ribose- CC
phosphate
CC linkages are replaced by N-(2-aminoethyl)glycine units linked
CC to
CC nucleotide bases via glycine amino N through a CC
methylenecarbonyl linker'
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FT source 1..9
FT Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 4.5e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTAGGG 6
3 TTAGGG 8

CC /note= 'N = 1-50 peptide nucleic acid nucleobases, selected
CC from U, T, A,
CC G, i or C' Location/Qualifiers
FH Key modified base 1
FT modified base 8.
FT Location/Qualifiers
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BASE COUNT 1 a 0 c 3 g 2 t 2 others
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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTAGGG 6
2 TTAGGG 7

RESULT 10
LOCUS AR026485 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 10 from patent US 5856096.
ACCESSION AR026485
VERSION AR026485.1 GI:5937325
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Windle, B.E., Qiu, M., Chen, S.-F., Fletcher, T.M. and Maine, I.
TITLE Rapid and sensitive assays for detecting and distinguishing between
processive and non-processive telomerase activities
JOURNAL Patent: US 5856096-A 10 05-JAN-1999;
FEATURES
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Best Local Similarity 100.0%; Pred. No. 5.3e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTAGGG 6
1 TTAGGG 6

RESULT 11
LOCUS AR243501 10 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 294 from patent US 6475789.
ACCESSION AR243501
VERSION AR243501.1 GI:27290712
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Cech, T.R., Lingner, J., Nakamura, T., Chapman, K.B., Morin, G.B.,
Harley, C.B. and Andrews, W.H.
TITLE Human telomerase catalytic subunit: diagnostic and therapeutic
methods
JOURNAL Patent: US 6475789-A 294 05-NOV-2002;
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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTAGGG 6
1 TTAGGG 6

RESULT 12
LOCUS AX152177 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 92 from Patent WO0138577.
ACCESSION AX152177
VERSION AX152177.1 GI:14533828
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Db 6 TTAGGG 1

RESULT 6
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LOCUS BD071049 8 bp DNA linear PAT 27-AUG-2002
DEFINITION Modulation of mammalian telomerase by peptide nucleic acids.
ACCESSION BD071049
VERSION BD071049.1 GI:22616652
KEYWORDS JP 2001517929-A/15.
SOURCE unidentified
ORGANISM unidentified

REFERENCE
1 (bases 1 to 8)
AUTHORS Shay,J.W., Wright,W.E., Piatyszek,M.A., Corey,D. and Norton,J.C.
TITLE Modulation of mammalian telomerase by peptide nucleic acids
JOURNAL Patent: JP 2001517929-A 15 09-OCT-2001;
COMMENT Geron Corp
OS Unidentified
PN JP 2001517929-A/15
PD 09-OCT-2001
PF 09-APR-1997 JP 1997536487
PR 09-APR-1996 US 08/630019
PI JERRY W SHAY,WOODRING E WRIGHT,MIECZYSLAW A PIATYSZEK,DAVID
PI COREY,
PI JAMES C NORTON
PC C07K14/00,A61K38/16,C12Q1/68
CC Strandedness: Single;
CC Topology: Linear;
CC /desc = 'peptide nucleic acid (PNA), where (deoxy(ribose- CC
phosphate
linkages are replaced by N-(2-aminoethyl)glycine units linked
to
nucleotide bases via glycine amino N through a CC
methylene-carbonyl linker'
FH Key Location/Qualifiers
FT source 1..8
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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
Db 7 TTAGGG 2

RESULT 8
BD071067
LOCUS BD071067 8 bp DNA linear PAT 27-AUG-2002
DEFINITION Modulation of mammalian telomerase by peptide nucleic acids.
ACCESSION BD071067
VERSION BD071067.1 GI:22616670
KEYWORDS JP 2001517929-A/33.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 8)
AUTHORS Shay,J.W., Wright,W.E., Piatyszek,M.A., Corey,D. and Norton,J.C.
TITLE Modulation of mammalian telomerase by peptide nucleic acids
JOURNAL Patent: JP 2001517929-A 33 09-OCT-2001;
COMMENT Geron Corp
OS Unidentified
PN JP 2001517929-A/33
PD 09-OCT-2001
PF 09-APR-1997 JP 1997536487
PR 09-APR-1996 US 08/630019
PI JERRY W SHAY,WOODRING E WRIGHT,MIECZYSLAW A PIATYSZEK,DAVID
PI COREY,
PI JAMES C NORTON
PC C07K14/00,A61K38/16,C12Q1/68
CC Strandedness: Single;
CC Topology: Linear;
CC /desc = 'peptide nucleic acid (PNA), where (deoxy(ribose- CC
phosphate
linkages are replaced by N-(2-aminoethyl)glycine units linked
to
nucleotide bases via glycine amino N through a CC
methylene-carbonyl linker'
FH Key Location/Qualifiers
FT source 1..8
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Location/Qualifiers
source 1..8
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/mol_type='genomic DNA'
/db_xref='taxon:32644'
BASE COUNT 1 a 0 c 4 g 3 t
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Query Match 100.0%; Score 6; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+09;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGGG 6
Db 2 TTAGGG 7

RESULT 7
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LOCUS BD071063 8 bp DNA linear PAT 27-AUG-2002
DEFINITION Modulation of mammalian telomerase by peptide nucleic acids.
ACCESSION BD071063
VERSION BD071063.1 GI:22616666
KEYWORDS JP 2001517929-A/29.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 8)
AUTHORS Shay,J.W., Wright,W.E., Piatyszek,M.A., Corey,D. and Norton,J.C.
TITLE Modulation of mammalian telomerase by peptide nucleic acids
JOURNAL Patent: JP 2001517929-A 29 09-OCT-2001;
COMMENT Geron Corp
OS Unidentified

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BASE COUNT	1 a	0 c	3 g	2 t
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Best Local Similarity		100.0%;	Pred. No. 6.8e+09;	
Matches	6;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
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Db	1 TTAGGG 6			
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LOCUS	AX268763		6 bp	DNA
DEFINITION	Sequence 11 from Patent WO0174342.			linear
ACCESSION	AX268763			
VERSION	AX268763.1		GI:16541835	
KEYWORDS				
SOURCE	synthetic construct			
ORGANISM	synthetic construct			
REFERENCE	1			
AUTHORS	Gilchrest,B.A., Yaar,M. and Eller,M.			
TITLE	Use of locally applied dna fragments			
JOURNAL	Patent: WO 0174342-A 11 11-OCT-2001;			
FEATURES	TRUSTEES OF BOSTON UNIVERSITY (US)			
source	Location/Qualifiers			
BASE COUNT	1 a	0 c	3 g	2 t
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Best Local Similarity		100.0%;	Pred. No. 6.8e+09;	
Matches	6;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1 TTAGGG 6			
Db	1 TTAGGG 6			
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LOCUS	AX268764		6 bp	DNA
DEFINITION	Sequence 12 from Patent WO0174342.			linear
ACCESSION	AX268764			
VERSION	AX268764.1		GI:16541836	
KEYWORDS				
SOURCE	synthetic construct			
ORGANISM	synthetic construct			
REFERENCE	1			
AUTHORS	Gilchrest,B.A., Yaar,M. and Eller,M.			
TITLE	Use of locally applied dna fragments			
JOURNAL	Patent: WO 0174342-A 12 11-OCT-2001;			
FEATURES	TRUSTEES OF BOSTON UNIVERSITY (US)			
source	Location/Qualifiers			
BASE COUNT	2 a	3 c	0 g	1 t
ORIGIN				
Query Match		100.0%;	Score 6;	DB 6; Length 6;
Best Local Similarity		100.0%;	Pred. No. 6.8e+09;	
Matches	6;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 11:36:21 ; Search time 552.38 Seconds  
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444.364 Million cell updates/sec

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Perfect score: 6  
Sequence: 1 ttaggg 6

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues  
Total number of hits satisfying chosen parameters: 1010434

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Minimum DB seq length: 0
Maximum DB seq length: 30
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Post-processing:	Minimum Match	0%
	Maximum Match	100%
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12: gb\_sy:\*  
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41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query			ID	Description
		Match	Length	DB		
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	2	6	100.0	6	6	AX058275 Sequence
	3	6	100.0	6	6	AX175285 Sequence
C	4	6	100.0	6	6	AX268763 Sequence
	5	6	100.0	6	6	AX268764 Sequence
	6	6	100.0	8	6	BD071049 Sequence
C	7	6	100.0	8	6	BD071063 Sequence
	8	6	100.0	8	6	BD071067 Sequence
	9	6	100.0	9	6	BD071050 Sequence
C	10	6	100.0	10	6	AR026485 Sequence
	11	6	100.0	10	6	AR243501 Sequence
	12	6	100.0	10	6	AX152177 Sequence
C	13	6	100.0	10	6	AX153381 Sequence
	14	6	100.0	10	6	AX153382 Sequence
	15	6	100.0	10	6	AX153383 Sequence
C	16	6	100.0	10	6	AX153524 Sequence
	17	6	100.0	10	6	BD011231 Sequence
	18	6	100.0	10	6	BD023724 Method fo
C	19	6	100.0	10	6	BD071041 Modulation
	20	6	100.0	10	6	BD071045 Modulation
	21	6	100.0	10	6	BD071051 Modulation
C	22	6	100.0	10	6	BD071054 Modulation
	23	6	100.0	10	6	BD071062 Modulation
	24	6	100.0	10	6	BD167218 Human liv
C	25	6	100.0	10	6	E36980 Human telom
	26	6	100.0	11	6	AR016034 Sequence
	27	6	100.0	11	6	AR026486 Sequence
C	28	6	100.0	11	6	AR026487 Sequence
	29	6	100.0	11	6	AR059195 Sequence
	30	6	100.0	11	6	AR075506 Sequence
C	31	6	100.0	11	6	AR161904 Sequence
	32	6	100.0	11	6	AR214804 Sequence
	33	6	100.0	11	6	AR301476 Sequence
C	34	6	100.0	11	6	AR301690 Sequence
	35	6	100.0	11	6	AR306454 Sequence
	36	6	100.0	11	6	AX033373 Sequence
C	37	6	100.0	11	6	AX268757 Sequence
	38	6	100.0	11	6	AX268761 Sequence
	39	6	100.0	11	6	AX283296 Sequence
C	40	6	100.0	11	6	AX394462 Sequence
	41	6	100.0	11	6	AX394499 Sequence
	42	6	100.0	11	6	AX471710 Sequence
C	43	6	100.0	11	6	AX623440 Sequence
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## ALIGNMENTS

RESULT 1	AX055801	6 bp	DNA	linear	PAT 13-JAN-2001
LOCUS	Sequence 5	from Patent WO073420.			
DEFINITION	AX055801				
ACCESSION	AX055801.1	GI:12228914			
VERSION					
KEYWORDS	synthetic construct				
ORGANISM	synthetic construct				
SOURCE	artificial sequences.				
REFERENCE	1 (bases 1 to 6)				
AUTHORS	Hahn, W.C. and Weinberg, R.A.				
TITLE	Creation of human tumorigenic cells and uses therefor				
JOURNAL	Patent: WO 073420-A 5 07-DEC-2000;				
	WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; DANA-FARBER				



Search completed: January 1, 2004, 01:10:39  
Job time : 234.165 secs

RESULT 14  
US-10-408-736-66/c  
; Sequence 66, Application US/10408736  
; Publication No. US20030177508A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pradip  
; APPLICANT: Das, Tapas  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Parker-Barnes, Jennifer M.  
; APPLICANT: Leonard, Amanda Eun-Yeong  
; APPLICANT: Thurmond, Jennifer M.  
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF  
; FILE REFERENCE: 6407.US.P1  
; CURRENT APPLICATION NUMBER: US/10/408,736  
; CURRENT FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: US/09/379,095A  
; PRIOR FILING DATE: 1999-08-23  
; PRIOR APPLICATION NUMBER: US 09/145,828  
; PRIOR FILING DATE: 1998-09-02  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 66  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Reverse Primer R0352  
US-10-408-736-66  
Query Match 59.0%; Score 11.8; DB 13; Length 18;  
Best Local Similarity 86.7%; Pred. No. 2.4e+04;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
6 CATGCATTACGTACG 20  
18 CAAGCTTTACGTACG 4  
RESULT 15  
US-09-940-185-3327  
; Sequence 3327, Application US/09940185  
; Publication No. US20030096239A1  
; GENERAL INFORMATION:  
; APPLICANT: Gunderson, Kevin  
; APPLICANT: Chee, Mark  
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides  
; FILE REFERENCE: A-69605-1  
; CURRENT APPLICATION NUMBER: US/09/940,185  
; CURRENT FILING DATE: 2001-08-27  
; PRIOR APPLICATION NUMBER: US 60/227,948  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: US 60/228,854  
; PRIOR FILING DATE: 2000-08-29  
; NUMBER OF SEQ ID NOS: 4768  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3327  
LENGTH: 24  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Computer Generated Probe Sequence.  
US-09-940-185-3327

Query Match 59.0%; Score 11.8; DB 11; Length 24;  
Best Local Similarity 86.7%; Pred. No. 2.4e+04;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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Db 8 GCATGCATGCCTTGC 22

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Db          9 GGAGGCATGATGACGT 25
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RESULT 10
US-10-230-562-43
; Sequence 43, Application US/10230562
; Publication No. US20030113886A1
; GENERAL INFORMATION:
; APPLICANT: Rouviere, Pierre E
; APPLICANT: Brzostowicz, Patricia C
; TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID
; TITLE OF INVENTION: INTERMEDIATES
; FILE REFERENCE: BC-1001
; CURRENT APPLICATION NUMBER: US/10/230,562
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/120,702
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 43
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-230-562-43
Query Match      61.0%; Score 12.2; DB 15; Length 30;
Best Local Similarity 82.4%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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9 GGAGGCATGATGACGT 25
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RESULT 11
US-10-098-263B-31016
Sequence 11016, Application US/10098263B
Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 31016
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-31016
Query Match      60.0%; Score 12; DB 15; Length 25;
Best Local Similarity 75.0%; Pred. No. 2e+04;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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RESULT 12
US-09-903-456-93/c
; Sequence 93, Application US/09903456
; Patent No. US20020138874A1
; GENERAL INFORMATION:
; APPLICANT: Mukerji, Pradipt
; APPLICANT: Mukerji, Pradipt

Db          9 GGAGGCATGATGACGT 25
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RESULT 13
US-10-156-911-93/c
; Sequence 93, Application US/10156911
; Publication No. US20030163845A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradipt
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng L.
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P4
; CURRENT APPLICATION NUMBER: US/10/156,911
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 09/903,456
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Reverse Primer R0352
US-10-156-911-93
Query Match      59.0%; Score 11.8; DB 13; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

6 CATGCATTACGTACG 20
|||||
18 CAAGCTTTACGTACG 4
|||||

RESULT 13
US-10-156-911-93/c
; Sequence 93, Application US/10156911
; Publication No. US20030163845A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradipt
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng L.
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P4
; CURRENT APPLICATION NUMBER: US/10/156,911
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 09/903,456
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Reverse Primer R0352
US-10-156-911-93
Query Match      59.0%; Score 11.8; DB 13; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

6 CATGCATTACGTACG 20
|||||
18 CAAGCTTTACGTACG 4
|||||
```

Db 17 ATGCTGCTTGTGATC 1

RESULT 6

US-10-245-805-20/c

Sequence 20, Application US/10245805

Publication No. US20030182672A1

GENERAL INFORMATION:

APPLICANT: GRAHAM, Michael Wayne

APPLICANT: RICE, Robert No. US20030182672A1man

APPLICANT: REED, Kenneth Clifford

APPLICANT: MORPHY, Kathleen Margaret

APPLICANT: Benitec Australia Ltd

APPLICANT: The State of Queensland through its Department of Primary Industries

TITLE OF INVENTION: GENETIC SILENCING

FILE REFERENCE: 54632200200

CURRENT APPLICATION NUMBER: US/10/245,805

CURRENT FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: PCT/AU01/00297

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: AU P6363

PRIOR FILING DATE: 2000-03-17

PRIOR APPLICATION NUMBER: AU PR2700

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 25

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 20

LENGTH: 23

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Double Stranded DNA Probe

US-10-245-805-20

Query Match 61.0%; Score 12.2; DB 13; Length 23;

Best Local Similarity 82.4%; Pred. No. 1.5e+04;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ATGCATGCATTACGTAC 19

DB 20 ATGCATGCTTTGCATAC 4

RESULT 7

US-10-245-805-21/c

Sequence 21, Application US/10245805

Publication No. US20030182672A1

GENERAL INFORMATION:

APPLICANT: GRAHAM, Michael Wayne

APPLICANT: RICE, Robert No. US20030182672A1man

APPLICANT: REED, Kenneth Clifford

APPLICANT: MORPHY, Kathleen Margaret

APPLICANT: Benitec Australia Ltd

APPLICANT: The State of Queensland through its Department of Primary Industries

TITLE OF INVENTION: GENETIC SILENCING

FILE REFERENCE: 54632200200

CURRENT APPLICATION NUMBER: US/10/245,805

CURRENT FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: PCT/AU01/00297

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: AU P6363

PRIOR FILING DATE: 2000-03-17

PRIOR APPLICATION NUMBER: AU PR2700

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 25

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 21

LENGTH: 23

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Double Stranded DNA Probe

US-10-245-805-21

Query Match 61.0%; Score 12.2; DB 13; Length 23;

Best Local Similarity 82.4%; Pred. No. 1.5e+04;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ATGCATGCATTACGTAC 19

DB 20 ATGCATGCTTTGCATAC 4

US-10-245-805-21

Query Match 61.0%; Score 12.2; DB 13; Length 23;

Best Local Similarity 82.4%; Pred. No. 1.5e+04;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ATGCATGCATTACGTAC 19

DB 20 ATGCATGCTTTGCATAC 4

RESULT 8

US-09-940-185-2034/c

Sequence 2034, Application US/09940185

Publication No. US20030096239A1

GENERAL INFORMATION:

APPLICANT: Gunderson, Kevin

APPLICANT: Chee, Mark

TITLE OF INVENTION: Probes and Decoder Oligonucleotides

FILE REFERENCE: A-69605-1

CURRENT APPLICATION NUMBER: US/09/940,185

CURRENT FILING DATE: 2001-08-27

PRIOR APPLICATION NUMBER: US 60/227,948

PRIOR FILING DATE: 2000-08-25

PRIOR APPLICATION NUMBER: US 60/228,854

PRIOR FILING DATE: 2000-08-29

NUMBER OF SEQ ID NOS: 4768

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2034

LENGTH: 24

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Computer Generated Probe Sequence.

US-09-940-185-2034

Query Match 61.0%; Score 12.2; DB 11; Length 24;

Best Local Similarity 82.4%; Pred. No. 1.5e+04;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TGCATGCATTACGTACG 20

DB 22 TGCAGGCACTACGGACG 6

RESULT 9

US-09-954-314-43

Sequence 43, Application US/09954314

Patent No. US20020127666A1

GENERAL INFORMATION:

APPLICANT: Rouviere, Pierre E.

APPLICANT: Brzostowicz, Patricia C.

TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIATES

FILE REFERENCE: BC1001 US NA

CURRENT APPLICATION NUMBER: US/09/954,314

CURRENT FILING DATE: 2001-09-17

PRIOR APPLICATION NUMBER: 60/120,702

PRIOR FILING DATE: 1999-February-19

NUMBER OF SEQ ID NOS: 49

SOFTWARE: Microsoft Office 97

SEQ ID NO 43

LENGTH: 30

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: primer

US-09-954-314-43

Query Match 61.0%; Score 12.2; DB 10; Length 30;

Best Local Similarity 82.4%; Pred. No. 1.6e+04;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGT 17

Db 1 GCATGCATGCATTACGTACG 20  
|||||

## RESULT 2

US-10-122-633-8  
; Sequence 8, Application US/10122633  
; Publication No. US20030032611A1  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrist, Barbara A.  
; APPLICANT: Eller, Mark S.  
; APPLICANT: Yaar, Mina  
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
; FILE OF INVENTION: Oligonucleotides  
; FILE REFERENCE: 0054.1088-019  
; CURRENT APPLICATION NUMBER: US/10/122,633  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US 09/540,843  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: PCT/US01/10162  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA Fragment

Query Match 100.0%; Score 20; DB 15; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCATGCATGCATTACGTACG 20  
|||||

## RESULT 3

US-10-194-035-95/c  
; Sequence 95, Application US/10194035  
; Publication No. US2003014229A1  
; GENERAL INFORMATION:  
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE  
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES  
; APPLICANT: KLINMAN, Dennis  
; APPLICANT: ISHII, Ken  
; APPLICANT: VERTHELYI, Daniela  
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE  
; FILE REFERENCE: 4239-63317  
; CURRENT APPLICATION NUMBER: US/10/194,035  
; CURRENT FILING DATE: 2002-07-12  
; PRIOR APPLICATION NUMBER: PCT/US01/01122  
; PRIOR FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: US 60/176,115  
; PRIOR FILING DATE: 2000-01-14  
; NUMBER OF SEQ ID NOS: 119  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 95  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA

Query Match 65.0%; Score 13; DB 13; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATGCATGCATT 13

Db 13 GCATGCATGCATT 1  
|||||

## RESULT 4

US-09-232-785-139  
; Sequence 139, Application US/09232785  
; Publication No. US20030049612A1  
; GENERAL INFORMATION:  
; APPLICANT: International Paper Co.  
; APPLICANT: Echt, Craig S.  
; APPLICANT: Nelson, C. Dana  
; TITLE OF INVENTION: MICROSATELLITE DNA MARKERS AND USES  
; FILE OF INVENTION: THEREOF  
; FILE REFERENCE: 4481/1E188US1  
; CURRENT APPLICATION NUMBER: US/09/232,785  
; CURRENT FILING DATE: 1999-01-19  
; PRIOR APPLICATION NUMBER: 09/232,884  
; PRIOR FILING DATE: 1999-01-15  
; NUMBER OF SEQ ID NOS: 397  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 139  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Pinus taeda L.  
; US-09-232-785-139

Query Match 61.0%; Score 12.2; DB 11; Length 20;  
Best Local Similarity 82.4%; Pred. No. 1.5e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TGCATGCATTACGTACG 20  
|||||

Db 1 TGCATGCATTACAAATG 17  
|||||

## RESULT 5

US-10-079-429-21/c  
; Sequence 21, Application US/10079429  
; Publication No. US20030027177A1  
; GENERAL INFORMATION:  
; APPLICANT: Haseltine et al.  
; TITLE OF INVENTION: Human DNA Mismatch Repair Proteins  
; FILE REFERENCE: PFI06P3D1  
; CURRENT APPLICATION NUMBER: US/10/079,429  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: PCT/US95/01035  
; PRIOR FILING DATE: 1995-01-25  
; PRIOR APPLICATION NUMBER: 08/468,024  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: 08/465,769  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: 08/294,312  
; PRIOR FILING DATE: 1994-08-23  
; PRIOR APPLICATION NUMBER: 08/210,143  
; PRIOR FILING DATE: 1994-03-16  
; PRIOR APPLICATION NUMBER: 08/187,757  
; PRIOR FILING DATE: 1994-01-27  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 21  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: hMLH1 sense primer

Query Match 61.0%; Score 12.2; DB 15; Length 20;  
Best Local Similarity 82.4%; Pred. No. 1.5e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ATGCATGCATTACGTAC 19

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 17:10:00 ; Search time 233.165 Seconds  
(without alignments)  
296.896 Million cell updates/sec

Title: US-09-540-843-8

Perfect score: 20

Sequence: 1 gcattgcatctacgtacg 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2263443 seqs, 1730637950 residues

Total number of hits satisfying chosen parameters: 998502

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	15	US-10-122-630-8
2	20	100.0	20	15	US-10-122-633-8
3	13	65.0	17	13	US-10-194-035-95
4	12.2	61.0	20	11	US-09-232-785-139
5	12.2	61.0	20	15	US-10-079-429-21
6	12.2	61.0	23	13	US-10-245-805-20
7	12.2	61.0	23	13	US-10-245-808-21
8	12.2	61.0	24	11	US-09-940-185-2034
9	12.2	61.0	30	10	US-09-954-314-43
10	12.2	61.0	30	15	US-10-230-562-43
11	12	60.0	25	15	US-10-098-2638-31016
12	11.8	59.0	18	10	US-09-903-456-93
13	11.8	59.0	18	13	US-10-156-911-93
14	11.8	59.0	18	13	US-10-408-736-66
15	11.8	59.0	24	11	US-09-940-185-3327

c	16	11.8	59.0	25	15	US-10-098-2638-60894	Sequence 60894, A
	17	11.8	59.0	25	15	US-10-098-2638-69160	Sequence 69160, A
	18	11.8	59.0	26	11	US-09-957-483-44	Sequence 44, Appl
c	19	11.8	59.0	29	13	US-10-012-762-3	Sequence 3, Appl
	20	11.8	59.0	30	15	US-10-118-495-12	Sequence 12, Appl
	21	11.8	59.0	30	15	US-10-118-495-14	Sequence 14, Appl
c	22	11.8	59.0	30	15	US-10-118-495-20	Sequence 20, Appl
	23	11.6	58.0	18	15	US-10-061-071-21	Sequence 21, Appl
c	24	11.6	58.0	20	8	US-08-983-605-4	Sequence 4, Appl
	25	11.6	58.0	23	10	US-09-822-295-11	Sequence 11, Appl
c	26	11.6	58.0	25	15	US-10-098-2638-30573	Sequence 30573, A
c	27	11.6	58.0	25	15	US-10-098-2638-30574	Sequence 30574, A
	28	11.6	58.0	25	15	US-10-098-2638-35044	Sequence 35044, A
	29	11.6	58.0	25	15	US-10-098-2638-97436	Sequence 97436, A
c	30	11.6	58.0	25	15	US-10-098-2638-97803	Sequence 97803, A
c	31	11.6	58.0	25	15	US-10-098-2638-105971	Sequence 105971, A
c	32	11.6	58.0	30	10	US-09-993-502-4	Sequence 4, Appl
	33	11.6	58.0	30	13	US-10-168-445-112	Sequence 112, App
c	34	11.6	58.0	30	13	US-10-168-445-153	Sequence 153, App
	35	11.4	57.0	20	13	US-10-352-615-18	Sequence 18, Appl
	36	11.4	57.0	29	13	US-10-314-512-14	Sequence 14, Appl
c	37	11.2	56.0	25	15	US-10-098-2638-55338	Sequence 55338, A
	38	11.2	56.0	25	15	US-10-098-2638-120655	Sequence 120655, A
c	39	11.2	55.0	28	13	US-10-379-836-15	Sequence 15, Appl
	40	11	55.0	11	10	US-09-263-959-422	Sequence 422, App
	41	11	55.0	11	10	US-09-263-959-820	Sequence 820, App
	42	11	55.0	17	13	US-10-194-035-93	Sequence 93, Appl
c	43	11	55.0	17	13	US-10-194-035-93	Sequence 93, Appl
	44	11	55.0	17	13	US-10-194-035-95	Sequence 95, Appl
	45	11	55.0	20	13	US-10-194-035-90	Sequence 90, Appl

#### ALIGNMENTS

RESULT 1  
US-10-122-630-8  
; Sequence 8, Application US/10122630  
; Publication No. US20030032610A1  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrist, Barbara A.  
; APPLICANT: Eller, Mark S.  
; APPLICANT: Yaar, Mina  
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using Oligonucleotides  
; TITLE OF INVENTION: Oligonucleotides  
; FILE REFERENCE: 0054.1088-018  
; CURRENT APPLICATION NUMBER: US/10/122,630  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US 08/467,012  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: PCT/US96/08386  
; PRIOR FILING DATE: 1996-06-03  
; PRIOR APPLICATION NUMBER: US 09/048,927  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: US 09/540,843  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: PCT/US01/10162  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA Fragment  
US-10-122-630-8

Query Match 100.0%; Score 20; DB 15; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATGATGCATTACGTACG 20



```

STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/724,753
FILING DATE: 28-NO. 6416953-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/123,638
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kappos, John
REGISTRATION NUMBER: 37,861
REFERENCE/DOCKET NUMBER: 221/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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Query Match      58.0%; Score 11.6; DB 4; Length 20;
Best Local Similarity 77.8%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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3 ATGCATGCATTACGTACG 20
||||| |||||
20 ATGCATACGTTTCAGTACG 3

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Search completed: January 1, 2004, 00:32:19
Job time : 77.8326 secs

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; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; US-08-232-233-3

Query Match 58.0%; Score 11.6; DB 1; Length 20;  
 Best Local Similarity 77.8%; Pred. No. 2.8e+03;  
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 ATGCATGCTTACGTACG 20  
 Db 20 ATGCATGCTTACGTACG 3

RESULT 13  
 US-08-703-601-3/c  
 Sequence 3, Application US/08703601  
 Patent No. 5849489  
 GENERAL INFORMATION:

APPLICANT: Michael J. Heller  
 TITLE OF INVENTION: SELF-ORGANIZING MOLECULAR PHOTONIC  
 TITLE OF INVENTION: STRUCTURES BASED ON CHROMOPHORE-  
 TITLE OF INVENTION: AND FLUOROPHORE-CONTAINING  
 TITLE OF INVENTION: POLYNUCLEOTIDES AND METHODS OF  
 TITLE OF INVENTION: THEIR USE  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: USA  
 ZIP: 90071

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
 SOFTWARE: WordPerfect (Version 5.1)  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/703,601

FILING DATE: August 23, 1996

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: 07/232,233

FILING DATE: May 5, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Kappos, John

REGISTRATION NUMBER: 37,861

REFERENCE/DOCKET NUMBER: 221/078

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-703-601-3

Query Match 58.0%; Score 11.6; DB 2; Length 20;  
 Best Local Similarity 77.8%; Pred. No. 2.8e+03;  
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 ATGCATGCTTACGTACG 20  
 Db 20 ATGCATGCTTACGTACG 3

RESULT 14  
 US-09-123-638-3/c  
 Sequence 3, Application US/09123638  
 Patent No. 6162603  
 GENERAL INFORMATION:

APPLICANT: Michael J. Heller  
 TITLE OF INVENTION: SELF-ORGANIZING MOLECULAR PHOTONIC  
 TITLE OF INVENTION: STRUCTURES BASED ON CHROMOPHORE-  
 TITLE OF INVENTION: AND FLUOROPHORE-CONTAINING  
 TITLE OF INVENTION: POLYNUCLEOTIDES AND METHODS OF  
 TITLE OF INVENTION: THEIR USE  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: USA  
 ZIP: 90071

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
 SOFTWARE: WordPerfect (Version 5.1)  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/123,638

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/703,601

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Kappos, John

REGISTRATION NUMBER: 37,861

REFERENCE/DOCKET NUMBER: 221/078

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-09-123-638-3

Query Match 58.0%; Score 11.6; DB 3; Length 20;  
 Best Local Similarity 77.8%; Pred. No. 2.8e+03;  
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 ATGCATGCTTACGTACG 20  
 Db 20 ATGCATGCTTACGTACG 3

RESULT 15  
 US-09-724-753-3/c  
 Sequence 3, Application US/09724753  
 Patent No. 6416953  
 GENERAL INFORMATION:

APPLICANT: Michael J. Heller  
 TITLE OF INVENTION: SELF-ORGANIZING MOLECULAR PHOTONIC  
 STRUCTURES BASED ON CHROMOPHORE-  
 AND FLUOROPHORE-CONTAINING  
 POLYNUCLEOTIDES AND METHODS OF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: unknown  
US-09-134-855-1

Query Match 60.0%; Score 12; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATGCATGCAT 12  
|||||  
DB 13 GCATGCATGCAT 2

## RESULT 10

US-09-145-828A-28/c  
Sequence 28, Application US/09145828A

Patent No. 6403349

## GENERAL INFORMATION:

APPLICANT: Abbott Laboratories  
APPLICANT: Mukerji, Pradip  
APPLICANT: Leonard, Amanda E. Y.  
APPLICANT: Huang, Yung-Sheng  
APPLICANT: Thurmond, Jennifer  
APPLICANT: Kirchner, Stephen J.  
APPLICANT: Parker-Barnes, Jennifer M.

TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF

FILE REFERENCE: 6407 US 01

CURRENT APPLICATION NUMBER: US/09/145,828A

CURRENT FILING DATE: 1998-09-02

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 28

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Primer R0352

US-09-145-828A-28

Query Match 59.0%; Score 11.8; DB 4; Length 18;  
Best Local Similarity 86.7%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

6 CATGCATTCAGTACG 20  
|||||  
18 CAAGCTTTCAGTACG 4

## RESULT 11

US-08-250-951-3/c

Sequence 3, Application US/08250951

Patent No. 532129

## GENERAL INFORMATION:

APPLICANT: Heller, Michael J

TITLE OF INVENTION: SELF-ORGANIZING MOLECULAR PHOTONIC

TITLE OF INVENTION: STRUCTURES BASED ON CHROMOPHORE- AND FLUOROPHORE-CONTAINING

TITLE OF INVENTION: POLYNUCLEOTIDES AND METHODS OF THEIR USE

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bingham & Fitting

STREET: 12526 High Bluff Drive, Suite 300

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92130

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/250,951

FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/790,262  
FILING DATE: 07-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: HEL0002P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-792-3680  
TELEFAX: 619-792-8477  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-250-951-3

Query Match 58.0%; Score 11.6; DB 1; Length 20;  
Best Local Similarity 77.8%; Pred. No. 2.8e+03;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 ATGCATGCATTCAGTACG 20  
|||||  
DB 20 ATGCATGCATTCAGTACG 3

## RESULT 12

US-08-232-233-3/c

Sequence 3, Application US/08232233

Patent No. 5565322

## GENERAL INFORMATION:

APPLICANT: Michael J. Heller

TITLE OF INVENTION: SELF-ORGANIZING MOLECULAR PHOTONIC

TITLE OF INVENTION: STRUCTURES BASED ON CHROMOPHORE- AND FLUOROPHORE-

TITLE OF INVENTION: CONTAINING POLYNUCLEOTIDES AND METHODS OF THEIR USE

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 611 West Sixth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90017

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/232,233

FILING DATE: May 4, 1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/790,262

FILING DATE: No. 5565322ember 7, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Murphy, David B.

REGISTRATION NUMBER: 31,125

REFERENCE/DOCKET NUMBER: 207/170

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

FEATURE:  
; OTHER INFORMATION: hmlh1 sense primer  
US-08-187-757D-19

Query Match 61.0%; Score 12.2; DB 4; Length 21;  
Best Local Similarity 82.4%; Pred. No. 1.4e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ATGCATGCATTACGTAC 19  
|||||  
Db 18 ATGCCTGCATTGTGATC 2

## RESULT 6

US-09-504-358-43  
; Sequence 43, Application US/09504358  
; Patent No. 6365376  
GENERAL INFORMATION:  
APPLICANT: Rouviere, Pierre E.  
APPLICANT: Brzostowicz, Patricia C.  
TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIATES  
FILE REFERENCE: BC1001 US NA  
CURRENT APPLICATION NUMBER: US/09/504,358  
CURRENT FILING DATE: 2000-02-15  
EARLIER APPLICATION NUMBER: 60/120,702  
EARLIER FILING DATE: 1999-February-19  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 43  
LENGTH: 30  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: primer  
US-09-504-358-43

Query Match 61.0%; Score 12.2; DB 4; Length 30;  
Best Local Similarity 82.4%; Pred. No. 1.4e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGT 17  
|||||  
Db 9 GGAGGCATGCATGACGT 25

## RESULT 7

US-09-954-314-43  
; Sequence 43, Application US/09954314  
; Patent No. 6465224  
GENERAL INFORMATION:  
APPLICANT: Rouviere, Pierre E.  
APPLICANT: Brzostowicz, Patricia C.  
TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIATES  
FILE REFERENCE: BC1001 US NA  
CURRENT APPLICATION NUMBER: US/09/954,314  
CURRENT FILING DATE: 2001-09-17  
PRIOR APPLICATION NUMBER: 60/120,702  
PRIOR FILING DATE: 1999-February-19  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 43  
LENGTH: 30  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: primer  
US-09-954-314-43

Query Match 61.0%; Score 12.2; DB 4; Length 30;  
Best Local Similarity 82.4%; Pred. No. 1.4e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCATGCATGCATTACGT 17

Db 9 GGAGGCATGCATGACGT 25  
|||||

## RESULT 8

US-09-134-855-1  
; Sequence 1, Application US/09134855  
; Patent No. 6107038  
GENERAL INFORMATION:  
APPLICANT: CHOUDHARY, Gargi  
APPLICANT: HAHNENBERGER, Karen  
APPLICANT: KUEKES, Philip J  
APPLICANT: LICHTENWALTER, Kay  
APPLICANT: HANCOCK, William S  
TITLE OF INVENTION: (As Amended) Method of Binding a Plurality of Chemicals  
TITLE OF INVENTION: on a Substrate by Electrophoretic Self-Assembly  
FILE REFERENCE: 5000-0050  
CURRENT APPLICATION NUMBER: US/09/134,855  
CURRENT FILING DATE: 1998-08-14  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 15  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (1)  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (1)  
OTHER INFORMATION: n is 2' fluorodeoxycytidine  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: unknown  
US-09-134-855-1

Query Match 60.0%; Score 12; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATGCATGCAT 12  
|||||  
Db 4 GCATGCATGCAT 15

## RESULT 9

US-09-134-855-1/c  
; Sequence 1, Application US/09134855  
; Patent No. 6107038  
GENERAL INFORMATION:  
APPLICANT: CHOUDHARY, Gargi  
APPLICANT: HAHNENBERGER, Karen  
APPLICANT: KUEKES, Philip J  
APPLICANT: LICHTENWALTER, Kay  
APPLICANT: HANCOCK, William S  
TITLE OF INVENTION: (As Amended) Method of Binding a Plurality of Chemicals  
TITLE OF INVENTION: on a Substrate by Electrophoretic Self-Assembly  
FILE REFERENCE: 5000-0050  
CURRENT APPLICATION NUMBER: US/09/134,855  
CURRENT FILING DATE: 1998-08-14  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 15  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (1)  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (1)  
OTHER INFORMATION: n is 2' fluorodeoxycytidine

QY 2 CATGCATGATTACG 16  
|||||  
Db 20 CATGCATGATTCCG 6

RESULT 2  
US-07-720-586-7  
; Sequence 7, Application US/07720586  
; Patent No. 5232831  
; GENERAL INFORMATION:  
; APPLICANT: Curt Millman  
; APPLICANT: Philip W. Hammond  
; TITLE OF INVENTION: NUCLEIC ACIDS PROBES  
; TITLE OF INVENTION: TO STREPTOCOCCUS PYOGENES  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM PS/2 Model 50Z or 55SX  
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
SOFTWARE: WordPerfect (Version 5.0)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07720,586  
FILING DATE: 19910628  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 193/121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-07-720-586-7

Query Match 63.0%; Score 12.6; DB 1; Length 26;  
Best Local Similarity 78.9%; Pred. No. 8.9e+02;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CATGCATGATTACG 20  
|||||  
Db 3 CTTGCATGATTAGGCACG 21

RESULT 3  
US-08-294-312B-21/c  
; Sequence 21, Application US/08294312B  
; Patent No. 6380369  
; GENERAL INFORMATION:  
; APPLICANT: Adams et al.  
; TITLE OF INVENTION: Human DNA Mismatch Repair Proteins  
; FILE REFERENCE: PFI06P2  
; CURRENT APPLICATION NUMBER: US/08/294,312B  
; CURRENT FILING DATE: 1994-08-23  
; PRIOR APPLICATION NUMBER: 08/210,143

; PRIOR FILING DATE: 1994-03-16  
; PRIOR APPLICATION NUMBER: 08/187,757  
; PRIOR FILING DATE: 1994-01-27  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 21  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: hMLH1 sense primer  
US-08-294-312B-21

Query Match 61.0%; Score 12.2; DB 4; Length 20;  
Best Local Similarity 82.4%; Pred. No. 1.4e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ATGCATGATTACGTAC 19  
|||||  
Db 17 ATGCCTGCATTGTGTAC 1

RESULT 4  
US-08-468-024B-21/c  
; Sequence 21, Application US/08468024B  
; Patent No. 6416984  
; GENERAL INFORMATION:  
; APPLICANT: Haseltine et al.  
; TITLE OF INVENTION: Human DNA Mismatch Repair Proteins  
; FILE REFERENCE: PFI06P3  
; CURRENT APPLICATION NUMBER: US/08/468,024B  
; CURRENT FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: 08/294,312  
; PRIOR FILING DATE: 1994-08-23  
; PRIOR APPLICATION NUMBER: 08/210,143  
; PRIOR FILING DATE: 1994-03-16  
; PRIOR APPLICATION NUMBER: 08/187,757  
; PRIOR FILING DATE: 1994-01-27  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 21  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: hMLH1 sense primer  
US-08-468-024B-21

Query Match 61.0%; Score 12.2; DB 4; Length 20;  
Best Local Similarity 82.4%; Pred. No. 1.4e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ATGCATGATTACGTAC 19  
|||||  
Db 17 ATGCCTGCATTGTGTAC 1

RESULT 5  
US-08-187-757D-19/c  
; Sequence 19, Application US/08187757D  
; Patent No. 6482606  
; GENERAL INFORMATION:  
; APPLICANT: Adams et al.  
; TITLE OF INVENTION: Human DNA Mismatch Repair Proteins  
; FILE REFERENCE: PFI06  
; CURRENT APPLICATION NUMBER: US/08/187,757D  
; CURRENT FILING DATE: 1994-01-27  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 19  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 14:40:05 ; Search time 77.7215 Seconds  
(without alignments)  
113.581 Million cell updates/sec

Title: US-09-540-843-8

Perfect score: 20

Sequence: 1 gcatgcattacgtacg 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 547746

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents NA:\*

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4: /cgn2\_6/prodata/1/ina/6B COMB.seq:\*

5: /cgn2\_6/prodata/1/ina/6C COMB.seq:\*

6: /cgn2\_6/prodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13.4	67.0	28	1	US-08-053-564-10
2	12.6	63.0	26	1	US-07-720-586-7
3	12.2	61.0	20	4	US-08-294-312B-21
4	12.2	61.0	20	4	US-08-468-024B-21
5	12.2	61.0	21	4	US-08-187-757D-19
6	12.2	61.0	30	4	US-09-504-358-43
7	12.2	61.0	30	4	US-09-954-314-43
8	12.2	60.0	15	3	US-09-134-855-1
9	12.2	60.0	15	3	US-09-134-855-1
10	11.8	59.0	18	4	US-09-145-828A-28
11	11.6	58.0	20	1	US-08-250-951-3
12	11.6	58.0	20	1	US-08-232-233-3
13	11.6	58.0	20	2	US-08-703-601-3
14	11.6	58.0	20	3	US-09-123-638-3
15	11.6	58.0	20	4	US-09-724-753-3
16	11.6	58.0	20	5	PCT-US92-09827-3
17	11.6	58.0	22	3	US-08-858-876A-12
18	11.6	58.0	22	3	US-09-472-880-12
19	11.6	58.0	23	3	US-09-081-345-11
20	11.6	58.0	24	3	US-08-105-761-8
21	11.6	58.0	24	3	US-09-333-208-4
22	11.6	58.0	24	3	US-09-333-254-4
23	11.6	58.0	24	4	US-09-183-270-4
24	11.6	58.0	24	5	PCT-US92-11076-8
25	11.6	58.0	27	3	US-08-886-886-4
26	11.6	58.0	28	1	US-08-053-564-10
27	11.6	58.0	28	4	US-09-601-943-3

c	28	11.6	58.0	30	1	US-08-384-708A-55	Sequence 55, Appl
c	29	11.6	58.0	30	2	US-09-001-826-13	Sequence 13, Appl
c	30	11.6	58.0	30	3	US-08-687-421-55	Sequence 55, Appl
c	31	11.6	58.0	30	4	US-09-264-854-13	Sequence 13, Appl
c	32	11.4	57.0	17	4	US-08-584-040-2218	Sequence 2218, Ap
c	33	11.4	57.0	17	4	US-09-371-772B-763	Sequence 763, App
c	34	11.4	57.0	17	4	US-09-371-772B-5107	Sequence 5107, Ap
c	35	11.4	57.0	17	4	US-09-371-772B-5108	Sequence 5108, Ap
c	36	11.4	57.0	20	4	US-08-894-454-18	Sequence 18, Appl
c	37	11.4	57.0	24	3	US-08-930-001-4	Sequence 4, Appli
c	38	11.4	57.0	28	3	US-09-111-085-14	Sequence 14, Appl
c	39	11.4	57.0	30	2	US-08-629-001A-34	Sequence 34, Appl
c	40	11.4	57.0	30	3	US-08-642-274D-113	Sequence 113, App
c	41	11.2	56.0	17	3	US-08-891-516-29	Sequence 29, Appl
c	42	11.2	56.0	17	3	US-08-837-034-29	Sequence 29, Appl
c	43	11.2	56.0	20	3	US-08-944-974A-3	Sequence 3, Appli
c	44	11.2	56.0	21	1	US-08-370-193A-6	Sequence 6, Appli
c	45	11.2	56.0	24	1	US-07-884-811-12	Sequence 12, Appl

## ALIGNMENTS

RESULT 1  
US-08-053-564-10/c  
; Sequence 10, Application US/08053564  
; Patent No. 5418153  
; GENERAL INFORMATION:  
; APPLICANT: MORI, MASASHI  
; APPLICANT: OKINO, TETSURO  
; APPLICANT: FURUSAWA, IWAQ  
; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF  
; TITLE OF INVENTION: EXOGENOUS GENE OR ITS PRODUCT  
; TITLE OF INVENTION: IN PLANT CELLS NO.2  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak &  
; ADDRESSEE: Seas  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version  
; SOFTWARE: #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/053,564  
; FILING DATE: 28-APR-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP HEI-4-152593  
; FILING DATE: 28-APR-1992  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)293-7060  
; TELEFAX: (202)293-7860  
; TELEX: 649113  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other nucleic acid  
; DESCRIPTION: synthesized oligonucleotide  
US-08-053-564-10

Query Match 67.0%; Score 13.4; DB 1; Length 28;  
Best Local Similarity 93.3%; Pred. No. 3.5e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Plate: 0102 row: 0 column: 13  
 Seq primer: CACACAGGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 30.  
 Location/Qualifiers

## FEATURES

1. .30  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0102013"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## BASE COUNT

11 a 4 c 7 g 8 t

## ORIGIN

Query Match 52.0%; Score 10.4; DB 28; Length 30;  
 Best Local Similarity 91.7%; Pred. No. 5.9e+05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 GCATGCATGCAT 12  
 |||||  
 4 GCATACATGCAT 15

## RESULT 15

## ACUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

AZ826822 30 bp DNA linear GSS 20-FEB-2001  
 2M0102013R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0102013 R, genomic survey sequence.

AZ826822 1 GI:12996730

GSS.

Mus musculus

Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 30)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly

, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0102 row: 0 column: 13  
 Seq primer: CACACAGGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 30.  
 Location/Qualifiers

## FEATURES

1. .30  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0102013"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## BASE COUNT

11 a 4 c 7 g 8 t

## ORIGIN

Query Match 52.0%; Score 10.4; DB 28; Length 30;  
 Best Local Similarity 91.7%; Pred. No. 5.9e+05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCATGCATGCAT 12  
 |||||  
 Db 17 GCATGCATGTAT 6

Search completed: December 31, 2003, 19:41:27  
 Job time : 2300.97 secs

Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 29.  
 Location/Qualifiers

## FEATURES

source

1. .29

/organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0212P03"  
 /sex="Female"

/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC2M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female); Purified genomic DNA from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT  
 ORIGIN

9 a 8 c 5 g 7 t

Query Match 52.0%; Score 10.4; DB 28; Length 29;  
 Best Local Similarity 91.7%; Pred. No. 5.9e+05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 GCATGATGCAT 12

|||||

13 GCATGCTTGCAT 24

## RESULT 13

AZ949216/c

LOCUS

2M0212P03R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
 clone UUGC2M0212P03 R, genomic survey sequence.

ACCESSION

AZ949216

VERSION

GSS

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished  
 Contact: Robert B. Weiss  
 University of Utah  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00

Plate: 0212 row: P column: 03  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 29.  
 Location/Qualifiers

## FEATURES

source

1. .29

/organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0212P03"  
 /sex="Female"

/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC2M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female); Purified genomic DNA from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 9 a 8 c 5 g 7 t  
 ORIGIN

Query Match 52.0%; Score 10.4; DB 28; Length 29;  
 Best Local Similarity 91.7%; Pred. No. 5.9e+05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 GCATGATGCAT 12

|||||

18 GCATGCTTGCAT 7

## RESULT 14

AZ826822

LOCUS

DEFINITION

ACCESSION

AZ826822

VERSION

GSS

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished  
 Contact: Robert B. Weiss  
 University of Utah  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu



ADIS DNA core facility at MP1Z  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weiss@adamp1z-koeln.mpg.de  
 Insert Length: 25 Std Error: 0.00  
 Plate: 17 row: K column: 24  
 Seq primer: T7; GTAATACCACTCACTATAGGC.

## FEATURES

source  
 1. 25  
 /organism="Beta vulgaris"  
 /mol\_type="mRNA"  
 /cultiivar="KWS2320 (double haploid, monogerm breeding line)"  
 /db\_xref="GABI:188822"  
 /db\_xref="taxon:161934"  
 /clone="024-017-K24"  
 /tissue\_type="storage root"  
 /lab\_host="EMPH10B"  
 /clone\_lib="MP1Z-ADIS-024-storage root"  
 /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KWS  
 Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
 orientation:  
 SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet project  
 local PI: Dr. Katharina Schneider, coordinator: Prof.  
 Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

## BASE COUNT

8 a 9 c 7 g 1 t

## ORIGIN

Query Match 52.0%; Score 10.4; DB 13; Length 25;  
 Best Local Similarity 70.0%; Pred. No. 5.7e+05;  
 Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

1 GCATGCGGCGTGGTGGCG 20  
 21 GTATGCGGCGTGGTGGCG 2

## RESULT 11

AZ760021 25 bp DNA linear GSS 16-FEB-2001  
 LOCUS 1M0553F20F Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
 DEFINITION clone UUGCLM0553F20 F, genomic survey sequence.

## ACCESSION

AZ760021 GI:12867408

## VERSION

GSS.

## KEYWORDS

Mus musculus (house mouse)

## SOURCE

Mus musculus

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 25)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0553 row: F column: 20

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends  
 High quality sequence stop: 25.

## FEATURES

source  
 Location/Qualifiers  
 1. 25  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGCLM0553F20"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGCLM library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT 4 a 9 c 5 g 7 t

## ORIGIN

Query Match 52.0%; Score 10.4; DB 28; Length 25;  
 Best Local Similarity 91.7%; Pred. No. 5.7e+05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCATGCGATGCAT 12

Db 23 GCATGCGAGGCAT 12

## RESULT 12

AZ949216 29 bp DNA linear GSS 27-APR-2001  
 LOCUS 2M0212P03R Mouse 10kb plasmid UUC2M library Mus musculus genomic  
 DEFINITION clone UUC2M0212P03 R, genomic survey sequence.

## ACCESSION

AZ949216 GI:13820443

## VERSION

GSS.

## KEYWORDS

Mus musculus (house mouse)

## SOURCE

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 29)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0212 row: P column: 03

```

VERSION      AZ810353.1  GI:12977531
KEYWORDS     GSS.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
REFERENCE    1 (bases 1 to 23)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
              M., Rose,M., Stokes,R., Tingey,A., von Niederhausern,A.
              and Wright,D., Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL
COMMENT      Unpublished
              Contact: Robert B. Weiss
              University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0074 row: N column: 18
              Seq primer: CACACAGAAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 23.

FEATURES             source
1..23
   /organism="Mus musculus"
   /mol_type="genomic DNA"
   /strain="C57BL/6J"
   /db_xref="taxon:10090"
   /clone="UUGC2M0074N18"
   /sex="Male"
   /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
   /clone_lib="Mouse 10kb plasmid UUGC1M library"
   /notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT      5 a      7 c      6 g      5 t
ORIGIN
Query Match      52.0%; Score 10.4; DB 28; Length 23;
Best Local Similarity 91.7%; Pred. No. 5.5e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCATGCGTGCAT 12
      |||||
Db      19 GCATGCGTGCAT 8

RESULT 9
BH907393
LOCUS      24 bp      DNA      linear      GSS 04-SEP-2002
DEFINITION SALK_042093.38.75.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_042093.38.75.x, genomic

survey sequence.
BH907393
VERSION      BH907393.1  GI:22720326
KEYWORDS     GSS.
SOURCE       Arabidopsis thaliana (thale cress)
ORGANISM     Arabidopsis thaliana
REFERENCE    1 (bases 1 to 24)
AUTHORS      Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadranab
              C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
              , Zimmerman,J. and Ecker,J.R.
              A Sequence-Indexed Library of Insertion Mutations in the
              Arabidopsis Genome
              Unpublished
              Contact: Joseph R. Ecker
              Salk Institute Genomic Analysis Laboratory (SIGAL)
              The Salk Institute for Biological Studies
              10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
              Tel: 858 453 4100 x1752
              Fax: 858 558 6379
              Email: ecker@salk.edu
              This is single pass sequence recovered from the left border of
              TDNA.
              Class: TDNA tagged.

FEATURES             Location/Qualifiers
1..24
   /organism="Arabidopsis thaliana"
   /mol_type="genomic DNA"
   /strain="Columbia 0"
   /db_xref="taxon:3702"
   /clone="SALK_042093.38.75.x"
   /clone_lib="Arabidopsis thaliana TDNA insertion lines"
   /note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT      10 a      2 c      5 g      7 t
ORIGIN
Query Match      52.0%; Score 10.4; DB 28; Length 24;
Best Local Similarity 91.7%; Pred. No. 5.6e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 ATGCATGCATTA 14
      |||||
Db      13 ATGTATGCATTA 24

RESULT 10
BH907393
LOCUS      25 bp      mRNA      linear      EST 06-DEC-2002
DEFINITION E012713-024-017-K24-T7 MP1Z-ADIS-024-storage root Beta vulgaris
            CDNA clone 024-017-K24 3-PRIME, mRNA sequence.

BASE COUNT      25 bp      mRNA      linear      EST 06-DEC-2002
ORIGIN
Query Match      52.0%; Score 10.4; DB 28; Length 23;
Best Local Similarity 91.7%; Pred. No. 5.5e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCATGCGTGCAT 12
      |||||
Db      19 GCATGCGTGCAT 8

RESULT 9
BH907393
LOCUS      24 bp      DNA      linear      GSS 04-SEP-2002
DEFINITION SALK_042093.38.75.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_042093.38.75.x, genomic

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Query Match      55.0%; Score 11; DB 28; Length 20;
Best Local Similarity 73.7%; Pred. No. 2.9e+05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCATCGATGCATTACGTAC 19
    |||||
Db 2 GCCTGCTGCCTTACTTCC 20

RESULT 6
A2477068
LOCUS      28 bp      DNA      linear      GSS 04-OCT-2000
DEFINITION  IM0296B23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
              clone UUGC1M0296B23 F, genomic survey sequence.
ACCESSION  A2477068
VERSION    A2477068.1 GI:10635267
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 28)
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL    Unpublished
COMMENT    Contact: Robert B. Weiss
            University of Utah
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0296 row: B column: 23
            Seq primer: CGTTGTAACGACGCGCCAGT
            Claes: plasmid ends
            High quality sequence stop: 28.
            Location/Qualifiers
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                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0296B23"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male). Was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnates/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
                9 a      5 c      6 g      8 t
BASE COUNT
ORIGIN

FEATURES
source
1..28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0296B23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male). Was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnates/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
9 a      5 c      6 g      8 t

Query Match      55.0%; Score 11; DB 28; Length 20;
Best Local Similarity 73.7%; Pred. No. 2.9e+05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCATCGATGCATTACGTAC 19
    |||||
Db 2 GCCTGCTGCCTTACTTCC 20

RESULT 7
BH910260
LOCUS      30 bp      DNA      linear      GSS 04-SEP-2002
DEFINITION  SALK_058679.37.45.x Arabidopsis thaliana TDNA insertion lines
              Arabidopsis thaliana genomic clone SALK_058679.37.45.x, genomic
              survey sequence.
ACCESSION  BH910260
VERSION    BH910260.1 GI:22723193
KEYWORDS   GSS.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
REFERENCE  1 (bases 1 to 30)
AUTHORS    Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
            ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
            , Zimmerman,J. and Ecker,J.R.
TITLE      A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
JOURNAL    Unpublished
COMMENT    Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
            Location/Qualifiers
                1..30
                /organism="Arabidopsis thaliana"
                /mol_type="genomic DNA"
                /strain="Columbia 0"
                /db_xref="taxon:3702"
                /clone="SALK_058679.37.45.x"
                /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                /note="PCR was performed on Arabidopsis thaliana lines
                each of which contains one or more TDNA insertion
                elements. The resultant fragment for each line was
                directly sequenced to determine the genomic sequence at
                the site of insertion. Details of the protocols used can
                be found at http://signal.salk.edu/tdna_protocols.html"
                13 a      6 c      3 g      8 t
BASE COUNT
ORIGIN

Query Match      53.0%; Score 10.6; DB 28; Length 30;
Best Local Similarity 76.5%; Pred. No. 4.8e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CATGCATGCATTACGTA 18
    |||||
Db 4 CATAAACGCAITACGCA 20

RESULT 8
A2810353/c
LOCUS      23 bp      DNA      linear      GSS 20-FEB-2001
DEFINITION  2M0074N18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
              clone UUGC2M0074N18 R, genomic survey sequence.
ACCESSION  A2810353

```

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source      1. .29
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Human adult lung 3' directed MboI cDNA"
/notes="Adult human lung, 3' directed MboI"
10 a      3 c      4 g      12 t

BASE COUNT
ORIGIN

Query Match      59.0%; Score 11.8; DB 14; Length 29;
Best Local Similarity 86.7%; Pred. No. 1.4e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GCATGCATGCATTAC 15
DB      15 GTATGCATGTATTAC 29

RESULT 4
LOCUS      AI568835
DEFINITION      th16g12.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:2118502 3'
similar to WP:BEED8.8 CE01892 ;, mRNA sequence.
ACCESSION      AI568835
VERSION      AI568835.1 GI:4532209
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 22)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strauberg, Ph.D.
Email: cgaps-x@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Insert Length: 1294 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. .22
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2118502"
/sex="male"
/dev_stage="adult"
/lab_host="DHIOB"
/clone_lib="NCI CGAP Pr28"
/notes="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; plasmid DNA from the
normalized library NCI CGAP Pr22 was prepared, and es
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clones IDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
5 a      6 c      3 g      8 t

BASE COUNT
ORIGIN

Query Match      57.0%; Score 11.4; DB 9; Length 22;

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Best Local Similarity 92.3%; Pred. No. 1.9e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CATGCATGCATTA 14
DB      2 CATCCATGCATTA 14

RESULT 5
LOCUS      AZ592714
DEFINITION      20 bp DNA linear GSS 13-DEC-2000
clone UUGC1M0403P13 R, genomic survey sequence.
ACCESSION      AZ592714
VERSION      AZ592714.1 GI:11714904
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Ielam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0403 row: P column: 13
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0403P13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
1 a      9 c      3 g      7 t

BASE COUNT
ORIGIN

FEATURES
source

```

Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0538 row: M column: 03  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 27.  
 Location/Qualifiers  
 1. .27

## FEATURES

source

/organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0538M03"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT  
 ORIGIN  
 10 a 7 c 5 g 5 t

Query Match 63.0%; Score 12.6; DB 28; Length 27;  
 Best Local Similarity 78.9%; Pred. No. 5.9e+04;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

2 CATGCATGCATTACGTACG 20

|||||  
 22 CATGCATGCATTGCTAATG 4

## RESULT 2

AZ478579/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AZ478579 26 bp DNA linear GSS 04-OCT-2000  
 1M0298E16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0298E16 R, genomic survey sequence.

AZ478579 1 GI:10637573

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 26)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly

, M., Rose, M., Ross, R., Stokes, R., Tingey, A., von Niederhausen, A.

and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0298 row: E column: 16  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 26.  
 Location/Qualifiers  
 1. .26

## FEATURES

source

/organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0298E16"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT  
 ORIGIN  
 8 a 6 c 3 g 9 t

Query Match 61.0%; Score 12.2; DB 28; Length 26;  
 Best Local Similarity 82.4%; Pred. No. 8.9e+04;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATGCATGCATTACGTA 18

|||||  
 21 CATGCAGGATTATGTA 5

## RESULT 3

D45819

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

D45819 29 bp mRNA linear EST 20-FEB-1995  
 HUMGS03038 Human adult lung 3' directed Mbol cDNA Homo sapiens CDNA  
 3', mRNA sequence.

D45819 1 GI:662773

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 29)

Itoh, K., Okubo, K., Yosii, J., Yokouchi, H. and Matsubara, K.

An expression profile of active genes in human lung

DNA Res. 1, 279-287 (1994)

95236275

7719923

Contact: Kohichi Itoh

Institute for Molecular and Cellular Biology

Osaka University

3-1, Yamadaoka, Suita, Osaka, 565, Japan

Tel: 06-877-5111 x3910

Fax: 06-877-1922.

## FEATURES

Location/Qualifiers

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 13:58:09 ; Search time 2297.97 Seconds  
(without alignments)  
211.530 Million cell updates/sec

Title: US-09-540-843-8

Perfect score: 20

Sequence: 1 gcatgcattacgtacg 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 33330

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_estc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_est3:\*

12: gb\_est4:\*

13: gb\_est5:\*

14: gb\_est6:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pin:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_pbg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	12.6	63.0	27	28	AZ660469 1M0538M03
C 2	12.2	61.0	26	28	AZ478579 1M0298E16
3	11.8	59.0	29	14	D45819 HUNG03038
4	11.4	57.0	22	9	A1568835 th16g12.x

5	11	55.0	20	28	AZ592714
6	10.6	53.0	28	28	AZ477068
7	10.6	53.0	30	28	BH910260
C 8	10.4	52.0	23	28	AZ810353
9	10.4	52.0	24	28	BH907393
C 10	10.4	52.0	25	13	BQ591292
C 11	10.4	52.0	25	28	AZ760021
C 12	10.4	52.0	29	28	AZ949216
C 13	10.4	52.0	29	28	AZ949216
C 14	10.4	52.0	30	28	AZ826822
C 15	10.4	52.0	30	28	AZ826822
16	10.2	51.0	20	28	AZ780308
17	10.2	51.0	24	28	AZ500040
C 18	10.2	51.0	24	28	AZ500040
C 19	10	50.0	23	28	AZ974350
C 20	10	50.0	23	28	AZ979817
C 21	10	50.0	25	28	AZ387185
22	10	50.0	27	28	AZ660469
23	10	50.0	29	28	AZ592381
C 24	9.8	49.0	20	14	D18242
C 25	9.8	49.0	23	9	AU013185
C 26	9.8	49.0	23	9	AU013203
C 27	9.8	49.0	23	9	AU013205
C 28	9.8	49.0	23	28	AZ974350
C 29	9.8	49.0	24	29	AZ45G10Q
C 30	9.8	49.0	27	28	AZ810112
C 31	9.8	49.0	28	28	AZ365824
C 32	9.8	49.0	28	28	AZ796047
C 33	9.8	49.0	29	28	AZ647129
C 34	9.8	49.0	30	28	AZ666770
C 35	9.6	48.0	19	28	AZ424532
C 36	9.6	48.0	21	28	AZ992327
37	9.6	48.0	24	28	AZ857110
38	9.6	48.0	25	28	BH900958
C 39	9.6	48.0	25	29	AZ254F12P
40	9.6	48.0	28	9	AU013446
41	9.6	48.0	28	9	AU013592
42	9.6	48.0	28	9	AU013668
43	9.6	48.0	29	28	AZ335197
C 44	9.6	48.0	29	29	TA71H09Q
45	9.6	48.0	30	28	AZ431599

#### ALIGNMENTS

RESULT 1  
AZ660469/c  
LOCUS  
DEFINITION  
1M0538M03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0538M03 R, genomic survey sequence.  
ACCESSION  
AZ660469  
VERSION  
AZ660469.1 GI:11797615  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 27)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R., 2003, Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

XX PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.  
 XX PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;  
 XX PI Picard FJ, Roy PH;  
 XX DR WPI; 2001-245006/25.  
 XX PT Nucleic acid sequences are used to generate universal probes and  
 XX PT primers which can be used to identify and detect the presence of algal,  
 XX PT archaeal, bacterial, fungal and parasitological species in a test sample -  
 XX PS Claim 21; Page 1456; 1580pp; English.  
 XX CC The present invention describes a method for generating a repertoire of  
 XX CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes  
 XX CC and/or primers are derived. The method comprises amplifying the nucleic  
 XX CC acids of determined algal, archaeal, bacterial, fungal and parasitological  
 XX CC species with a combination of defined primer pairs. The method can be  
 XX CC used for producing probes and/or primers for detecting one or more  
 XX CC related microorganisms e.g. algae, archaea, bacteria, fungi and  
 XX CC parasites, for universal detection and for specific and ubiquitous  
 XX CC detection and identification of an algal, archaeal, bacterial, fungal  
 XX CC and parasitological species, genus, family and group. A nucleic acid (I)  
 XX CC obtained using the method of the invention can be used for the universal  
 XX CC detection of any bacterium, fungus or parasite in a sample and for the  
 XX CC detection of at least one antimicrobial agent resistance gene or at  
 XX CC least one toxin gene. hexA nucleic acids are used for the specific and  
 XX CC ubiquitous detection and for identification of Streptococcus pneumoniae.  
 XX CC (I) can be used to design a therapeutic agent which is effective against  
 XX CC microorganisms. Microbial species or genus or family or phylum or group  
 XX CC which can be detected include Abiotrophia adiacens, Bordetella sp.,  
 XX CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,  
 XX CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp.,  
 XX CC Neisseria gonorrhoeae and Staphylococcus sp. Using DNA based tests  
 XX CC provides faster results than substrate specificity tests as results can  
 XX CC be determined in an hour and improved accuracy is also achieved.  
 XX CC AAH00010 to AAH002304 represent nucleotide sequences and primers/probes  
 XX CC which are given in the exemplification of the present invention.  
 XX CC Sequence 23 BP; 8 A; 6 C; 4 G; 5 T; 0 other;  
 XX CC Query Match 61.0%; Score 12.2; DB 22; Length 23;  
 XX CC Best Local Similarity 82.4%; Pred. No. 8.2e+03;  
 XX CC Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 XX CC 2 CATGCATGCATTACGTA 18  
 XX CC |||||  
 XX CC 3 CAAGCATGCATTATGCA 19  
 XX CC |||||  
 XX CC RESULT 15  
 XX CC ABX14112/c  
 XX CC ID ABX14112 standard; DNA; 24 BP.  
 XX CC AC ABX14112;  
 XX CC DT 25-FEB-2003 (first entry)  
 XX CC DE Human zinc finger protein 8.8 specific RT-PCR primer, #2.  
 XX CC KW Zinc finger protein 8.8; human; RT-PCR; ss; tumour; haemopathy;  
 XX CC KW human immunodeficiency virus; HIV; immunological disease; inflammation;  
 XX CC KW antagonist; reverse transcription; primer.  
 XX CC OS Homo sapiens.  
 XX CC PN CN1352050-A.  
 XX CC PD 05-JUN-2002.  
 XX CC PF 02-NOV-2000; 2000CN-0127133.

PR 02-NOV-2000; 2000CN-0127133.  
 XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
 XX PI Mao Y, Xie Y;  
 XX DR WPI; 2002-644445/70.  
 XX PT New polypeptide-human zinc finger protein 8.8 and polynucleotide for  
 XX PT encoding such polypeptide -  
 XX PS Example 2; Page 16 (disclosure); 32pp; Chinese.  
 XX CC The present invention discloses a novel human zinc finger protein 8.8,  
 XX CC polynucleotide coding for the polypeptide and method for producing this  
 XX CC polypeptide by using DNA recombination technology. The invention also  
 XX CC discloses the method for curing several diseases, such as malignant  
 XX CC tumour, haemopathy, human immunodeficiency virus (HIV) infection,  
 XX CC immunological diseases and various inflammations by using the  
 XX CC polypeptide. The invention also discloses an antagonist for resisting  
 XX CC said polypeptide and its therapeutic action and also discloses the  
 XX CC application of the polynucleotide for coding this novel zinc finger  
 XX CC protein 8.8. The sequence presented is the reverse transcription  
 XX CC (RT)-PCR primer, #2, which was used to isolate human zinc finger protein  
 XX CC 8.8 cDNA.  
 XX CC Sequence 24 BP; 5 A; 5 C; 9 G; 5 T; 0 other;  
 XX CC Query Match 61.0%; Score 12.2; DB 24; Length 24;  
 XX CC Best Local Similarity 82.4%; Pred. No. 8.2e+03;  
 XX CC Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 XX CC QY 1 GCATGCATGCATTACGT 17  
 XX CC |||||  
 XX CC Db 20 GCCTGCATGCATGACCT 4  
 XX CC |||||  
 XX CC Search completed: December 31, 2003, 15:08:16  
 XX CC Job time : 578.975 secs

PA (QUEE-) STATE QUEENSLAND DEPT PRIMARY IND.  
 XX  
 PI Graham MW, Rice RN, Murphy KM, Reed KC;  
 XX  
 XX WPI; 2001-596939/67.  
 DR  
 XX Genetic construct for generating transgenic animal cells and in gene  
 PT therapy of vertebrate animal, comprises nucleotide sequence identical  
 PT to endogenous target sequence in the genome of vertebrate animal cell  
 PT  
 XX  
 XX Example 19; Page 114; 176pp; English.  
 PS  
 XX The invention relates to a method of inducing, promoting or otherwise  
 CC facilitating a change in the phenotype of an animal cell or group of  
 CC animal cells. The modulation of phenotypic expression is conveniently  
 CC accomplished via genotypic manipulation through such means as reducing  
 CC translation of transcript to proteinaceous product. The ability to  
 CC induce, promote or otherwise facilitate the silencing of expressible  
 CC genetic sequences provides a means for modulating the phenotype in,  
 CC for example, the medical, veterinary and the animal husbandry  
 CC industries. Genetic construct comprising nucleotide sequence  
 CC substantially identical to target endogenous sequence of nucleotides  
 CC in the genome of a vertebrate animal cell, is useful for altering  
 CC the phenotype of a vertebrate animal cell, where the phenotype is  
 CC conferred or otherwise facilitated by the expression of an endogenous  
 CC gene, and also in the generation of animal cells. It is also useful  
 CC in gene therapy in a vertebrate animal (e.g. human, primate, livestock  
 CC animal, laboratory test animal or a murine species, avian species, fish  
 CC or reptile. The present sequence is a double-stranded DNA probe derived  
 CC from simian virus 40 (SV40) enhancer sequence and is used for  
 CC electromobility shift assay (EMSA) of Oct-factor proteins, N-Oct-1 and  
 CC N-Oct-3. This sequence is used in the co-suppression of Bn-2  
 CC transcription factor, which belongs to a class of Oct-factors, in WM96L  
 CC melanoma cells in vitro.  
 XX  
 SQ Sequence 23 BP; 8 A; 5 C; 5 G; 5 T; 0 other;  
 Query Match 61.0%; Score 12.2; DB 22; Length 23;  
 Best Local Similarity 82.4%; Pred. No. 8.2e+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 ATGCATGCATTACGTAC 19  
 Db ||||| |||||  
 20 ATGCATGCTTTCATAC 4  
 RESULT 13  
 AAH21016/c  
 ID AAD21016 standard; DNA; 23 BP.  
 XX  
 AC AAD21016;  
 XX  
 DT 15-JAN-2002 (first entry)  
 XX  
 DE Oct-dpm8, probe used for EMSA of Oct-factor proteins.  
 XX  
 KW Genetic silencing; medical industry; animal husbandry;  
 KW veterinary; gene therapy; electromobility shift assay; EMSA;  
 KW Oct-factor protein; N-Oct-1; N-Oct-3; probe; ds.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200170949-A1.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 16-MAR-2001; 2001WO-AU00297.  
 XX  
 PR 17-MAR-2000; 2000AU-0006363.  
 PR 24-JAN-2001; 2001AU-0002700.  
 XX  
 PA (BENI-) BENITEC AUSTRALIA LTD.

PA (QUEE-) STATE QUEENSLAND DEPT PRIMARY IND.  
 XX  
 PI Graham MW, Rice RN, Murphy KM, Reed KC;  
 XX  
 XX WPI; 2001-596939/67.  
 DR  
 XX Genetic construct for generating transgenic animal cells and in gene  
 PT therapy of vertebrate animal, comprises nucleotide sequence identical  
 PT to endogenous target sequence in the genome of vertebrate animal cell  
 PT  
 XX  
 XX Example 19; Page 114; 176pp; English.  
 PS  
 XX The invention relates to a method of inducing, promoting or otherwise  
 CC facilitating a change in the phenotype of an animal cell or group of  
 CC animal cells. The modulation of phenotypic expression is conveniently  
 CC accomplished via genotypic manipulation through such means as reducing  
 CC translation of transcript to proteinaceous product. The ability to  
 CC induce, promote or otherwise facilitate the silencing of expressible  
 CC genetic sequences provides a means for modulating the phenotype in,  
 CC for example, the medical, veterinary and the animal husbandry  
 CC industries. Genetic construct comprising nucleotide sequence  
 CC substantially identical to target endogenous sequence of nucleotides  
 CC in the genome of a vertebrate animal cell, is useful for altering  
 CC the phenotype of a vertebrate animal cell, where the phenotype is  
 CC conferred or otherwise facilitated by the expression of an endogenous  
 CC gene, and also in the generation of animal cells. It is also useful  
 CC in gene therapy in a vertebrate animal (e.g. human, primate, livestock  
 CC animal, laboratory test animal or a murine species, avian species, fish  
 CC or reptile. The present sequence is a double-stranded DNA probe used for  
 CC electromobility shift assay (EMSA) of Oct-factor proteins, N-Oct-1 and  
 CC N-Oct-3. This sequence is used in the co-suppression of Bn-2  
 CC transcription factor, which belongs to a class of Oct-factors, in WM96L  
 CC melanoma cells in vitro.  
 XX  
 SQ Sequence 23 BP; 9 A; 4 C; 6 G; 4 T; 0 other;  
 Query Match 61.0%; Score 12.2; DB 22; Length 23;  
 Best Local Similarity 82.4%; Pred. No. 8.2e+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 ATGCATGCATTACGTAC 19  
 Db ||||| |||||  
 20 ATGCATGCTTTCCTTAC 4  
 RESULT 14  
 AAH02033  
 ID AAH02033 standard; DNA; 23 BP.  
 XX  
 AC AAH02033;  
 XX  
 DT 24-JUL-2001 (first entry)  
 XX  
 DE S. pneumoniae pbpla gene detection nucleotide sequence SEQ ID NO:2026.  
 XX  
 KW Species specific; genus specific; family specific; probe; detection;  
 KW identification; algal; archaeal; bacterial; fungal; parasitological;  
 KW microorganism; diagnosis; translation elongation factor Tu; toxin;  
 KW translation elongation factor G; RecA recombinase; resistance;  
 KW catalytic subunit of proton-translocating ATPase; antimicrobial;  
 KW vaccine; primer; ss.  
 XX  
 OS Streptococcus pneumoniae.  
 XX  
 PN WO200123604-A2.  
 XX  
 PD 05-APR-2001.  
 XX  
 PF 28-SEP-2000; 2000WO-CA01150.  
 XX  
 PR 28-SEP-1999; 99CA-2283458.  
 PR 19-MAY-2000; 2000CA-2307010.



AD45370 standard; DNA; 20 BP.  
AD45370;  
27-DEC-2002 (first entry)  
Human MLH1 cDNA amplifying PCR primer, 5283.  
Human; DNA repair protein; therapeutic; cancer; therapy; immunogen;  
MLH1 protein; PCR; primer; ss.  
Homo sapiens.  
US6416984-B1.  
09-JUL-2002.  
06-JUN-1995; 95US-0468024.  
27-JAN-1994; 94US-0187757.  
16-MAR-1994; 94US-0210143.  
23-AUG-1994; 94US-0294312.  
25-JAN-1995; 95WO-US01035.  
(HUMA-) HUMAN GENOME SCI INC.  
Haseltine WA, Ruben SM, Wei Y, Adams MD, Fleischmann RD;  
Fraser CM, Fuldner RA, Kirkness EF, Rosen CA;  
WPI; 2002-634734/68.  
Novel isolated human DNA repair polypeptide useful for diagnosing,  
preventing or treating cancer, or for in vitro purposes related to  
scientific research, synthesis of DNA and manufacture of DNA vectors  
Disclosure; Column 61; 69pp; English.  
The present invention relates to novel human DNA repair proteins (e.g.  
MLH1, MLH3) and polynucleotides encoding such proteins. Sequences  
of the invention are useful for therapeutic purposes, e.g., for treating  
cancer, for diagnosing or preventing cancer, as an immunogen to produce  
antibodies or for in vitro purposes related to scientific research,  
synthesis of DNA and manufacture of DNA vectors. The present DNA sequence  
is a PCR primer which is used for amplifying human MLH1 cDNA.  
Sequence 20 BP; 7 A; 4 C; 5 G; 4 T; 0 other;  
Query Match 61.0%; Score 12.2; DB 24; Length 20;  
Best Local Similarity 82.4%; Pred. No. 8.1e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
3 ATGCATGCATTACGTAC 19  
|||||  
17 ATGCCTGCATTGTGTAC 1  
RESULT 11  
ABX12523/c  
ID ABX12523 standard; DNA; 21 BP.  
AC ABX12523;  
XX  
XX  
XX 10-MAY-2003 (first entry)  
XX  
XX Human mut L homologue 1 (HMLH1) sequencing primer #2.  
XX  
XX Human; DNA repair protein; HMLH1; human mut L homologue 1; cancer;  
XX lung cancer; prostate cancer; ovarian cancer; breast cancer;  
XX colon cancer; stomach cancer; DNA replication error;  
XX Genetic recombination error; hereditary susceptibility to cancer;  
XX cytostatic; gene therapy; sequencing; primer; ss.  
XX  
XX Homo sapiens.  
OS

XX US6482606-B1.  
XX  
XX 19-NOV-2002.  
XX  
XX 27-JAN-1994; 94US-0187757.  
XX  
XX 27-JAN-1994; 94US-0187757.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Adams MD, Fleischmann RD, Fraser CM, Fuldner RA, Kirkness EF;  
XX Haseltine WA, Rosen CA, Ruben S, Wei Y;  
XX WPI; 2003-298135/29.  
XX  
XX New human DNA mismatch repair polynucleotides and proteins, useful for  
XX diagnosing or treating cancers (e.g. lung, prostate, ovarian or breast  
XX cancer), or for correcting errors made during DNA replication and  
XX genetic recombination -  
XX  
XX Disclosure; Column 11-12; 28pp; English.  
XX  
XX The invention describes an isolated polynucleotide encoding a human DNA  
XX repair protein, which is designated human mut L homologue 1 (HMLH1). The  
XX DNA repair polynucleotide is useful for diagnostic or therapeutic  
XX purposes. The polynucleotide may be used in diagnosing or treating  
XX cancers, e.g. lung cancer, prostate cancer, ovarian cancer, breast  
XX cancer, colon cancer or stomach cancer. The DNA repair polynucleotide is  
XX particularly useful for correcting errors made during DNA replication and  
XX genetic recombination e.g. by gene therapy. The polynucleotide is  
XX particularly useful for diagnosing a hereditary susceptibility to  
XX cancer. This sequence represents a primer used to sequence a region of  
XX the DNA repair protein human mut L homologue 1 (HMLH1) gene in order to  
XX detect mutations in the gene.  
XX  
XX Sequence 21 BP; 8 A; 4 C; 5 G; 4 T; 0 other;  
XX  
XX Query Match 61.0%; Score 12.2; DB 25; Length 21;  
XX Best Local Similarity 82.4%; Pred. No. 8.1e+03;  
XX Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 3 ATGCATGCATTACGTAC 19  
|||||  
Db 18 ATGCCTGCATTGTGTAC 2  
RESULT 12  
AAD21015/c  
ID AAD21015 standard; DNA; 23 BP.  
XX  
XX AAD21015;  
XX  
XX 15-JAN-2002 (first entry)  
XX  
XX Oct-WT, SV40 probe used for EMSA of Oct-factor proteins.  
XX  
XX Genetic silencing; medical industry; animal husbandry; probe;  
XX veterinary; gene therapy; electrophoresis shift assay; EMSA;  
XX Oct-factor protein; N-Oct-1; N-Oct-3; simian virus 40; SV40; ds.  
XX  
XX Rhesus macaque polyoma virus.  
XX  
XX WO200170949-A1.  
XX  
XX 27-SEP-2001.  
XX  
XX 16-MAR-2001; 2001WO-AU00297.  
XX  
XX 17-MAR-2000; 2000AU-0006363.  
XX  
XX 24-JAN-2001; 2001AU-0002700.  
XX  
XX (BENI-) BENITEC AUSTRALIA LTD.  
XX  
XX

Probe #2 (AA046967) hybridises to, and is specific for, the 16S rRNA of S.pyogenes. Hybridisation was enhanced by the use of "helper probes" AA046971 and AA046972. The probe can be used alone or in a mix with other S.pyogenes-specific probes to distinguish S.pyogenes from closely related bacteria (i.e. other Streptococcus spp.).

Sequence 26 BP; 5 A; 8 C; 6 G; 7 T; 0 other;

Query Match 63.0%; Score 12.6; DB 14; Length 26;  
Best Local Similarity 78.9%; Pred. No. 5.2e+03;  
Matches 15; Conservative .0; Mismatches 4; Indels 0; Gaps 0;

2 CATGCATGCATTACGTACG 20  
||||| ||||| |||||  
3 CTTGCATGTATTAGGCACG 21

AAAL15194 standard; DNA; 27 BP.

AAAL15194;

04-SEP-2000 (first entry)

PCR primer for DNA downstream of tata.

Virulence protein; tata; tatB; tatC; tatE; mdoG; creC; yggN;  
eck1; iroD; iroC; iroE; md2; msi; vaccine; infection;  
Gram negative bacterium; PCR primer; ss.

Escherichia coli.

WO2000028038-A2.

18-MAY-2000.

09-NOV-1999; 99WO-GB03721.

09-NOV-1998; 98GB-0024569.  
09-NOV-1998; 98GB-0024570.  
17-DEC-1998; 98GB-0027814.  
17-DEC-1998; 98GB-0027815.  
17-DEC-1998; 98GB-0027816.  
17-DEC-1998; 98GB-0027818.  
13-JAN-1999; 99GB-0000708.  
13-JAN-1999; 99GB-0000710.  
13-JAN-1999; 99GB-0000711.  
28-JAN-1999; 99GB-0001915.

(MICR-) MICROSCIENCE LTD.

Crooke HR, Clarke EE, Everest PH, Dougan G, Holden DW, Shea JE;  
Feldman RG;

WPI; 2000-376550/32.

Peptide encoded by an operon including genes from Escherichia coli for screening potential drugs, detecting virulence and treating conditions associated with infection by a Gram negative bacterium -

Example 6; Page 10; 122pp; English.

PCR primers AAAL15193-94 were used to amplify DNA downstream of tata. The specification describes virulence proteins which are encoded by an operon including tata, tatB, tatC, tatE, mdoG, creC, recG, yggN, eck1, iroD, iroC, iroE, md2 or msi-16 genes obtained from Escherichia coli K1. The virulence proteins and polynucleotides, and their vaccines are useful for screening potential drugs, for the detection of virulence, and for treating or preventing conditions associated with infection by a Gram negative bacterium particularly Escherichia coli.

```

SQ Sequence 27 BP; 8 A; 10 C; 4 G; 5 T; 0 other;

Query Match          63.0%; Score 12.6; DB 21; Length 27;
Best Local Similarity 78.9%; Pred. No. 5.2e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CATGCATGCATTACGTACG 20
Db 1 CATGCATGCATCCATATG 19

RESULT 9
AAAT74107
XX ID AAA74107 standard; DNA; 20 BP.
XX AC AAA74107;
XX DT 29-NOV-2000 (first entry)
XX DE Forward PCR primer for loblolly pine locus RIPPT658.
XX KW PCR primer; loblolly pine; Simple Sequence Repeat; SSR;
XX KW microsatellite DNA repeat; genetic marker; mapping; inheritance study;
XX KW population genetics study; plant breeding programme; ss.
XX OS Pinus taeda.
XX OS WO200042210-A2.
XX PN 20-JUL-2000.
XX PD 06-JAN-2000; 2000WO-US00325.
XX PF 15-JAN-1999; 99US-0232884.
XX PR 19-JAN-1999; 99US-0232785.
XX XX
XX (INTO ) INT PAPER CO.
XX PA (ECHT/) ECHT C S.
XX PA (NELS/) NELSON C D.
XX PA (USDA ) US SEC OF AGRIC.
XX XX
XX ECHT CS, Nelson CD;
XX WPI; 2000-482836/42.
XX XX
XX PT Polynucleotide having simple sequence repeat useful as markers in
XX PT plants for genetic characterization e.g. genetic mapping study, an
XX PT inheritance study of a commercially important trait in a plant breeding
XX PT program -
XX XX
XX Claim 6; Page 23; 57pp; English.
XX XX
XX CC The present invention relates to loblolly pine polynucleotides with one
XX CC or more Simple Sequence Repeats (SSRs) (see AAA74205-A74322). SSRs are
XX CC also known as microsatellite DNA repeats. The SSRs are useful as genetic
XX CC markers for genetic mapping, population genetics studies and inheritance
XX CC studies in various plant breeding programmes. The present sequence is a
XX CC PCR primer used for detecting the presence of a SSR locus in a pine
XX CC genomic DNA sample.
XX XX
SQ Sequence 20 BP; 7 A; 4 C; 3 G; 6 T; 0 other;

Query Match          61.0%; Score 12.2; DB 21; Length 20;
Best Local Similarity 82.4%; Pred. No. 8.1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TGCATGCATTACGTACG 20
Db 1 TGCATGCATTACAAATG 17

RESULT 10
AAAT45370/C

```

and comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY-3'. The central CpG motif is unmethylated, and the oligonucleotides have phosphorothioate linkages which make them more resistant to degradation. The invention also relates to an oligonucleotide delivery complex comprising an oligonucleotide of the invention and a targeting agent, and a pharmaceutical composition comprising the oligonucleotide delivery complex. The oligonucleotides are able to induce either a cell-mediated (T-cell) response or a humoral (B-cell, antibody) response, with oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3' being able to induce a humoral response. It is thought that after administration, the oligonucleotide acts on antigen-presenting cells (e.g., macrophages and dendritic cells), which then release cytokines, leading to activation of natural killer (NK) cells. A cell-mediated or humoral response can then occur by activation of T- or B-cells. The induction of an immune response is useful for treating, preventing or ameliorating an allergic reaction (preferably asthma), or an infection, where an immunogenic CpG oligonucleotide is administered either alone or in combination with an anti-allergic agent or anti-infectious agent. The allergic conditions which may be treated include eczema, allergic rhinitis, hayfever, urticaria, food allergies and other atopic conditions, and the infections which may be treated include viral, bacterial, fungal and protozoal infections such as tuberculosis, AIDS, leishmania and schistosomiasis. Immune response induction may also be used in the treatment of an autoimmune disorder (e.g., lupus erythematosus, rheumatoid arthritis and multiple sclerosis), a disease associated with immune system deficiency, and symptoms resulting from exposure to an agent of biological warfare. An immunogenic CpG oligonucleotide, either alone or in combination with an anti-cancer agent, is useful for treating solid tumour cancer. The induction of an immune response is used in antisense therapy and to improve the efficacy of a vaccine. The oligonucleotide is preferably administered to lymphocytes *ex vivo*, producing activated lymphocytes which are then administered to the host. The present sequence represents an immunogenic CpG oligodeoxynucleotide of the invention.

Sequence 17 BP; 8 A; 3 C; 3 G; 3 T; 0 other;

Query Match 65.0%; Score 13; DB 22; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCATGCGATGCATT 13  
|||||||  
13 GCATGCGATGCATT 1

RESULT 6  
AAQ46523/c  
ABK46523 standard; DNA; 17 BP.

ABK46523;

05-JUN-2002 (first entry)

Immunostimulatory unmethylated CpG oligodeoxynucleotide #113.

unmethylated CpG; oligodeoxynucleotide; ODN; virucide; vaccine;  
Paramyxoviridae; F protein; respiratory syncytial virus; RSV;  
viral bronchiolitis; pneumonia; infectious pulmonary disease;  
bronchopulmonary dysplasia; congenital heart condition; ss.

Synthetic.

WO200211761-A2.

14-FEB-2002.

09-AUG-2001; 2001WO-US41633.

10-AUG-2000; 2000US-224011P.

01-SEP-2000; 2000US-229307P.

XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.  
PA Mond JJ, Prince G, Klinman DM;  
PI WPI; 2002-227118/28.  
DR Vaccine for immunising patient against respiratory syncytial virus, has  
XX epitopes of paramyxoviridae F protein, and cytosine followed by guanine  
PT linked by phosphate bond-oligodeoxynucleotides -  
XX Claim 4; Page 9; 30pp; English.

XX The invention describes a vaccine comprising one or more epitopes of a  
CC paramyxoviridae F protein, and one or more CpG (cytosine followed by  
CC guanine linked by phosphate bond)-oligodeoxynucleotides (ODNs). The  
CC vaccine is useful for vaccinating a patient especially against viruses  
CC of the paramyxoviridae family e.g. respiratory syncytial virus (RSV),  
CC the primary cause of viral bronchiolitis and pneumonia in infants and  
CC children, and infectious pulmonary disease in infants. RSV has been  
CC particularly implicated in death of infants that are premature, have  
CC bronchopulmonary dysplasia, or congenital heart conditions. This  
CC sequence represents an oligodeoxynucleotide that can be used in the  
CC creation of the vaccine.

XX Sequence 17 BP; 8 A; 3 C; 3 G; 3 T; 0 other;

Query Match 65.0%; Score 13; DB 24; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATGCGATGCATT 13  
|||||||  
DB 13 GCATGCGATGCATT 1

RESULT 7

AAQ46972  
ID AAQ46972 standard; DNA; 26 BP.

XX AAQ46972;

XX 25-JAN-1994 (first entry)

XX Helper Probe #7 to detect Streptococcus pyogenes rRNA.

XX group A beta-haemolytic Streptococcus; S. pyogenes; ribosomal RNA;  
XX respiratory tract infection; sinusitis; pharyngitis; meningitis;  
XX tonsillitis; septicemia; pyoderma; endocarditis; impetigo;  
XX helper probe; ss.

XX Synthetic.

XX US5232831-A.

XX 03-AUG-1993.

XX 28-JUN-1991; 91US-0720586.

XX 28-JUN-1991; 91US-0720586.

XX (GEPR-) GEN PROBE INC.

XX Hammond PW, Milliman CL;

XX WPI; 1993-257892/32.

XX New nucleotide polymers used as probes for detection of  
PT Streptococcus pyogenes - capable of distinguishing it from  
PT related species when used alone or as a mix

XX Claim 7; Column 13; 9pp; English.

XX Primers DK15 (AAT29050) and DK16 (AAT29051) were used for the PCR  
 CC amplification of the ribosome binding site and signal peptide  
 CC coding regions of the *Bacillus stearothermophilus* maltogenic  
 CC alpha-amylase gene in pDN520. The PCR product was used to  
 CC construct pPEF1, which also carried a gene (AAT29043) for Oerskovia  
 CC xanthineolytica beta-1,3-glucanase (AAK97362). Transformation of  
 CC *Bacillus subtilis* strain DN1895 or protease-deficient strain ToC46  
 CC allowed prodn. of the Oerskovia lytic enzyme.  
 XX  
 SQ Sequence 28 BP; 10 A; 5 C; 8 G; 5 T; 0 other;  
 Query Match 68.0%; Score 13.6; DB 17; Length 28;  
 Best Local Similarity 80.0%; Pred. No. 1.6e+03;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 1 GCATGATGCATTACGTACG 20  
 4 GCAAGCTTGCAATACGAAG 23  
 RESULT 4  
 AAC09645/C  
 AAC09645 standard; DNA; 17 BP.  
 AAC09645;  
 26-SEP-2001 (first entry)  
 Immunoreactive CpG sequence-containing oligonucleotide #95.  
 CpG sequence; immune response; non-B cell activation; interferon gamma;  
 IFN-gamma; humoral; antibody production; interleukin-6 production;  
 therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;  
 bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;  
 coryza; hay fever; urticaria; hives; food allergy; atopic condition;  
 hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;  
 lupus erythematosus; rheumatoid arthritis; multiple sclerosis;  
 schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;  
 Leishmania; Ebola; Anthrax; Listeria; ss.  
 Synthetic.  
 WO200151500-A1.  
 19-JUL-2001.  
 12-JAN-2001; 2001WO-US01122.  
 14-JAN-2000; 2000US-0176115.  
 (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 Klinman D, Ishii K, Verthelyi D;  
 WPI; 2001-442129/47.  
 Oligodeoxynucleotides for inducing an immune response to treat and  
 prevent an allergic reaction, cancer, an autoimmune disorder and  
 symptoms resulting from exposure to bio-warfare agents, comprise  
 multiple CpG sequences -  
 Claim 5; Page 43; 48pp; English.  
 AAC09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10  
 nucleotides comprising multiple CpG sequences, where one of the CpG  
 sequences is different from another of the multiple CpG sequences.  
 The ODN are useful for inducing an immune response, preferably a cell-  
 mediated immune response, involving non-B cell activation, interferon  
 gamma (IFN-gamma) production or a humoral immune response involving B  
 cell activation, antibody and interleukin-6 production in a host, for  
 treating, preventing or ameliorating an allergic reaction, e.g. asthma,  
 cancer, e.g. solid tumour cancer, a disease associated with the immune

CC system e.g. autoimmune disorder or an immune system deficiency, infection  
 CC or a symptom resulting from exposure to bio-warfare agent in a human. The  
 CC induction of immune response improves the efficacy of a vaccine and is  
 CC used in antisense therapy. The ODN are useful for treating, preventing or  
 CC ameliorating allergic reactions, including eczema, allergic rhinitis or  
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies  
 CC and other atopic conditions, for improving the efficacy of vaccines  
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and  
 CC malaria, for treating immune system deficiencies, e.g. lupus  
 CC erythematosus and autoimmune diseases such as rheumatoid arthritis and  
 CC multiple sclerosis, infections including Francisella, schistosomiasis,  
 CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and  
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,  
 CC Anthrax and Listeria.  
 XX  
 SQ Sequence 17 BP; 8 A; 3 C; 3 G; 3 T; 0 other;  
 Query Match 65.0%; Score 13; DB 22; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 GCATGATGCATT 13  
 13 GCATGATGCATT 1  
 QY  
 Db  
 RESULT 5  
 AAC0675/C  
 ID AAC0675 standard; DNA; 17 BP.  
 AAC0675;  
 14-FEB-2001 (first entry)  
 Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:95.  
 CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;  
 immunogenic; cytokine release; natural killer cell; NK cell activation;  
 cell-mediated immune response; T-cell response; humoral response;  
 B-cell response; antibody production; immune response induction;  
 vaccine; allergy; asthma; infection; bacterial; viral; fungal; protozoal;  
 parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;  
 rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;  
 immune deficiency; biological warfare agent; cytostatic; antiarthritic;  
 antimicrobial; antiallergic; protozoicide; tuberculostatic;  
 antiasthmatic; dermatological; phosphorothioate; ss.  
 Synthetic.  
 WO200061151-A2.  
 19-OCT-2000.  
 12-APR-2000; 2000WO-US09839.  
 12-APR-1999; 99US-0128898.  
 (KLIN/) KLINMAN D.  
 PA (ISHI/) ISHII K.  
 PA (VERT/) VERTHELYI D.  
 PI Klinman D, Ishii K, Verthelyi D;  
 DR WPI; 2001-006880/01.  
 Novel oligonucleotides useful for the prevention and treatment of  
 PT allergies, cancer, and autoimmune disorders and for ameliorating  
 PT symptoms resulting from exposure to a bio-warfare agent -  
 XX  
 PS Claim 4; Page 38; 46pp; English.  
 CC The invention relates to novel immunogenic CpG oligodeoxynucleotides  
 CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long

PT DNA fragments useful for increasing p53 activity in a cell and reducing  
 PT susceptibility to UV-induced hyperproliferative diseases -  
 XX  
 PS Claim 11; Page 30; 44pp; English.

XX AA210692-97 represent DNA fragments that are used for increasing p53  
 CC activity in a cell. The oligonucleotides are UV mimetics and  
 CC protect cells against subsequent exposure to UV-irradiation or  
 CC chemicals. The oligonucleotides are useful for increasing p53 activity  
 CC in a cell, reducing the susceptibility to UV-induced hyperproliferative  
 CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic  
 CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging  
 CC and reducing susceptibility to skin cancer.

XX Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.83;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCATGCGATTCATTACGTACG 20  
 1 GCATGCGATTCATTACGTACG 20

RESULT 2  
 AAS14912  
 ID AAS14912 standard; DNA; 20 BP.

AAS14912;

14-FEB-2002 (first entry)

Melanogenesis associated oligonucleotide #8.

Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;  
 anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;  
 immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;  
 tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;  
 carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;  
 conjunctivitis; allergic rhinitis; vitiligo; se.

Synthetic.

Key Location/Qualifiers  
 modified\_base 1  
 /\*tag= a  
 /mod\_base= g  
 /note= "Phosphorylated"

WO200174342-A2.

11-OCT-2001.

30-MAR-2001; 2001WO-US10162.

31-MAR-2000; 2000US-0540843.

(UYBO-) UNIV BOSTON.

Gilchrest BA, Yaar M, Eller M;

WPI; 2001-626338/72.

Inhibiting proliferation of epithelial cells, useful e.g. for treating  
 PT carcinoma, using specific oligonucleotides that mimic the effects of  
 PT ultra-violet light -

Claim 1; Page 39; 74pp; English.

XX The invention describes inhibition of mammalian epithelial cell  
 CC proliferation by treating cells with at least one oligonucleotide, or  
 CC its fragment. The compounds, which have cytostatic, anti-allergic,

CC anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and  
 CC immunosuppressive activities, function as 'ultra-violet mimics' to induce  
 CC DNA repair processes (or a protective response to later exposure to  
 CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer  
 CC or a tumour necrosis factor inhibitor. Probably they mimic products of  
 CC DNA damage, or processed DNA-damage intermediates, by inducing the p53  
 CC pathway, resulting in transient arrest of cell growth, allowing more time  
 CC for DNA repair to occur before cell division takes place. The method is  
 CC especially used to treat carcinoma but may also be used to treat other  
 CC hyperproliferative states (e.g. psoriasis or precancerous conditions);  
 CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat  
 CC allergically mediated inflammation (atopic or contact dermatitis,  
 CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in  
 CC cells caused by radiation or chemicals; increase melanin production  
 CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to  
 CC promote apoptosis in epithelial cells that contain damaged DNA. Also  
 CC oligonucleotides that contain non-hydrolyzable backbones are used to  
 CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This  
 CC sequence is melanogenesis associated oligonucleotide #8, a synthetic  
 CC peptide that resembles the fragment excised during excision repair of  
 CC Thymine dimers and one of the oligonucleotides used to inhibit mammalian  
 CC epithelial cell proliferation, described in the method of the invention.

XX Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 20; DB 23; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.83;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATGCGATTCATTACGTACG 20  
 Db 1 GCATGCGATTCATTACGTACG 20

RESULT 3

AAT29051  
 ID AAT29051 standard; DNA; 28 BP.

AC AAT29051;

DT 03-OCT-1996 (first entry)

XX Maltogenic alpha-amylase signal peptide PCR primer DK16.

XX Beta-1,3-glucanase; Cellulomonas cellulans; Bacillus subtilis;  
 KW lytic enzyme; beta-glucan degradation; cell wall lysis;  
 KW pigment; colorant; flavour; yeast extract; protoplast;  
 KW Oerskovia xanthineolytica; polymerase chain reaction; primer;  
 KW PCR; alpha-amylase; signal peptide; Bacillus stearothermophilus;  
 KW ss.

OS Synthetic.

XX WO9612013-A1.

PN 25-APR-1996.

XX 16-OCT-1995; 95WO-DK00414.

XX 14-OCT-1994; 94DK-0001192.

XX (NOVO) NOVO-NORDISK AS.

PI Asenjo JA, Diers I, Ferrer P, Halkier T, Hedegaard L;

PI Savva D;

XX WPI; 1996-222000/22.

XX DNA construct encoding enzyme with beta-1,3-glucanase activity -  
 PT useful for modifying or degrading beta-glucan contg. material and in  
 PT the prepn. of e.g. food colourants, flavourings and yeast extracts  
 XX Example 7; Page 22; 60pp; English.

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 11:36:21 ; Search time 577.975 Seconds  
(without alignments)  
93.410 Million cell updates/sec

Title: US-09-540-843-8

Perfect score: 20

Sequence: 1 gcattgcatcattacgtacg 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 2101872

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	20	100.0	20	AAZ10697	Oligonucleotide se
2	20	100.0	20	AAZ14912	Melanogenesis asso
3	13.6	68.0	28	AAT29051	Maltogenic alpha-a
C 4	13	65.0	17	AAZ09645	Immunoreactive Cpg
C 5	13	65.0	17	AAZ08675	Immunoreactive Cpg oi
C 6	13	65.0	17	ABK46523	Immunostimulatory
7	12.6	63.0	26	AAQ46972	Helper Probe #7 to
8	12.6	63.0	27	AAA15194	PCR primer for DNA

9	12.2	61.0	20	21	AAA74107	Forward PCR primer
C 10	12.2	61.0	20	24	AAZ45370	Human MLH1 cDNA am
C 11	12.2	61.0	21	25	ABX12523	Human mut L homolo
C 12	12.2	61.0	23	22	AAZ21015	Oct-WT, SV40 probe
C 13	12.2	61.0	23	22	AAZ21016	Oct-dpm8, probe us
C 14	12.2	61.0	23	22	AAH2033	S. pneumoniae pbpl
C 15	12.2	61.0	24	24	ABQ02027	Human zinc finger
C 16	12.2	61.0	24	24	ABQ14112	Oligonucleotide ad
C 17	12.2	61.0	24	24	ABQ07960	Oligonucleotide ad
C 18	12.2	61.0	24	24	ABQ08001	Oligonucleotide ad
C 19	12	60.0	12	19	AAV11148	Oligonucleotide #1
C 20	12	60.0	15	21	AAZ92016	Isotachophoresis m
C 21	12	60.0	15	21	AAZ92016	Isotachophoresis m
C 22	12	60.0	22	22	AAH22273	OX40 reverse PCR p
C 23	12	60.0	24	24	ABA99666	Human monoclonal a
C 24	12	60.0	24	24	ABT88044	Capture oligonucle
C 25	12	60.0	24	24	ABT88045	Capture oligonucle
C 26	12	60.0	26	13	AAQ24823	Primer EBA-D. Syn
C 27	12	60.0	29	21	AAZ88292	Oligonucleotide SE
C 28	12	60.0	29	21	AAZ88292	Oligonucleotide SE
C 29	11.8	59.0	17	20	AAV93571	Human B-raf subst
C 30	11.8	59.0	18	21	AAZ94246	Vector pZLL revers
C 31	11.8	59.0	18	24	ABK46375	Vector forward pri
C 32	11.8	59.0	20	22	ABA03463	Green filamentous
C 33	11.8	59.0	22	22	AAH01139	S. pneumoniae pbpl
C 34	11.8	59.0	23	22	AAZ32383	NAAT related fluor
C 35	11.8	59.0	24	24	ABQ03320	Oligonucleotide ad
C 36	11.8	59.0	26	24	AAI68073	2-methyl-epothilon
C 37	11.8	59.0	29	22	AAZ06023	Yeast cystathionin
C 38	11.8	59.0	29	22	AAZ24346	Human papillomavir
C 39	11.8	59.0	30	25	AAZ54428	E7 mRNA PCR primer
C 40	11.8	59.0	30	25	ABS58064	Rhodobacter sphaer
C 41	11.8	59.0	30	25	ABS58066	Rhodobacter sphaer
C 42	11.8	59.0	30	25	ABS58068	Rhodobacter sphaer
C 43	11.8	59.0	30	25	ABS58074	Rhodobacter sphaer
C 44	11.6	58.0	18	21	AAZ45519	PCR primer used to
C 45	11.6	58.0	18	22	AAZ62258	Primer derived fro

#### ALIGNMENTS

RESULT 1  
AAZ10697  
ID AAZ10697 standard; DNA; 20 BP.  
XX AAZ10697;  
AC AAZ10697;  
XX 23-NOV-1999 (first entry)  
DT 23-NOV-1999 (first entry)  
XX Oligonucleotide sequence that increases p53 activity in a cell.  
DE Oligonucleotide sequence that increases p53 activity in a cell.  
XX p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;  
KW UV-induced hyperproliferative disease; psoriasis; vitiligo;  
KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;  
KW skin cancer; ss.  
XX Synthetic.  
OS Synthetic.  
XX GB2336157-A.  
PN GB2336157-A.  
XX 13-OCT-1999.  
PD 13-OCT-1999.  
XX 24-MAR-1999; 99GB-0006758.  
PF 24-MAR-1999; 99GB-0006758.  
XX 26-MAR-1998; 98US-0048927.  
PR 26-MAR-1998; 98US-0048927.  
XX (UYBO-) UNIV BOSTON.  
PA (UYBO-) UNIV BOSTON.  
XX Gilchrist BA, Year M, Eller M;  
PI Gilchrist BA, Year M, Eller M;  
XX WPI; 1999-543520/46.  
DR WPI; 1999-543520/46.  
XX



REFERENCE 1 (bases 1 to 15)  
AUTHORS Choudhary,G., Hannenberger,K., Kuekes,P.J., Lichtenwalter,K. and Hancock,W.S.  
TITLE Method of binding a plurality of chemicals on a substrate by electrophoretic self-assembly  
JOURNAL Patent: US 6107038-A 1 22-AUG-2000;  
FEATURES Location/Qualifiers  
source 1..15  
BASE COUNT 4 a 3 c 3 g 4 t 1 others  
ORIGIN /organism="unknown"

Query Match 60.0%; Score 12; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
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1 GCATGCATGCAT 12  
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13 GCATGCATGCAT 2

RESULT 15  
AX133943  
FOCUS 15 bp DNA linear PAT 15-MAY-2001  
DEFINITION Sequence 2 from Patent WO0127327.  
ACCESSION AX133943  
VERSION AX133943.1 GI:14139884  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Brennan,T.M., Chatelain,F. and Berninger,M.  
TITLE Method and apparatus for performing large numbers of reactions using array assembly  
JOURNAL Patent: WO 0127327-A 2 19-APR-2001;  
FEATURES Protogene Laboratories, Inc. (US)  
Location/Qualifiers  
source 1..15  
BASE COUNT 4 a 4 c 4 g 3 t  
ORIGIN /organism="Homo sapiens"  
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Job time : 1844.27 secs



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Best Local Similarity	82.4%;	Pred. No. 1.6e+05;			
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QY	2	CATGTCGATTCACGTA 18			
Db	3	CAAGCATGCAATATGCA 19			
RESULT 10					
AX445579/c					
LOCUS	AX445579	24 bp	DNA	linear	PAT 03-JUL-2002
DEFINITION	Sequence 2034 from Patent WO216649.				
ACCESSION	AX445579				
VERSION	AX445579.1	GI:21692860			
KEYWORDS	synthetic construct				
ORGANISM	synthetic construct				
REFERENCE	1	artificial sequences.			
AUTHORS	Gunderson, K.				
TITLE	Probes and decoder oligonucleotides				
JOURNAL	Patent: WO 0216649-A 2034 28-FEB-2002;				
FEATURES	Illumina, Inc. (US)				
source	Location/Qualifiers				
BASE COUNT	2 a	7 c	8 g	7 t	
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Query Match	61.0%;	Score 12.2;	DB 6;	Length 24;	
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QY	4	TGCATGCATTCAGTACG 20			
Db	22	TGCAGGCACTACGGACG 6			
RESULT 11					
AX203427					
LOCUS	AX203427	30 bp	DNA	linear	PAT 20-JUN-2002
DEFINITION	Sequence 43 from patent US 6365376.				
ACCESSION	AX203427				
VERSION	AX203427.1	GI:21499813			
KEYWORDS	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1	(bases 1 to 30)			
AUTHORS	Brzostowicz, P.C. and Rouviere, P.E.				
TITLE	Genes and enzymes for the production of adipic acid intermediates				
JOURNAL	Patent: US 6365376-A 43 02-APR-2002;				
FEATURES	Location/Qualifiers				
source	1. .30				
BASE COUNT	9 a	7 c	10 g	4 t	
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Query Match	61.0%;	Score 12.2;	DB 6;	Length 30;	
Best Local Similarity	82.4%;	Pred. No. 1.6e+05;			
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Db	9	GGAGGCATGCATGACGT 25			
RESULT 12					
AX236687					
LOCUS	AX236687	30 bp	DNA	linear	PAT 20-DEC-2002
DEFINITION	Sequence 43 from patent US 6465224.				
ACCESSION	AX236687				
VERSION	AX236687.1	GI:27280788			
KEYWORDS	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1	(bases 1 to 30)			
AUTHORS	Brzostowicz, P.C. and Rouviere, P.E.				
TITLE	Oxidation of a cyclohexanone derivative using a Brevibacterium				
JOURNAL	Patent: US 6465224-A 43 15-OCT-2002;				
FEATURES	cyclohexanone monooxygenase				
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Db	9	GGAGGCATGCATGACGT 25			
RESULT 13					
ARI06386					
LOCUS	ARI06386	15 bp	DNA	linear	PAT 14-FEB-2001
DEFINITION	Sequence 1 from patent US 6107038.				
ACCESSION	ARI06386				
VERSION	ARI06386.1	GI:12820916			
KEYWORDS	Unknown.				
ORGANISM					

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Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
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Db 1 GCATGCATGCATTACGTACG 20

RESULT 2
LOCUS AX194495/c 28 bp DNA linear PAT 29-SEP-1997
DEFINITION Synthetic oligonucleotide.
ACCESSION E06768
VERSION E06768.1 GI:2174950
KEYWORDS JP 1994046874-A/10.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 28)
AUTHORS Mori,M., Okuno,T. and Furusawa,I.
TITLE EXOGENOTE IN PLANT CELL AND PRODUCTION OF ITS PRODUCT
JOURNAL Patent: JP 1994046874-A 10 22-FEB-1994;
NIPPON NOH YAKU CO LTD
COMMENT OS Artificial gene
OC Artificial sequence; Genes.
PN JP 1994046874-A/10
PD 22-FEB-1994
PF 27-APR-1993 JP 199312189
PR 28-APR-1992 JP 92P 152593
PI MORI MASAYUKI, OKUNO TETSUO, FURUSAWA IMAO
PC C12P21/02,A01H5/00,C12N5/10,C12N15/11,C12N15/83,(C12N15/11, PC
C12R1:92);
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CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No.
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9 a 6 c 5 g 8 t

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Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 20 CATGCATGCATTCCG 6

RESULT 3
LOCUS I12026/c 28 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 10 from Patent US 5418153.
ACCESSION I12026
VERSION I12026.1 GI:909467
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

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9 a 6 c 5 g 8 t

BASE COUNT
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Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 20 CATGCATGCATTCCG 6

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LOCUS AX194495/c 17 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 95 from Patent WO0151500.
ACCESSION AX194495
VERSION AX194495.1 GI:15385151
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Klinman,D., Ishii,K. and Verthelyi,D.
TITLE Oligodeoxynucleotide and its use to induce an immune response
JOURNAL Patent: WO 0151500-A 95 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
FEATURES
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Location/Qualifiers
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/db_xref="taxon:32630"
/note="Synthetic DNA"
8 a 3 c 3 g 3 t

BASE COUNT
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Best Local Similarity 100.0%; Pred. No. 6.1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 13 GCATGCATGCATT 1

RESULT 5
LOCUS AX465445/c 17 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 113 from Patent WO0211761.
ACCESSION AX465445
VERSION AX465445.1 GI:21899808
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Mond,J.J., Prince,G. and Klinman,D.M.
TITLE Vaccine against RSV
JOURNAL Patent: WO 0211761-A 113 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
FEATURES
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/mol_type="genomic DNA"
10 a 3 c 3 g 3 t

BASE COUNT
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Qy 1 GCATGCATGCATT 13
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Db 13 GCATGCATGCATT 1
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
444.364 Million cell updates/sec

Title: US-09-540-843-8

Perfect score: 20

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Scoring table: IDENTITY NUC

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Total number of hits satisfying chosen parameters: 1010434

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 2: gb\_hg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	20	100.0	20	6	AX268760	AX268760 Sequence
2	13.4	67.0	28	6	E06768	E06768 Synthetic o
3	13.4	67.0	28	6	I12026	I12026 Synthetic 10
4	13	65.0	17	6	AX194495	AX194495 Sequence
5	13	65.0	17	6	AX465445	AX465445 Sequence
6	12.2	61.0	20	6	AR217681	AR217681 Sequence
7	12.2	61.0	20	6	BD181114	BD181114 Human DNA
8	12.2	61.0	21	6	AR255705	AR255705 Sequence
9	12.2	61.0	23	6	AX111293	AX111293 Sequence
10	12.2	61.0	24	6	AX445579	AX445579 Sequence
11	12.2	61.0	30	6	AR203427	AR203427 Sequence
12	12.2	61.0	30	6	AR236687	AR236687 Sequence
13	12	60.0	15	6	AR106386	AR106386 Sequence
14	12	60.0	15	6	AR106386	AR106386 Sequence
15	12	60.0	15	6	AX133943	AX133943 Sequence
16	12	60.0	15	6	AX133943	AX133943 Sequence
17	12	60.0	20	6	AX683917	AX683917 Sequence
18	12	60.0	23	6	A83415	A83415 Sequence 1
19	12	60.0	24	6	AX291062	AX291062 Sequence
20	12	60.0	24	6	BD133367	BD133367 Amino aci
21	11.8	59.0	18	6	AR213170	AR213170 Sequence
22	11.8	59.0	18	6	AX464822	AX464822 Sequence
23	11.8	59.0	20	6	AX300892	AX300892 Sequence
24	11.8	59.0	22	6	AX110397	AX110397 Sequence
25	11.8	59.0	24	6	AX446872	AX446872 Sequence
26	11.8	59.0	26	6	AX403021	AX403021 Sequence
27	11.6	58.0	18	6	AX010676	AX010676 Sequence
28	11.6	58.0	18	6	AX039554	AX039554 Sequence
29	11.6	58.0	20	6	AR065159	AR065159 Sequence
30	11.6	58.0	20	6	AR136789	AR136789 Sequence
31	11.6	58.0	20	6	AR217384	AR217384 Sequence
32	11.6	58.0	20	6	I23329	I23329 Sequence 3
33	11.6	58.0	20	6	I27356	I27356 Sequence 3
34	11.6	58.0	22	6	AR164805	AR164805 Sequence
35	11.6	58.0	22	6	AX189772	AX189772 Sequence
36	11.6	58.0	23	6	AR149923	AR149923 Sequence
37	11.6	58.0	24	6	AR148349	AR148349 Sequence
38	11.6	58.0	24	6	AR153693	AR153693 Sequence
39	11.6	58.0	24	6	AR215094	AR215094 Sequence
40	11.6	58.0	24	6	AX289339	AX289339 Sequence
41	11.6	58.0	27	6	AR106598	AR106598 Sequence
42	11.6	58.0	27	6	AX077732	AX077732 Sequence
43	11.6	58.0	28	6	AR221944	AR221944 Sequence
44	11.6	58.0	28	6	E06768	E06768 Synthetic o
45	11.6	58.0	28	6	I12026	I12026 Sequence 10

## ALIGNMENTS

RESULT 1	AX268760	Sequence 8 from Patent WO0174342.	20 bp	DNA	Linear	PAT 29-OCT-2001
LOCUS	AX268760	Sequence 8 from Patent WO0174342.	20 bp	DNA	Linear	PAT 29-OCT-2001
DEFINITION	AX268760	Sequence 8 from Patent WO0174342.	20 bp	DNA	Linear	PAT 29-OCT-2001
ACCESSION	AX268760	Sequence 8 from Patent WO0174342.	20 bp	DNA	Linear	PAT 29-OCT-2001
VERSION	AX268760.1	GI:16541832				
KEYWORDS		synthetic construct				
SOURCE		synthetic construct				
ORGANISM		artificial sequences.				
REFERENCE	1					
AUTHORS		Gilchrest,B.A., Yaar,M. and Eller,M.				
TITLE		Use of locally applied dna fragments				
JOURNAL		Patent: WO 0174342-A 8 11-OCT-2001;				
		TRUSTEES OF BOSTON UNIVERSITY (US)				



APPLICANT: Ribozyne Pharmaceuticals Inc.  
 TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection

FILE REFERENCE: MEH800-801-F  
 CURRENT APPLICATION NUMBER: US/09/817,879

CURRENT FILING DATE: 2001-03-26  
 NUMBER OF SEQ ID NOS: 9703

SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 4624

LENGTH: 13  
 TYPE: RNA

ORGANISM: Artificial Sequence  
 FEATURE:

NAME/KEY: misc\_feature  
 LOCATION:

OTHER INFORMATION: oligonucleotide substrate

US-09-817-879-4624

Query Match 100.0%; Score 7; DB 13; Length 13;  
 Best Local Similarity 71.4%; Pred. No. 1.1e+05;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7

6 AGAUGA 12

RESULT 15

US-09-875-440-22/c

Sequence 22, Application US/09875440

Patent No. US20020156035A1

GENERAL INFORMATION:

APPLICANT: Reinhard, Christoph

APPLICANT: Jefferson, Anne B.

APPLICANT: Winter, Jill A.

APPLICANT: Randazzo, Filippo

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING

NEOPLASTIC DISEASE USING NET-4 MODULATORS

FILE REFERENCE: PP-01701.002/200130.522

CURRENT APPLICATION NUMBER: US/09/875,440

CURRENT FILING DATE: 2001-06-05

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 22

LENGTH: 14

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Oligonucleotide NET-4 oligo 868 used for in-situ

hybridization

US-09-875-440-22

Query Match 100.0%; Score 7; DB 10; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7

13 AGTATGA 7

Search completed: January 1, 2004, 01:10:38

Job time : 82.6076 secs

QY 1 AGTATGA 7  
|||||  
Db 10 AGTATGA 4

## RESULT 10

US-10-033-145-1423/c  
; Sequence 1423, Application US/10033145  
; Publication No. US2002015151A1  
; GENERAL INFORMATION:  
; APPLICANT: GENZYME CORPORATION  
; APPLICANT: ROBERTS, BRUCE  
; APPLICANT: SHANKARA, SRINIVAS  
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES  
; FILE REFERENCE: GA0201C  
; CURRENT APPLICATION NUMBER: US/10/033,145  
; CURRENT FILING DATE: 2001-11-05  
; PRIOR APPLICATION NUMBER: PCT/US99/13800  
; PRIOR FILING DATE: 1999-06-18  
; NUMBER OF SEQ ID NOS: 2137  
; SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1423  
LENGTH: 10  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-033-145-1423

Query Match 100.0%; Score 7; DB 14; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATGA 7  
|||||  
Db 7 AGTATGA 1

## RESULT 11

US-10-150-779A-15/c  
; Sequence 15, Application US/10150779A  
; Publication No. US20030125241A1  
; GENERAL INFORMATION:  
; APPLICANT: WISSENBACH, MARGIT  
; APPLICANT: KOCH, TROELS  
; APPLICANT: ORUM, HENRICK  
; APPLICANT: HANSEN, BO  
; TITLE OF INVENTION: THERAPEUTIC USES OF LNA-MODIFIED OLIGONUCLEOTIDES IN  
; FILE REFERENCE: 55704 (45120)  
; CURRENT APPLICATION NUMBER: US/10/150,779A  
; CURRENT FILING DATE: 2003-02-07  
; PRIOR APPLICATION NUMBER: 60/291,830  
; PRIOR FILING DATE: 2001-05-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: oligonucleotide  
US-10-150-779A-15

Query Match 100.0%; Score 7; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATGA 7  
|||||  
Db 11 AGTATGA 5

## RESULT 12

US-10-150-779A-16/c  
; Sequence 16, Application US/10150779A  
; Publication No. US20030125241A1  
; GENERAL INFORMATION:  
; APPLICANT: WISSENBACH, MARGIT  
; APPLICANT: KOCH, TROELS  
; APPLICANT: ORUM, HENRICK  
; APPLICANT: HANSEN, BO  
; TITLE OF INVENTION: THERAPEUTIC USES OF LNA-MODIFIED OLIGONUCLEOTIDES IN  
; FILE REFERENCE: 55704 (45120)  
; CURRENT APPLICATION NUMBER: US/10/150,779A  
; CURRENT FILING DATE: 2003-02-07  
; PRIOR APPLICATION NUMBER: 60/291,830  
; PRIOR FILING DATE: 2001-05-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 16  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: DNA oligonucleotide with phosphorothioate backbone  
US-10-150-779A-16

Query Match 100.0%; Score 7; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATGA 7  
|||||  
Db 11 AGTATGA 5

## RESULT 13

US-09-740-332-4624  
; Sequence 4624, Application US/09740332  
; Publication No. US20030125270A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
; FILE REFERENCE: RPI 400/003  
; CURRENT APPLICATION NUMBER: US/09/740,332  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9704  
; SOFTWARE: PatentIn version 3.0  
SEQ ID NO 4624  
LENGTH: 13  
TYPE: RNA  
ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-740-332-4624

Query Match 100.0%; Score 7; DB 11; Length 13;  
Best Local Similarity 71.4%; Pred. No. 1.1e+05;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATGA 7  
|||:|  
Db 6 AGUAUGA 12

## RESULT 14

US-09-817-879-4624  
; Sequence 4624, Application US/09817879  
; Publication No. US20030171311A1  
; GENERAL INFORMATION:

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA Fragment  
US-10-122-630-1

Query Match 100.0%; Score 7; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.7e+08;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATGA 7  
|||||  
Db 2 AGTATGA 8

RESULT 6

US-10-122-633-1  
Sequence 1, Application US/10122633  
Publication No. US20030032611A1

GENERAL INFORMATION:  
APPLICANT: Gilchrist, Barbara A.  
APPLICANT: Eller, Mark S.  
APPLICANT: Yaar, Mina  
TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
Oligonucleotides  
FILE REFERENCE: 0054.1088-019  
CURRENT APPLICATION NUMBER: US/10/122,633  
CURRENT FILING DATE: 2002-04-12  
PRIOR APPLICATION NUMBER: US 09/540,843  
PRIOR FILING DATE: 2000-03-31  
PRIOR APPLICATION NUMBER: PCT/US01/10162  
PRIOR FILING DATE: 2001-03-30  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 9  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic DNA Fragment

US-10-122-633-1

Query Match 100.0%; Score 7; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.7e+08;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATGA 7  
|||||  
Db 2 AGTATGA 8

RESULT 7

US-09-398-399-31  
Sequence 31, Application US/09398399  
Patent No. US20020051973A1

GENERAL INFORMATION:  
APPLICANT: DELENSTARR, GLENDA C.  
APPLICANT: LEFKOWITZ, STEVEN M.  
APPLICANT: LUEBKE, KEVIN J.  
APPLICANT: OVERMAN, LESLIE B.  
APPLICANT: SAMPRAS, NICHOLAS M.  
APPLICANT: SAMPSON, JEFFREY R.  
APPLICANT: WOLBER, PAUL K.  
TITLE OF INVENTION: TECHNIQUES FOR ASSESSING NONSPECIFIC BINDING OF NUCLEIC  
ACIDS TO SURFACES  
FILE REFERENCE: 10981620-1  
CURRENT APPLICATION NUMBER: US/09/398,399  
CURRENT FILING DATE: 1999-09-17  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 31  
LENGTH: 10  
TYPE: DNA  
ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Probe  
US-09-398-399-31

Query Match 100.0%; Score 7; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATGA 7  
|||||  
Db 1 AGTATGA 7

RESULT 8

US-09-899-381-31  
Sequence 31, Application US/09899381  
Patent No. US20020068293A1

GENERAL INFORMATION:  
APPLICANT: Delenstarr, Glend C.  
APPLICANT: Wolber, Paul K.  
APPLICANT: Sana, Theodore R.  
TITLE OF INVENTION: Arrays Having Background Features and  
Methods for Using the Same  
FILE REFERENCE: 10010760-1  
CURRENT APPLICATION NUMBER: US/09/899,381  
CURRENT FILING DATE: 2001-07-05  
PRIOR APPLICATION NUMBER: 09/398,399  
PRIOR FILING DATE: 1999-09-17  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 31  
LENGTH: 10  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic probe  
US-09-899-381-31

Query Match 100.0%; Score 7; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATGA 7  
|||||  
Db 1 AGTATGA 7

RESULT 9

US-10-329-465-30/c  
Sequence 30, Application US/10329465  
Publication No. US20030165949A1

GENERAL INFORMATION:  
APPLICANT: Wang et al.  
TITLE OF INVENTION: GENES ABNORMALLY EXPRESSED IN MYELOID LEUKEMIA CELLS WITH AN MLL-1  
FUSION  
FILE REFERENCE: 27373/37928A  
CURRENT APPLICATION NUMBER: US/10/329,465  
CURRENT FILING DATE: 2002-12-23  
PRIOR APPLICATION NUMBER: US 60/343,826  
PRIOR FILING DATE: 2001-12-27  
NUMBER OF SEQ ID NOS: 315  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 30  
LENGTH: 10  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Synthetic oligonucleotide  
US-10-329-465-30

Query Match 100.0%; Score 7; DB 13; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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Db      1 AGTATGA 7
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Query Match      100.0%; Score 7; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.8e+08;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
US-10-122-630-7
; Sequence 3, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-018
; CURRENT APPLICATION NUMBER: US/10/122,630
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US96/08386
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: US 09/048,927
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-7

Query Match      100.0%; Score 7; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.8e+08;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      1 AGTATGA 7
|||||||
Query Match      100.0%; Score 7; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.8e+08;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
US-10-122-633-3
; Sequence 3, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-3

Query Match      100.0%; Score 7; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.8e+08;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      1 AGTATGA 7
|||||||
Query Match      100.0%; Score 7; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.8e+08;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
US-10-122-633-7
; Sequence 7, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-7

Query Match      100.0%; Score 7; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.8e+08;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      1 AGTATGA 7
|||||||
Query Match      100.0%; Score 7; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.8e+08;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
US-10-122-630-1
; Sequence 1, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-018
; CURRENT APPLICATION NUMBER: US/10/122,630
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US96/08386
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: US 09/048,927
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: DNA
US-10-122-630-1
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 17:10:00 ; Search time 81.6076 Seconds  
(without alignments)  
296.896 Million cell updates/sec

Title: US-09-540-843-7  
Perfect score: 7  
Sequence: 1 agtatga 7

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2263443 seqs, 1730637950 residues

Total number of hits satisfying chosen parameters: 998502

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA: \*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq: \*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq: \*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq: \*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq: \*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq: \*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq: \*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq: \*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq: \*  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq: \*  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq: \*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq: \*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq: \*  
13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq2: \*  
14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq: \*  
15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq: \*  
16: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq: \*  
17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq: \*  
18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	15	US-10-122-630-3
2	7	100.0	7	15	US-10-122-630-7
3	7	100.0	7	15	US-10-122-633-3
4	7	100.0	7	15	US-10-122-633-7
5	7	100.0	9	15	US-10-122-630-1
6	7	100.0	9	15	US-10-122-633-1
7	7	100.0	10	9	US-09-398-399-31
8	7	100.0	10	9	US-09-899-381-31
9	7	100.0	10	13	US-10-329-465-30
10	7	100.0	10	14	US-10-033-145-1423
11	7	100.0	12	15	US-10-150-779A-15
12	7	100.0	12	15	US-10-150-779A-16
13	7	100.0	13	11	US-09-740-332-4624
14	7	100.0	13	13	US-09-817-879-4624
15	7	100.0	14	10	US-09-875-440-22

Sequence 527, App  
Sequence 528, App  
Sequence 529, App  
Sequence 1527, App  
Sequence 1569, App  
Sequence 1570, App  
Sequence 30, Appl  
Sequence 527, App  
Sequence 528, App  
Sequence 529, App  
Sequence 1527, App  
Sequence 1569, App  
Sequence 1570, App  
Sequence 1, Appl  
Sequence 2, Appl  
Sequence 4558, App  
Sequence 4571, App  
Sequence 4558, App  
Sequence 4571, App  
Sequence 88, Appl  
Sequence 569, App  
Sequence 2749, App  
Sequence 2750, App  
Sequence 2751, App  
Sequence 2752, App  
Sequence 2753, App  
Sequence 2754, App  
Sequence 2755, App  
Sequence 2756, App

ALIGNMENTS

RESULT 1  
US-10-122-630-3  
; Sequence 3, Application US/10122630  
; Publication No. US20030032610A1  
; GENERAL INFORMATION:  
; APPLICANT: Glitchrest, Barbara A.  
; APPLICANT: Eller, Mark S.  
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
; TITLE OF INVENTION: Oligonucleotides  
; FILE REFERENCE: 0054.1088-018  
; CURRENT APPLICATION NUMBER: US/10/122,630  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US 08/467,012  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: PCT/US96/08386  
; PRIOR FILING DATE: 1996-06-03  
; PRIOR APPLICATION NUMBER: US 09/048,927  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: US 09/540,843  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: PCT/US01/10162  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Fastseq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 7  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA Fragment  
US-10-122-630-3

Query Match 100.0%; Score 7; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.8e+08;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGTATGA 7

STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-485-133-28

Query Match 100.0%; Score 7; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7  
| | | | |  
Db 9 AGTATGA 15

## RESULT 14

US-09-094-714A-33/c

Sequence 33, Application US/09094714A

Patent No. 6117847

## GENERAL INFORMATION:

APPLICANT: C. Frank Bennett, Nicholas M. Dean  
TITLE OF INVENTION: OLIGONUCLEOTIDES FOR ENHANCED MODULATION OF  
TITLE OF INVENTION: PROTEIN KINASE C EXPRESSION  
NUMBER OF SEQUENCES: 69  
CURRENT APPLICATION DATA:

ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 6117847ris, LLP

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

## COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 8.0

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/094,714A

FILING DATE: June 15, 1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/601,269

FILING DATE: 14-FEB-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/478,178

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/089,996

FILING DATE: 09-JUL-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/852,852

FILING DATE: 16-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: Paul K. Legaard

REGISTRATION NUMBER: 38,534

REFERENCE/DOCKET NUMBER: ISIS-2943

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 15

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-094-714A-33

Query Match 100.0%; Score 7; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7  
| | | | |  
Db 12 AGTATGA 6

## RESULT 15

US-09-094-714A-34/c

Sequence 34, Application US/09094714A

Patent No. 6117847

## GENERAL INFORMATION:

APPLICANT: C. Frank Bennett, Nicholas M. Dean  
TITLE OF INVENTION: OLIGONUCLEOTIDES FOR ENHANCED MODULATION OF  
TITLE OF INVENTION: PROTEIN KINASE C EXPRESSION  
NUMBER OF SEQUENCES: 69  
CURRENT APPLICATION DATA:

ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 6117847ris, LLP

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

## COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 8.0

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/094,714A

FILING DATE: June 15, 1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/601,269

FILING DATE: 14-FEB-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/478,178

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/089,996

FILING DATE: 09-JUL-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/852,852

FILING DATE: 16-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: Paul K. Legaard

REGISTRATION NUMBER: 38,534

REFERENCE/DOCKET NUMBER: ISIS-2943

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 15

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-094-714A-34

Query Match 100.0%; Score 7; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7  
| | | | |  
Db 14 AGTATGA 8

Search completed: January 1, 2004, 00:32:19

Job time : 28.3136 secs

NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/585,684B  
FILING DATE: January 16, 1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/000,951  
FILING DATE: July 7, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/078  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 130:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-585-684B-130

Query Match 100.0%; Score 7; DB 2; Length 15;  
Best Local Similarity 71.4%; Pred. No. 8.6e+03;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATGA 7  
||:|  
DB 5 AGUAUGA 11

RESULT 12  
US-08-585-684B-1315  
Sequence 1315, Application US/08585684B  
Patent No. 5877021  
GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Daniel T.  
APPLICANT: Jarvis, Thale  
APPLICANT: McSwigen, James  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
INDUCTION OF GRAFT TOLERANCE  
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE  
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES  
NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:

NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:

NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:

NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:

NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:

NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:

NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
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STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:

NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
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STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:

NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:

NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:

NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:

NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:

NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:

NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:

NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:

NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:

NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:

NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:

NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:

NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:

NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS

TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
INFORMATION FOR SEQ ID NO: 327:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-334-847-327

Query Match 100.0%; Score 7; DB 1; Length 15;  
Best Local Similarity 71.4%; Pred. No. 8.6e+03;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7  
||:|:  
5 AGAUGA 11

RESULT 9  
US-08-671-071B-2/c  
Sequence 2, Application US/08671071B  
Patent No. 5811270  
GENERAL INFORMATION:  
APPLICANT: Grandgenett, Duane  
TITLE OF INVENTION: An in vitro method for concerted integration of  
TITLE OF INVENTION: donor DNA molecules using retroviral integrase proteins.  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Grandgenett, Duane  
STREET: 8610 Henrietta Ave  
CITY: Brentwood  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63144

COMPUTER READABLE FORM:  
MEDIUM TYPE: Distette, 3.5 inch;  
COMPUTER: Gateway 2000, 4DX2-66E (Intel)  
OPERATING SYSTEM: IBM clone  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/671,071B  
FILING DATE: 06/27/96  
CLASSIFICATION: 435  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 962-0064  
TELEFAX: (314) 577-8406  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 bases  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
HYPOTHETICAL: no  
ANTI-SENSE: no  
ORIGINAL SOURCE: Combination of avian or HIV-1 retrovirus  
ORIGINAL SOURCE: DNA, p1AN7 plasmid and pGEM plasmid.  
IMMEDIATE SOURCE: Same as in 2.vi.  
FEATURE:  
OTHER INFORMATION: The sequence is the bottom strand of  
OTHER INFORMATION: M-2 US and the pGEM target of the top clone shown in  
OTHER INFORMATION: Figure 14 of original application.

US-08-671-071B-2  
Query Match 100.0%; Score 7; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 AGTATGA 7  
9 AGTATGA 3

RESULT 10  
US-08-747-121-4/c  
Sequence 4, Application US/08747121  
Patent No. 5874290  
GENERAL INFORMATION:  
APPLICANT: Murphy, Gerald  
APPLICANT: Boynton, Alton  
APPLICANT: Sehgal, Anil  
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID  
TITLE OF INVENTION: SEQUENCES OF A D2-2 GENE ASSOCIATED WITH  
TITLE OF INVENTION: BRAIN TUMORS AND METHODS BASED THEREON  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/747,121  
FILING DATE: 08-NOV-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Baldwin, Geraldine F  
REGISTRATION NUMBER: 31,232  
REFERENCE/DOCKET NUMBER: 8511-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 7909090  
TELEFAX: (212) 8698864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Modified Base  
LOCATION: 1  
OTHER INFORMATION: Where N is any nucleotide

US-08-747-121-4  
Query Match 100.0%; Score 7; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 AGTATGA 7  
15 AGTATGA 9

RESULT 11  
US-08-585-684B-130  
Sequence 130, Application US/08585684B  
Patent No. 5877021  
GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Daniel T.  
APPLICANT: Jarvis, Thale  
APPLICANT: McSwiggen, James  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE  
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES

US-08-585-684B-130  
Query Match 100.0%; Score 7; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 AGTATGA 7  
15 AGTATGA 9

US-08-671-071B-2  
Query Match 100.0%; Score 7; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 AGTATGA 7  
9 AGTATGA 3

;  
; TITLE OF INVENTION: AND METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/744,905A  
; FILING DATE: 08-NOV-1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Baldwin, Geraldine F  
; REGISTRATION NUMBER: 31,232  
; REFERENCE/DOCKET NUMBER: 8511-009  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)7909090  
; TELEFAX: (212)8698864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Modified Base  
; LOCATION: 1  
; OTHER INFORMATION: Where N is any nucleotide  
;  
; S-08-744-905A-4  
;  
; Query Match 100.0%; Score 7; DB 2; Length 14;  
; Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
;  
; 1 AGTATGA 7  
; |||||  
; 14 AGTATGA 8  
;  
; RESULT 7  
; NS-08-334-847-24  
; Sequence 24, Application US/08334847  
; Patent No. 5693532  
; GENERAL INFORMATION:  
; APPLICANT: McSwiggen, James  
; APPLICANT: Draper, Kenneth  
; APPLICANT: Pavco, Pam  
; APPLICANT: Woolf, Tod  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; OPERATING SYSTEM: INHIBITING RESPIRATORY  
; TITLE OF INVENTION: SYNCYTIAL VIRUS  
; NUMBER OF SEQUENCES: 909  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
;  
; Copied from 09980559 on 05/19/2004

;  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/334,847  
; FILING DATE: NO. 5693532ember 4, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 209/032  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-334-847-24  
;  
; Query Match 100.0%; Score 7; DB 1; Length 15;  
; Best Local Similarity 71.4%; Pred. No. 8.6e+03;  
; Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
;  
; QY 1 AGTATGA 7  
; |||||  
; Db 5 AGUAUGA 11  
;  
; RESULT 8  
; US-08-334-847-327  
; Sequence 327, Application US/08334847  
; Patent No. 5693532  
; GENERAL INFORMATION:  
; APPLICANT: McSwiggen, James  
; APPLICANT: Draper, Kenneth  
; APPLICANT: Pavco, Pam  
; APPLICANT: Woolf, Tod  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; OPERATING SYSTEM: INHIBITING RESPIRATORY  
; TITLE OF INVENTION: SYNCYTIAL VIRUS  
; NUMBER OF SEQUENCES: 909  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/334,847  
; FILING DATE: NO. 5693532ember 4, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 209/032  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-334-847-24

EARLIER FILING DATE: 1995-06-06  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 9  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: DNA Fragment  
US-09-048-927-1

Query Match 100.0%; Score 7; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+07;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7  
|||||  
2 AGTATGA 8

RESULT 3  
US-09-922-445-12/c  
Sequence 12, Application US/09922445  
Patent No. 6528268  
GENERAL INFORMATION:

APPLICANT: Andersson, Maria K.  
APPLICANT: Berglund, Lars G. T.  
APPLICANT: Reneland, Rikard H.  
APPLICANT: Adam, Gail I. R.  
TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTION OF HEART FAILURE  
FILE REFERENCE: GG126US  
CURRENT APPLICATION NUMBER: US/09/922,445  
CURRENT FILING DATE: 2001-08-03  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 12  
LENGTH: 13  
TYPE: DNA  
ORGANISM: synthetic  
US-09-922-445-12

Query Match 100.0%; Score 7; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7  
|||||  
9 AGTATGA 3

RESULT 4  
US-09-922-445-22  
Sequence 22, Application US/09922445  
Patent No. 6528268  
GENERAL INFORMATION:

APPLICANT: Andersson, Maria K.  
APPLICANT: Berglund, Lars G. T.  
APPLICANT: Reneland, Rikard H.  
APPLICANT: Adam, Gail I. R.  
TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTION OF HEART FAILURE  
FILE REFERENCE: GG126US  
CURRENT APPLICATION NUMBER: US/09/922,445  
CURRENT FILING DATE: 2001-08-03  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 22  
LENGTH: 13  
TYPE: DNA  
ORGANISM: synthetic  
US-09-922-445-22

Query Match 100.0%; Score 7; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 8.6e+03;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AGTATGA 7  
|||||  
Db 5 AGTATGA 11

RESULT 5  
US-08-485-133-27  
Sequence 27, Application US/08485133  
Patent No. 5976789  
GENERAL INFORMATION:  
APPLICANT: Allibert, Patrice A.  
APPLICANT: Cros, Philippe  
APPLICANT: Mach, Bernard F.  
APPLICANT: Mandrand, Bernard F.  
APPLICANT: Tiercy, Jean-Marie  
TITLE OF INVENTION: SYSTEM OF PROBES ENABLING HLA-DR TYPING  
TITLE OF INVENTION: TO BE PERFORMED, AND TYPING METHOD USING SAID PROBES  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OLIFF & BERRIDGE  
STREET: P.O. Box 19928  
CITY: Alexandria  
STATE: Virginia  
ZIP: 22320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,133  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/030,143  
FILING DATE: 11-MAR-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Berridge, William P.  
REGISTRATION NUMBER: 30,024  
REFERENCE/DOCKET NUMBER: WPB 28596A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6400  
TELEFAX: 703-836-2787  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-485-133-27

Query Match 100.0%; Score 7; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7  
|||||  
Db 8 AGTATGA 14

RESULT 6  
US-08-744-905A-4/c  
Sequence 4, Application US/08744905A  
Patent No. 5990294  
GENERAL INFORMATION:  
APPLICANT: Murphy, Gerald  
APPLICANT: Boynton, Alton  
APPLICANT: Sehgal, Anil  
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID  
SEQUENCES OF C4-2, A TUMOR SUPPRESSOR GENE,

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 14:40:05 ; Search time 27.2025 Seconds  
(without alignments)  
113.581 Million cell updates/sec

Title: US-09-540-843-7

Perfect score: 7  
Sequence: 1 agtatga 7

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 547746

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued Patents NA:\*

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4: /cgn2\_6/prodata/1/ina/6B COMB.seq:\*  
5: /cgn2\_6/prodata/1/ina/6C COMB.seq:\*  
6: /cgn2\_6/prodata/1/ina/6D COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	7	100.0	9	3	US-09-048-927-1
3	7	100.0	13	4	US-09-922-445-12
4	7	100.0	13	4	US-09-922-445-22
5	7	100.0	14	2	US-08-485-133-27
6	7	100.0	14	2	US-08-744-905A-4
7	7	100.0	15	1	US-08-334-847-24
8	7	100.0	15	1	US-08-334-847-327
9	7	100.0	15	1	US-08-671-071B-2
10	7	100.0	15	2	US-08-747-121-4
11	7	100.0	15	2	US-08-585-684B-130
12	7	100.0	15	2	US-08-585-684B-1315
13	7	100.0	15	2	US-08-485-133-28
14	7	100.0	15	3	US-09-094-714A-33
15	7	100.0	15	3	US-09-094-714A-34
16	7	100.0	15	3	US-09-049-190-6
17	7	100.0	15	3	US-09-049-190-7
18	7	100.0	15	3	US-09-038-073-130
19	7	100.0	15	3	US-09-038-073-1315
20	7	100.0	15	4	US-08-932-140C-6
21	7	100.0	15	4	US-08-932-140C-7
22	7	100.0	15	4	US-08-253-977-2
23	7	100.0	16	1	US-07-977-284A-59
24	7	100.0	16	1	US-08-719-593B-24
25	7	100.0	16	2	US-08-256-426B-59
26	7	100.0	16	3	US-08-458-814-1
27	7	100.0	17	1	US-08-390-850-461

#### ALIGNMENTS

##### RESULT 1

US-09-048-927-3  
; Sequence 3, Application US/09048927  
; Patent No. 6147056  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrest, Barbara A.  
; APPLICANT: Yaar, Mina  
; TITLE OF INVENTION: Use of Locally Applied DNA Fragments  
; FILE REFERENCE: BU94-68A2  
; CURRENT APPLICATION NUMBER: US/09/048,927  
; EARLIER FILING DATE: 1998-03-26  
; EARLIER APPLICATION NUMBER: 08/952,697  
; EARLIER FILING DATE: 1996-06-03  
; EARLIER APPLICATION NUMBER: 08/467,012  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 7  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: DNA Fragment  
US-09-048-927-3

Query Match 100.0%; Score 7; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 5.9e+07;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7  
Db 1 AGTATGA 7

##### RESULT 2

US-09-048-927-1  
; Sequence 1, Application US/09048927  
; Patent No. 6147056  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrest, Barbara A.  
; APPLICANT: Yaar, Mina  
; TITLE OF INVENTION: Use of Locally Applied DNA Fragments  
; FILE REFERENCE: BU94-68A2  
; CURRENT APPLICATION NUMBER: US/09/048,927  
; EARLIER FILING DATE: 1998-03-26  
; EARLIER APPLICATION NUMBER: 08/952,697  
; EARLIER FILING DATE: 1996-06-03  
; EARLIER APPLICATION NUMBER: 08/467,012

Sequence 461, App  
Sequence 365, App  
Sequence 367, App  
Sequence 369, App  
Sequence 371, App  
Sequence 813, App  
Sequence 815, App  
Sequence 6, Appli  
Sequence 2, Appli  
Sequence 443, App  
Sequence 444, App  
Sequence 6, Appli  
Sequence 55, Appl  
Sequence 8, Appl  
Sequence 10, Appl  
Sequence 48, Appl  
Sequence 8, Appli



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survey sequence.
ACCESSION   BH857761
VERSION     BH857761.1  GI:21708582
KEYWORDS    GSS
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
            ; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE   1 (bases 1 to 25)
AUTHORS     Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
            , C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
            , Zimmerman,J. and Ecker,J.R.
TITLE       A Sequence-Indexed Library of Insertion Mutations in the
JOURNAL     Arabidopsis Genome
COMMENT     Unpublished
            Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel.: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA. This sequence lies within an annotated intron of AC3g22930.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source           1..25
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_015664.41.95.x"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains one or more TDNA insertion
                     elements. The resultant fragment for each line was
                     directly sequenced to determine the genomic sequence at
                     the site of insertion. Details of the protocols used can
                     be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT          9 a 5 c 0 g 11 t
ORIGIN
Query Match       100.0%; Score 7; DB 28; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches           7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 AGTATGA 7
|||||||
8 AGTATGA 2

RESULT 15
AC345685/c
LOCUS        26 bp DNA linear GSS 29-SEP-2000
DEFINITION   clone UUGC1M0080C06 R, genomic survey sequence.
ACCESSION    AZ345685
VERSION      AZ345685.1  GI:10424922
KEYWORDS     GSS.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1 (bases 1 to 26)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            , M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D. Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished
COMMENT     Contact: Robert B. Weiss

```

```

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: C column: 06
Seq primer: CACACAGGAAACACCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
1..26
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080C06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT          7 a 7 c 0 g 12 t
ORIGIN
Query Match       100.0%; Score 7; DB 28; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.4e+05;
Matches           7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY              1 AGTATGA 7
|||||||
Db              9 AGTATGA 3

Search completed: December 31, 2003, 19:41:24
Job time : 804.291 secs

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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWB42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor-mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 5 a 6 c 5 g 9 t

## ORIGIN

Query Match 100.0%; Score 7; DB 28; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATGA 7

DB 22 AGTATGA 16

## RESULT 12

BH852860

## LOCUS

DEFINITION SALK\_075689.48-55.x Arabidopsis thaliana TDNA insertion lines  
Arabidopsis thaliana genomic clone SALK\_075689.48-55.x, genomic  
survey sequence.

## ACCESSION

BH852860

## VERSION

BH852860.1

## KEYWORDS

GSS.

## SOURCE

Arabidopsis thaliana (thale cress)

## ORGANISM

Arabidopsis thaliana

## REFERENCE

1 (bases 1 to 25)

## AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab

,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.

, Zimmermann,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within an annotated exon of At3g41627.

Class: TDNA tagged.

Location/Qualifiers

1. .25

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SALK\_075689.48-55.x"

/notes="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

BASE COUNT 9 a 2 c 6 g 8 t

## FEATURES

source

1. .25

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SALK\_075689.48-55.x"

/notes="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

9 a 2 c 6 g 8 t

## ORIGIN

Query Match 100.0%; Score 7; DB 28; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATGA 7

DB 12 AGTATGA 18

## RESULT 13

BH852866

## LOCUS

DEFINITION SALK\_075697.38-25.x Arabidopsis thaliana TDNA insertion lines  
Arabidopsis thaliana genomic clone SALK\_075697.38-25.x, genomic  
survey sequence.

## ACCESSION

BH852866

## VERSION

BH852866.1

## KEYWORDS

GSS.

## SOURCE

Arabidopsis thaliana (thale cress)

## ORGANISM

Arabidopsis thaliana

## REFERENCE

1 (bases 1 to 25)

## AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab

,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.

, Zimmermann,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within an annotated exon of At3g41627.

Class: TDNA tagged.

Location/Qualifiers

1. .25

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SALK\_075697.38-25.x"

/notes="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

9 a 2 c 6 g 8 t

## BASE COUNT

Query Match 100.0%; Score 7; DB 28; Length 25;

Best Local Similarity 100.0%; Pred. No. 2.3e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATGA 7

DB 12 AGTATGA 18

## RESULT 14

BH857761

## LOCUS

DEFINITION SALK\_015664.41-95.x Arabidopsis thaliana TDNA insertion lines  
Arabidopsis thaliana genomic clone SALK\_015664.41-95.x, genomic

BASE COUNT 9 a 2 c 6 g 8 t

/db\_xref="taxon:9606"  
 /clone="IMAGE:232513"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares pineal gland N3HPC"  
 /note="Organ: pineal gland; Vector: pT7T3D (Pharmacia)  
 with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;  
 1st strand cDNA was primed with a Not I - oligo(dT) primer  
 [5', TGTTACCAATCTGAAGTCGGAGCGCGCGTCTTTTCTTTTCTTTT 3']  
 , double-stranded cDNA was size selected, ligated to Eco  
 RI adaptors (Pharmacia), digested with Not I and cloned  
 into the Not I and Eco RI sites of a modified pT7T3 vector  
 (Pharmacia). Library constructed by Bento Soares and  
 M.Fatima Bonaldo."

BASE COUNT 6 a 5 c 6 g 8 t

## ORIGIN

Query Match 100.0%; Score 7; DB 14; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7

|||||

19 AGTATGA 13

## RESULT 10

AZ605844/c

LOCUS IM0427J22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC1M0427J22 F, genomic survey sequence.

AZ605844

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 25)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
 ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
 and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

Unpublished

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0427 row: J column: 22

Seq primer: CGTTGTAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 25.

Location/Qualifiers

1. .25

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0427J22"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD22 [gi|4732114|gb|AF129072.1], a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT 7 a 6 c 5 g 7 t

## ORIGIN

Query Match 100.0%; Score 7; DB 28; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7

|||||

17 AGTATGA 11

## RESULT 11

AZ802490/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 25)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
 ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
 and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

Unpublished

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0061 row: I column: 22

Seq primer: CGTTGTAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 25.

Location/Qualifiers

1. .25

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0061I22"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 6 a 8 c 3 g 7 t

ORIGIN

Query Match 100.0%; Score 7; DB 28; Length 24;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7

|||||

8 AGTATGA 2

#### RESULT 8

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..24

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0085E05"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

Location/Qualifiers

1..24

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0085E05"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

Location/Qualifiers

1..24

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:3862504"

Location/Qualifiers

1..25

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:3862504"

/clone lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 7 a 6 c 3 g 8 t

ORIGIN

Query Match 100.0%; Score 7; DB 28; Length 24;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7

|||||

19 AGTATGA 13

#### RESULT 9

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..25

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:3862504"

Location/Qualifiers

1..25

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:3862504"

Location/Qualifiers

1..25

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:3862504"

Location/Qualifiers

1..25

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:3862504"

Location/Qualifiers

1..25

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:3862504"

Location/Qualifiers

1..25

Tel: 510 670 9338  
 Fax: 510 670 9302  
 Email: tim@lynxen.com  
 Sequence obtained from LYNX Therapeutics Megasort technology.  
 Collected from the down-regulated gate.  
 High quality sequence stop: 24.  
 Location/Qualifiers  
 1. .24  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /cell\_type="monocytic leukemia"  
 /cell\_line="THP-1 (TIB-202)"  
 /clone\_lib="DNC15"  
 /note="Vector: PCR1; Cloning of PCR products from micro-beads carrying 3' end of down-regulated cDNA. THP-1 cells non-induced (treated with DMSO only)."

BASE COUNT  
 9 a 6 c 1 g 8 t

FEATURES  
 source  
 1. .24  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /cell\_type="monocytic leukemia"  
 /cell\_line="THP-1 (TIB-202)"  
 /clone\_lib="DNC15"  
 /note="Vector: PCR1; Cloning of PCR products from micro-beads carrying 3' end of down-regulated cDNA. THP-1 cells non-induced (treated with DMSO only)."

Query Match 100.0%; Score 7; DB 9; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7  
 |||||  
 23 AGTATGA 17

RESULT 6  
 LOCUS AZ423817 24 bp DNA linear GSS 03-OCT-2000  
 DEFINITION 1M0203P19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0203P19 F, genomic survey sequence.  
 ACCESSION AZ423817.1 GI:10547830  
 VERSION 1  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 24)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
 and Wright,D., Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0203 row: P column: 19  
 Seq primer: CGTTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 24.  
 Location/Qualifiers  
 1. .24  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0203P19"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT  
 7 a 3 c 2 g 12 t

Query Match 100.0%; Score 7; DB 28; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7  
 |||||  
 17 AGTATGA 11

RESULT 7  
 LOCUS AZ478673 24 bp DNA linear GSS 04-OCT-2000  
 DEFINITION 1M0298J20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0298J20 R, genomic survey sequence.  
 ACCESSION AZ478673.1 GI:10637794  
 VERSION 1  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 24)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
 and Wright,D., Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0298 row: J column: 20  
 Seq primer: CACACAGGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 24.  
 Location/Qualifiers  
 1. .24  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0298J20"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0462 row: J column: 10  
 Seq primer: CGTTGTAACAGCGGCACG  
 Class: plasmid ends  
 High quality sequence stop: 22.

## FEATURES

source

1. .22  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0462J10"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Copied from 09980559 on 05/19/2004

## BASE COUNT

ORIGIN

Query Match 100.0%; Score 7; DB 28; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7

|||||

11 AGTATGA 5

## RESULT 4

LOCUS

AZ658158 22 bp DNA linear GSS 14-DEC-2000  
 1M0534H17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0534H17 R, genomic survey sequence.

AZ658158

VERSION

AZ658158.1 GI:11795304

GSS.

Mus musculus

Mus musculus

(house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly

, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.

and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0534 row: H column: 17

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

## FEATURES

source

1. .22  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0534H17"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## BASE COUNT

ORIGIN

Query Match 100.0%; Score 7; DB 28; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7

|||||

4 AGTATGA 10

## RESULT 5

LOCUS

AW059679 24 bp mRNA linear EST 23-AUG-2000  
 A0059679.1 GI:6652001  
 Homo sapiens (human)

AW059679

DEFINITION

AW059679

ACCESSION

AW059679.1

VERSION

AW059679.1

GI:6652001

EST.

Homo sapiens

Homo sapiens

(human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 24)

Brenner, S., Williams, S.R., Vernass, E.H., Storch, T., Moon, K.,

McCollum, C., Mao, J.I., Kirchner, J.J., Eietr, S., Dubridge, R.B.,

Burcham, T., and Albrecht, G.

In vitro cloning of complex mixtures of DNA on microbeads: Physical

separation of differentially expressed cDNAs

Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)

20144098

MEDLINE

PUBMED

10677516

COMMENT

Contact: Burcham TS

LYNX Therapeutics, Inc.

25861 Industrial Blvd., Hayward, CA 94545, USA

Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0086 row: E column: 01  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers

## FEATURES

source

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0086E01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
6 a 1 c 6 g

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BASE COUNT  
 ORIGIN

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Query Match      100.0%; Score 7; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 AGTATGA 7
|||||
10 AGTATGA 16

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RESULT 2  
 LOCUS

AZ990856 19 bp DNA linear GSS 27-APR-2001  
 2M0274F14R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
 clone UUGC2M0274F14 R, genomic survey sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE

AZ990856.1 GI:13862083  
 GSS.  
 Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 19)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
 ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
 and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss  
 University of Utah Genome Center

University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606

Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0274 row: F column: 14  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers

## FEATURES

source

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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0274F14"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
8 a 5 c 6 t

```

BASE COUNT  
 ORIGIN

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Query Match      100.0%; Score 7; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AGTATGA 7
|||||
18 AGTATGA 12

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RESULT 3  
 AZ623945/c

LOCUS

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 1M0462J10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0462J10 F, genomic survey sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE

AZ623945.1 GI:11746135  
 GSS.  
 Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 22)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
 ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
 and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss  
 University of Utah Genome Center

University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 13:58:09 ; Search time 804.291 Seconds  
(without alignments)  
211.530 Million cell updates/sec

Title: US-09-540-843-7  
Perfect score: 7  
Sequence: 1 agtatga 7

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 33330

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hct:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hct:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estcom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_man:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_pbg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	7	100.0	19	28	AZ817238 2M0086E01
2	7	100.0	19	28	AZ990856 2M0274F14
3	7	100.0	22	28	AZ623945 1M0462J10
4	7	100.0	22	28	AZ658158 1M0534H17

C 5	7	100.0	24	9	AW059679
C 6	7	100.0	24	28	AZ423817
C 7	7	100.0	24	28	AZ478673
C 8	7	100.0	24	28	AZ816657
C 9	7	100.0	25	14	H96935
C 10	7	100.0	25	18	AZ605844
C 11	7	100.0	25	28	AZ802490
C 12	7	100.0	25	28	BH852860
C 13	7	100.0	25	28	BH852866
C 14	7	100.0	25	28	BH857761
C 15	7	100.0	26	28	AZ345685
C 16	7	100.0	26	28	AZ473354
C 17	7	100.0	27	14	D45824
C 18	7	100.0	27	18	AI187C01P
C 19	7	100.0	28	9	AI790546
C 20	7	100.0	28	28	AZ861130
C 21	7	100.0	28	28	BH904074
C 22	7	100.0	29	28	BH856420
C 23	7	100.0	29	29	AZ230F03P
C 24	7	100.0	30	14	C21099
C 25	7	100.0	30	29	AL766985
C 26	6	85.7	16	12	BG928185
C 27	6	85.7	17	12	BG929060
C 28	6	85.7	17	14	C21103
C 29	6	85.7	19	9	AI747751
C 30	6	85.7	19	28	AZ406137
C 31	6	85.7	19	28	AZ464990
C 32	6	85.7	19	28	AZ579566
C 33	6	85.7	19	28	AZ647364
C 34	6	85.7	19	28	AZ815067
C 35	6	85.7	20	13	BQ593049
C 36	6	85.7	20	28	AZ336039
C 37	6	85.7	20	28	AZ359199
C 38	6	85.7	20	28	AZ579536
C 39	6	85.7	20	28	AZ615402
C 40	6	85.7	20	28	AZ665083
C 41	6	85.7	20	28	AZ795800
C 42	6	85.7	20	29	TA199G02Q
C 43	6	85.7	21	28	AZ346766
C 44	6	85.7	21	28	AZ383946
C 45	6	85.7	21	28	AZ477879

## ALIGNMENTS

RESULT 1  
AZ817238  
LOCUS  
DEFINITION  
2M0086E01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0086E01 R, genomic survey sequence.  
ACCESSION  
AZ817238  
VERSION  
AZ817238.1 GI:12987146  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL  
Unpublished  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177





Novel isolated human Phospholipase A2, Group IB pancreas polynucleotide, for therapeutic purposes, for studying expression and function of the polynucleotide and for expressing the phospholipase protein -

Claim 19; Page 13; 51pp; English.

The invention relates to an isolated human Phospholipase A2, Group IB (pancreas) (PLA2G1B) polynucleotide comprising a sequence which is a polymorphic variant for a reference sequence for the PLA2G1B gene or its fragment, or a polymorphic variant of a reference sequence for a PLA2G1B cDNA or its fragment. Also included are haplotyping/genotyping the PLA2G1B gene of an individual, predicting the haplotype pair for the PLA2G1B gene of an individual, identifying an association between a trait and at least one haplotype or haplotype pair of the PLA2G1B gene, an isolated genotyping oligonucleotide for detecting a polymorphism in the PLA2G1B gene, a recombinant non-human organism transformed or transfected with the PLA2G1B sequence, where the organism expresses a PLA2G1B protein encoded by the first nucleotide sequence or by the polymorphic variant sequence, an isolated polypeptide comprising a sequence which is a polymorphic variant of a reference sequence for the PLA2G1B protein or its fragment, an anti-PLA2G1B monoclonal antibody, screening for drugs targeting PLA2G1B, a computer system for storing and analysing polymorphism data for the PLA2G1B gene and a genome anthology for PLA2G1B gene. The PLA2G1B variant is useful in studying the expression and function of PLA2G1B, and in expressing PLA2G1B protein for use in screening for candidate drugs to treat diseases related to PLA2G1B activity (e.g. pancreatitis and pancreatic cancer) and for therapeutic purposes. The transgenic organism is useful for studying expression of the PLA2G1B isogenes in vivo, for in vivo screening and testing of drugs targeted against PLA2G1B protein, and for testing the efficacy of therapeutic agents and compounds in a biological system. The antibody is useful for studying the effect of the variation on the biological activity of PLA2G1B as well as on the binding affinity of candidate drugs targeting PLA2G1B. The PLA2G1B gene is located on chromosome 12q23-q24.1. The present sequence is an allele specific oligonucleotide (ASO) primer extension primer 3' end used to detect the polymorphisms in PLA2G1B.

Sequence 10 BP; 3 A; 3 C; 0 G; 4 T; 0 other;

Query Match 100.0%; Score 7; DB 24; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.7e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7  
|||||  
9 AGTATGA 3

Search completed: December 31, 2003, 15:08:15  
Job time : 202.291 secs

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FT FT /mod_base= OTHER
FT FT /note= "This sequence is a peptide nucleic acid. (i.e. it
FT FT contains a polyamide backbone instead of a deoxyribose
FT FT backbone"
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FT FT /*tag= b
FT FT /mod_base= OTHER
FT FT /note= "The base is modified with Lys-NH2"
XX PN WO200242316-A2.
XX PD 30-MAY-2002.
XX PF 23-NOV-2001; 2001WO-DK00779.
XX PR 24-NOV-2000; 2000DK-0001776.
XX PR 06-MAR-2001; 2001DK-0000371.
XX PR 16-JUL-2001; 2001DK-0001117.
XX PR (PANT-) PANTHECO AS.
XX PR Nielsen PE, Poeschl A;
XX PR WPI; 2002-490198/52.
XX PR
XX PR New peptide nucleic acid oligomer, useful as antisense molecules to
XX PR treat bacterial and viral infections, has single units comprising
XX PR different amino acid backbones such as aminoethylglycine -
XX PR
XX PR Example 7; Page 34; 40pp; English.
XX PR
XX PR The invention comprises peptide nucleic acid (PNA) oligomers, where the
XX PR single units of the oligomers comprise different amino acid backbones
XX PR selected from any amino acid, such as: including aminoethylglycine (aeg);
XX PR aminoethylprolyl (aep); and aminoethylpyrrolidine (pyr). The PNA
XX PR oligomers of the invention are useful for the downregulation of specific
XX PR genes by targeting the genes at the mRNA or DNA level. The PNA oligomers
XX PR are useful for treating bacterial and viral infections, cancer, metabolic
XX PR diseases and immunological disorders. The PNA oligomers are also useful
XX PR in PCR monitoring/modulation by PNA-clamping. The present DNA sequence
XX PR represents a PNA oligomer of the invention.
XX PR
XX PR Sequence 10 BP; 2 A; 4 C; 0 G; 4 T; 0 other;
XX PR
XX PR Query Match 100.0%; Score 7; DB 24; Length 10;
XX PR Best Local Similarity 100.0%; Pred. No. 5.7e+04;
XX PR Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX PR 1 AGTATGA 7
XX PR |||||
XX PR 8 AGTATGA 2
XX PR
XX PR RESULT 14
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XX PR
XX PR AC ABK99556;
XX PR
XX PR 21-OCT-2002 (first entry)
XX PR
XX PR Nucleic acid microarray probe #3.
XX PR
XX PR Nucleic acid microarray; probe; ss.
XX PR
XX PR Synthetic.
XX PR
XX PR US2002068293-A1.
XX PR
XX PR 06-JUN-2002.
XX PR
XX PR 02-JUL-2001; 2001US-0899381.
XX PR
XX PR
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XX PR 17-SEP-1999; 99US-0398399.
XX PR (DELE/) DELENSTARR G C.
XX PR (WOLB/) WOLBER P K.
XX PR (SANA/) SANA T R.
XX PR
XX PR Delenstarr GC, Wolber PK, Sana TR;
XX PR WPI; 2002-582474/62.
XX PR
XX PR Nucleic acid arrays for qualitatively or quantitatively determining the
XX PR presence of analyte target nucleic acid in a sample comprises both
XX PR hybridisation features and background features -
XX PR
XX PR Claim 8; Page 17; 38pp; English.
XX PR
XX PR The invention relates to a nucleic acid array (I) comprising at least
XX PR one hybridisation feature and at least one background feature. (I) is
XX PR useful for detecting the presence of an analyte nucleic acid in a sample.
XX PR The detection comprises contacting the nucleic acid array with the sample
XX PR under stringent hybridisation conditions, subtracting the background
XX PR signal from the hybridisation signal to obtain a background corrected
XX PR hybridisation signal and relating the background corrected hybridisation
XX PR signal to the presence of the analyte target nucleic acid in the sample
XX PR The method further comprises a labeling step comprising labeling any
XX PR analyte target nucleic acids present in the sample with a member of a
XX PR signal producing system prior to contacting the array with the sample.
XX PR CC ABK99529-ABK99544 and ABK99549-ABK99578 represent nucleic acid probes
XX PR of the invention.
XX PR
XX PR Sequence 10 BP; 5 A; 1 C; 2 G; 2 T; 0 other;
XX PR
XX PR Query Match 100.0%; Score 7; DB 24; Length 10;
XX PR Best Local Similarity 100.0%; Pred. No. 5.7e+04;
XX PR Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX PR
XX PR Oy 1 AGTATGA 7
XX PR |||||
XX PR Db 1 AGTATGA 7
XX PR
XX PR RESULT 15
XX PR ABK47394/c
XX PR ID ABK47394 standard; DNA; 10 BP.
XX PR
XX PR AC ABK47394;
XX PR
XX PR 18-JUN-2002 (first entry)
XX PR
XX PR Human PLA2G1B ASO primer extension primer 3' end #5.
XX PR
XX PR Human; ss; primer; SNP; single nucleotide polymorphism; pancreatitis;
XX PR pancreatic cancer; Phospholipase A2 group IIB; PLA2G1B; gene therapy;
XX PR haplotype; genotype; chromosome 12q23-q24.1; transgenic; drug screening;
XX PR ASO; allele specific oligonucleotide; primer extension.
XX PR
XX PR Homo sapiens.
XX PR
XX PR WO200212562-A2.
XX PR
XX PR 14-FEB-2002.
XX PR
XX PR 06-AUG-2001; 2001WO-US24663.
XX PR
XX PR 04-AUG-2000; 2000US-223179P.
XX PR
XX PR (GENA-) GENAISSANCE PHARM INC.
XX PR
XX PR Kazemi A, Klieb SE, Koshy B;
XX PR WPI; 2002-303982/34.
XX PR
XX PR
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XX WO200077214-A2.  
 XX 21-DEC-2000.  
 XX 14-JUN-2000; 2000WO-US16223.  
 XX 16-JUN-1999; 99US-0335032.  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 XX Velculescu V, Vogelstein B, Kinzler K;  
 XX WPI; 2001-061874/07.  
 XX  
 XX Yeast gene coding sequences comprising NORF genes with serial analysis  
 XX of gene expression (SAGE) tags, useful for studying, monitoring and  
 XX affecting phases of the cell cycle -  
 XX  
 XX Example; Page 272; 419pp; English.  
 XX  
 XX The present invention describes an isolated DNA molecule comprising a  
 XX coding sequence of a yeast gene selected from a group of 745 NORF (not  
 XX previously assigned open reading frame; or nonannotated ORF) genes  
 XX comprising a SAGE (serial analysis of gene expression) tag. Also  
 XX described are: (1) a method (M1) of using NORF genes to affect the cell  
 XX cycle comprising administering a NORF gene whose expression varies by at  
 XX least 10% between any two phases of the cell cycle selected from log  
 XX phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 XX antifungal drugs comprising: (a) contacting a test substance with a  
 XX yeast cell; and (b) monitoring expression of a NORF gene whose  
 XX expression varies as in M1, where a test substance which modifies the  
 XX expression of the yeast gene is a candidate antifungal drug; (3) a method  
 XX (M3) for identifying human genes which are involved in cell cycle  
 XX progression comprising contacting human DNA with a probe which comprises  
 XX at least 10 contiguous nucleotides of a NORF gene whose expression varies  
 XX as in M1; and (4) a method (M4) for identifying a candidate drug as a  
 XX member of a class of drugs having a characteristic effect on gene  
 XX expression in a yeast cell comprising contacting a yeast cell with a  
 XX candidate drug and monitoring expression in the yeast cell of at least 1  
 XX NORF gene whose expression is affected by the class of drugs. The NORF  
 XX genes may be used to study, monitor and affect phases of the cell cycle,  
 XX the differentially expressed genes may be used as markers of phases of  
 XX the cell cycle. The methods may be used to identify candidate drugs which  
 XX affect the cell cycle and for identification of antifungal drugs.  
 XX AAF33268 to AAF44064 represent SAGE tags used in the exemplification of  
 XX the present invention. AAF33262 to AAF33267 represent linkers and PCR  
 XX primers used in the SAGE method, in the exemplification of the present  
 XX invention.  
 XX  
 XX Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 other;  
 XX  
 XX Query Match 100.0%; Score 7; DB 22; Length 10;  
 XX Best Local Similarity 100.0%; Pred. No. 5.7e+04;  
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 AGTATGA 7  
 XX | | | | |  
 XX Db 3 AGTATGA 9  
 XX  
 XX RESULT 12  
 XX AAD44180  
 XX ID AAD44180 standard; DNA; 10 BP.  
 XX AC AAD44180;  
 XX XX  
 XX DT 13-DEC-2002 (first entry)  
 XX XX  
 XX DE Probe #3 used to illustrate the method of the invention.  
 XX Target nucleotide; analyte; signal; drug discovery; probe; ss.  
 XX FT

OS Unidentified.  
 XX US2002051973-A1.  
 XX 02-MAY-2002.  
 XX 17-SEP-1999; 99US-0398399.  
 XX 17-SEP-1999; 99US-0398399.  
 XX (DELE/) DELENSTARR G C.  
 XX (LEFK/) LEFKOWITZ S M.  
 XX (LUEB/) LUEBKE K J.  
 XX (OVER/) OVERMAN L B.  
 XX (SAMP/) SAMPSON N M.  
 XX (SAMP/) SAMPSON J R.  
 XX (WOLB/) WOLBER P K.  
 XX Delenstarr GC, Lefkowitz SM, Luebke KJ, Overman LB, Sampson NM;  
 XX Sampson JR, Wolber PK;  
 XX WPI; 2002-443693/47.  
 XX  
 XX Detecting a target nucleotide sequence in an analyte, for use in e.g.  
 XX drug discovery, comprises using a set of features having  
 XX oligophosphodiester probes, and subtracting a background signal from an  
 XX observed signal -  
 XX  
 XX Claim 7; Page 19; 35pp; English.  
 XX  
 XX The invention relates to a method for detecting the presence and/or  
 XX amount of a target nucleotide sequence in an analyte. The method  
 XX comprising: contacting an aliquot of an analyte suspected of containing  
 XX the target sequence with a set of features comprising oligophosphodiester  
 XX probes; and subtracting a background signal from an observed signal to  
 XX determine the presence and/or amount of the target sequence in the  
 XX analyte. The method is used to detect the presence and/or amount of a  
 XX target sequence in an analyte. The method is used for estimating  
 XX background noise in a nucleic acid hybridisation assay and for validating  
 XX a test-background feature. The method is useful in chemical, biological  
 XX medical and diagnostic techniques, and for drug discovery. The present  
 XX sequence is a probe used to illustrate the method of the invention.  
 XX  
 XX Sequence 10 BP; 5 A; 1 C; 2 G; 2 T; 0 other;  
 XX  
 XX Query Match 100.0%; Score 7; DB 24; Length 10;  
 XX Best Local Similarity 100.0%; Pred. No. 5.7e+04;  
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 AGTATGA 7  
 XX | | | | |  
 XX Db 1 AGTATGA 7  
 XX  
 XX RESULT 13  
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 XX ID AAL44343 standard; DNA; 10 BP.  
 XX AC AAL44343;  
 XX XX  
 XX DT 24-OCT-2002 (first entry)  
 XX XX  
 XX DE Peptide nucleic acid (PNA) oligomer #3.  
 XX KW PNA oligomer; PNA; peptide nucleic acid; polyamide backbone; ss;  
 XX aminoethylglycine; aeg; aminoethylprolyl; aep; aminoethylpyrrolidine;  
 XX pyr; gene downregulation; bacterial infection; viral infection; cancer;  
 XX metabolic disease; immunological disorder; PNA-clamping.  
 XX  
 XX OS Synthetic.  
 XX Key Location/Qualifiers  
 XX modified\_base 1..10  
 XX FT



XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
 KW antimetastatic; vaccine; diagnosis; ss.  
 XX Homo sapiens.  
 XX WO9965928-A2.  
 XX 23-DEC-1999.  
 XX 18-JUN-1999; 99WO-US13647.  
 XX 19-JUN-1998; 98US-0089853.  
 XX 19-JUN-1998; 98US-0089997.  
 XX 19-JUN-1998; 98US-0090039.  
 XX 19-JUN-1998; 98US-0090040.  
 XX 19-JUN-1998; 98US-0090041.  
 XX (GENZ ) GENZYME CORP.  
 XX (ROBE/) ROBERTS B L.  
 XX (SHAN/) SHANKARA S.  
 XX Roberts BL, Shankara S;  
 XX WPI; 2000-106079/09.  
 XX Isolated polynucleotides differentially expressed between metastatic  
 KW and non-metastatic breast cancer cells, useful for diagnosis,  
 KW prevention and treatment of cancer -  
 XX Claim 1; Page 208; 219pp; English.  
 XX AAZ80767 to AAZ83941 represent tags corresponding to distinct  
 KW transcripts that are preferentially transcribed in the metastatic breast  
 KW tumour tissue (i.e. are upregulated in metastatic breast tumour cells).  
 KW AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts  
 KW that are preferentially transcribed in the primary or non-metastatic  
 KW breast tumour tissue (i.e. are downregulated in metastatic breast tumour  
 KW cells). These transcripts can be used for diagnosis, prognosis,  
 KW monitoring and treatment of breast cancer, particularly where metastatic.  
 KW Diagnosis is by standard immunoassays or hybridisation/amplification  
 KW reactions. Compounds that modulate expression of the transcripts are  
 KW potentially useful for treatment of (metastatic) breast cancer, while  
 KW promoters from the transcripts are used to direct expression, in selected  
 KW cell types, of e.g. therapeutic genes (also ribozymes or antisense  
 KW sequences), particularly an antigen-encoding sequence for use in gene or  
 KW cell-based vaccines. Polypeptides encoded by the transcripts are also  
 KW useful in vaccines; for diagnosing breast cancer and for raising  
 KW specific antibodies (Ab). Ab are used to detect the polypeptides or as  
 KW therapeutic agents. Host cells that produce the polypeptides can be used  
 KW to expand and isolate populations of educated, antigen-specific immune  
 KW effector cells, e.g. cytotoxic T lymphocytes, and these used for  
 KW adoptive immunotherapy.  
 XX SQ Sequence 10 BP; 5 A; 0 C; 3 G; 2 T; 0 other;  
 XX Query Match 100.0%; Score 7; DB 21; Length 10;  
 XX Best Local Similarity 100.0%; Pred. No. 5.7e+04;  
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGTATGCA 7  
 DB 4 AGTATGCA 10  
 XX  
 XX RESULT 8  
 XX AAH32760  
 XX ID AAH32760 standard; cDNA; 10 BP.  
 XX AC AAH32760;  
 XX 13-AUG-2001 (first entry)

XX LPS activated human monocyte expression gene cDNA tag SEQ.133.  
 XX Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;  
 KW expressed sequence tag; diagnosis; human disease; treatment; ss.  
 XX Homo sapiens.  
 XX JP2001069993-A.  
 XX 21-MAR-2001.  
 XX 28-APR-2000; 2000JP-0131079.  
 XX 08-JUL-1999; 99JP-0195103.  
 XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
 XX WPI; 2001-304369/32.  
 XX LPS activated human monocyte expression gene group -  
 XX Claim 10; Page 28; 52pp; Japanese.  
 XX The present invention describes an lipopolysaccharide (LPS) activated  
 KW human monocyte expression gene group consisting of the high-ranking 50  
 KW genes of the highest expression among the genes expressed by human  
 KW monocyte stimulated by LPS in which the cDNA of each gene has the base  
 KW sequence of (AAH32628 to AAH32677) continuous to the base sequence  
 KW 5'-CATG-3' nearest to the polyA region. The gene group is useful for the  
 KW development of new means for the diagnosis and the treatment of various  
 KW human diseases in which human monocyte plays an important role.  
 KW AAH32628 to AAH32943 represent specifically claimed LPS activated human  
 KW monocyte expression gene cDNA tags from the present invention. AAH32944  
 KW represents an LPS activated human monocyte expression gene cDNA sequence  
 KW encoding AAB98009, which are given in the exemplification of the present  
 KW invention.  
 XX SQ Sequence 10 BP; 4 A; 0 C; 4 G; 2 T; 0 other;  
 XX Query Match 100.0%; Score 7; DB 22; Length 10;  
 XX Best Local Similarity 100.0%; Pred. No. 5.7e+04;  
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGTATGCA 7  
 DB 1 AGTATGCA 7  
 XX  
 XX RESULT 9  
 XX AAF38936  
 XX ID AAF38936 standard; DNA; 10 BP.  
 XX AC AAF38936;  
 XX 23-MAR-2001 (first entry)  
 XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5675.  
 XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX Saccharomyces cerevisiae.  
 XX WO200077214-A2.  
 XX 21-DEC-2000.  
 XX 14-JUN-2000; 2000WO-US16223.  
 XX 16-JUN-1999; 99US-0335032.

pathway, resulting in transient arrest of cell growth, allowing more time for DNA repair to occur before cell division takes place. The method is especially used to treat carcinoma but may also be used to: treat other hyperproliferative states (e.g. psoriasis or precancerous conditions); reduce photoaging, oxidative stress or damage; prevent skin cancer; treat allergically mediated inflammation (atopic or contact dermatitis, allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in cells caused by radiation or chemicals; increase melanin production (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to promote apoptosis in epithelial cells that contain damaged DNA. Also oligonucleotides that contain non-hydrolyzable backbones are used to inhibit apoptosis, in response to DNA damage, in epithelial cell. This sequence is melanogenesis associated oligonucleotide #1, one of the oligonucleotides used to inhibit mammalian epithelial cell proliferation, described in the method of the invention.

Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;

Query Match 100.0%; Score 7; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.9e+08;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7

|||||  
2 AGTATGA 8

#### RESULT 6

AAZ78995/c  
AAZ78995 standard; DNA; 10 BP.

AAZ78995;

10-APR-2000 (first entry)

Human dendritic cell SAGE tag, SEQ ID NO:1423.

SAGE tag; serial analysis of gene expression; antigen-presenting cell; APC; monocyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL; cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

Homo sapiens.

W09965924-A2.

23-DEC-1999.

18-JUN-1999; 99WO-US13800.

19-JUN-1998; 98US-0089833.

19-JUN-1998; 98US-0089844.

19-JUN-1998; 98US-0089853.

19-JUN-1998; 98US-0089878.

19-JUN-1998; 98US-0089991.

19-JUN-1998; 98US-0089992.

19-JUN-1998; 98US-0089993.

19-JUN-1998; 98US-0089994.

19-JUN-1998; 98US-0089997.

19-JUN-1998; 98US-0089999.

19-JUN-1998; 98US-0090000.

19-JUN-1998; 98US-0090035.

19-JUN-1998; 98US-0090036.

19-JUN-1998; 98US-0090040.

19-JUN-1998; 98US-0090041.

19-JUN-1998; 98US-0090042.

19-JUN-1998; 98US-0090043.

19-JUN-1998; 98US-0090044.

19-JUN-1998; 98US-0090045.

19-JUN-1998; 98US-0090047.

19-JUN-1998; 98US-0090048.

19-JUN-1998; 98US-0090049.

PR 19-JUN-1998; 98US-0090076.  
PR 19-JUN-1998; 98US-0090077.  
PR 19-JUN-1998; 98US-0090078.  
PR 19-JUN-1998; 98US-0090079.  
PR 19-JUN-1998; 98US-0090080.  
PR 08-DEC-1998; 98US-0111715.  
XX

(GENZ ) GENZYME CORP.

(ROBE/) ROBERTS B L.

(SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

PI

XX WPI; 2000-106077/09.

DR

PT Isolated polynucleotides differentially expressed in antigen-presenting

PT cells, useful in gene vaccines against cancer -

XX Claim 1; Page 105; 130pp; English.

XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene

CC expression) tags used to identify mRNA transcripts encoding

CC immunostimulatory cofactor proteins which are preferentially or

CC differentially expressed in monocyte-derived dendritic cells compared

CC with monocytes. Some of the transcripts correspond to known genes or

CC ESTs (expressed sequence tags) which were previously unknown to be

CC preferentially or differentially expressed in dendritic cells, while

CC other transcripts correspond to novel genes. Antigen-presenting cell

CC (APC)-associated costimulatory factors play an important role in the

CC activation of the cytotoxic immune response, particularly against tumour

CC cells. Tumour antigen presentation via the MHC (major histocompatibility

CC complex) and subsequent recognition by T-cell receptors is alone

CC insufficient to activate a robust cytotoxic immune response that can

CC lyse the tumour cells, immunostimulatory cofactors also being required

CC for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid

CC sequences identified using the SAGE tags have several potential uses.

CC They may be used in vaccines to induce an immune response, particularly

CC against a tumour antigen; to modulate the genotype of an APC; to screen

CC for agents that modulate expression of differentially expressed genes in

CC an APC; and as hybridisation probes/amplification primers for the

CC diagnosis, prognosis and monitoring of diseases related to abnormal

CC expression of these genes. Detection of the dendritic cell

CC to identify cells as belonging to the monocyte lineage. Cells containing

CC these genes can be used in active immunotherapy (or to stimulate

CC production of a population of antigen-specific effector cells) and

CC vectors containing them are used in gene therapy. Co-administration of

CC tumour antigens and APC-associated costimulatory factors ensures adequate

CC antigen presentation to endogenous APCs and upregulates the APCs for the

CC presentation of co-stimulatory signals, migration to T cell-rich sites,

CC secretion of T cell growth factors and secretion of chemokines for

CC recruitment of immune effector cells.

XX

SQ Sequence 10 BP; 4 A; 2 C; 1 G; 3 T; 0 other;

Query Match 100.0%; Score 7; DB 21; Length 10;

Best Local Similarity 100.0%; Pred. No. 5.7e+04;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATGA 7

|||||

7 AGTATGA 1

Db

RESULT 7

AAZ86425

ID: AAZ86425 standard; DNA; 10 BP.

XX AAZ86425;

AC

XX

DT 07-APR-2000 (first entry)

XX Metastatic breast tumour cell downregulated transcript tag #5659.

DE

CC The invention describes inhibition of mammalian epithelial cell  
 CC proliferation by treating cells with at least one oligonucleotide, or  
 CC its fragment. The compounds, which have cytostatic, anti-allergic,  
 CC anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and  
 CC immunosuppressive activities, function as 'ultra-violet mimics' to induce  
 CC DNA repair processes (or a protective response to later exposure to  
 CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer  
 CC or a tumour necrosis factor inhibitor. Probably they mimic products of  
 CC DNA damage, or processed DNA-damage intermediates, by inducing the p53  
 CC pathway, resulting in transient arrest of cell growth, allowing more time  
 CC for DNA repair to occur before cell division takes place. The method is  
 CC especially used to treat carcinoma but may also be used to: treat other  
 CC hyperproliferative states (e.g. psoriasis or precancerous conditions);  
 CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat  
 CC allergically mediated inflammation (atopic or contact dermatitis,  
 CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in  
 CC cells caused by radiation or chemicals; increase melanin production  
 CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to  
 CC promote apoptosis in epithelial cells that contain damaged DNA. Also  
 CC oligonucleotides that contain non-hydrolyzable backbones are used to  
 CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This  
 CC sequence is melanogenesis associated oligonucleotide #7, one of the  
 CC oligonucleotides used to inhibit mammalian epithelial cell  
 CC proliferation, described in the method of the invention.

CC Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 7; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. NO. 3.7e+08;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGTATGA 7  
 Db |||||  
 1 AGTATGA 7

# RESULT 4

AZ10692  
 AZ10692 standard; DNA; 9 BP.

AZ10692;

23-NOV-1999 (first entry)

Oligonucleotide sequence that increases p53 activity in a cell.

p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;  
 UV-induced hyperproliferative disease; psoriasis; vitiligo;  
 atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;  
 skin cancer; ss.

Synthetic.

GB2336157-A.

13-OCT-1999.

24-MAR-1999; 99GB-0006758.

26-MAR-1998; 98US-0048927.

(UYBO-) UNIV BOSTON.

Gilchrest BA, Yaar M, Eller M;

WPI; 1999-543520/46.

DNA fragments useful for increasing p53 activity in a cell and reducing  
 susceptibility to UV-induced hyperproliferative diseases -

Claim 11; Page 29; 44pp; English.

AZ10692-97 represent DNA fragments that are used for increasing p53

CC activity in a cell. The oligonucleotides are are UV mimetics and  
 CC protect cells against subsequent exposure to UV-irradiation or  
 CC chemicals. The oligonucleotides are useful for increasing p53 activity  
 CC in a cell, reducing the susceptibility to UV-induced hyperproliferative  
 CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic  
 CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging  
 CC and reducing susceptibility to skin cancer.

SQ Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;

Query Match 100.0%; Score 7; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. NO. 2.9e+08;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATGA 7

Db |||||

2 AGTATGA 8

# RESULT 5

AAS14905

ID AAS14905 standard; DNA; 9 BP.

XX AC AAS14905;

XX 14-FEB-2002 (first entry)

XX Melanogenesis associated oligonucleotide #1.

XX Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;  
 XX anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;  
 XX immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;  
 XX tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;  
 XX carcinoma; oxidative stress; skin cancer; allergic mediated inflammation;  
 XX conjunctivitis; allergic rhinitis; vitiligo; ss.

OS Synthetic.

PH Key Location/Qualifiers

FT modified\_base 1

FT /\*tag= a

FT /mod\_base= g

FT /note= "Optionally phosphorylated"

XX WO200174342-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10162.

XX 31-MAR-2000; 2000US-0540843.

XX (UYBO-) UNIV BOSTON.

XX Gilchrest BA, Yaar M, Eller M;

XX WPI; 2001-626338/72.

XX Inhibiting proliferation of epithelial cells, useful e.g. for treating  
 PT carcinoma, using specific oligonucleotides that mimic the effects of  
 PT ultra-violet light -

XX Claim 1; Page 36; 74pp; English.

XX The invention describes inhibition of mammalian epithelial cell  
 CC proliferation by treating cells with at least one oligonucleotide, or  
 CC its fragment. The compounds, which have cytostatic, anti-allergic,  
 CC anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and  
 CC immunosuppressive activities, function as 'ultra-violet mimics' to induce  
 CC DNA repair processes (or a protective response to later exposure to  
 CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer  
 CC or a tumour necrosis factor inhibitor. Probably they mimic products of  
 CC DNA damage, or processed DNA-damage intermediates, by inducing the p53



PT DNA fragments useful for increasing p53 activity in a cell and reducing  
 PT susceptibility to UV-induced hyperproliferative diseases -  
 XX Claim 11; Page 30; 4pp; English.

XX AA210692-97 represent DNA fragments that are used for increasing p53  
 CC activity in a cell. The oligonucleotides are UV mimetics and  
 CC protect cells against subsequent exposure to UV-irradiation or  
 CC chemicals. The oligonucleotides are useful for increasing p53 activity  
 CC in a cell, reducing the susceptibility to UV-induced hyperproliferative  
 CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic  
 CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging  
 CC and reducing susceptibility to skin cancer.

XX Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 7; DB 20; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+08;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATGA 7  
 Db 1 AGTATGA 7

RESULT 2  
 AAS14907  
 ID AAS14907 standard; DNA; 7 BP.

XX AAS14907;

XX 14-FEB-2002 (first entry)

XX Melanogenesis associated oligonucleotide #3.

XX Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;  
 XX anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;  
 XX immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;  
 XX tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;  
 XX carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;  
 XX conjunctivitis; allergic rhinitis; vitiligo; ss.

XX Synthetic.

XX WO200174342-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10162.

XX 31-MAR-2000; 2000US-0540843.

XX (UYBO-) UNIV BOSTON.

XX Gilchrist BA, Yaar M, Eller M;

XX WPI; 2001-626338/72.

XX Inhibiting proliferation of epithelial cells, useful e.g. for treating  
 PT carcinoma, using specific oligonucleotides that mimic the effects of  
 PT ultra-violet light -

XX Claim 1; Page 36; 74pp; English.

XX The invention describes inhibition of mammalian epithelial cell  
 CC proliferation by treating cells with at least one oligonucleotide, or  
 CC its fragment. The compounds, which have cytostatic, anti-allergic,  
 CC anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and  
 CC immunosuppressive activities, function as 'ultra-violet mimics' to induce  
 CC DNA repair processes (or a protective response to later exposure to  
 CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer  
 CC or a tumour necrosis factor inhibitor. Probably they mimic products of  
 CC DNA damage, or processed DNA-damage intermediates, by inducing the p53

CC pathway, resulting in transient arrest of cell growth, allowing more time  
 CC for DNA repair to occur before cell division takes place. The method is  
 CC especially used to treat carcinoma but may also be used to: treat other  
 CC hyperproliferative states (e.g. psoriasis or precancerous conditions);  
 CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat  
 CC allergically mediated inflammation (atopic or contact dermatitis,  
 CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in  
 CC cells caused by radiation or chemicals; increase melanin production  
 CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to  
 CC promote apoptosis in epithelial cells that contain damaged DNA. Also  
 CC oligonucleotides that contain non-hydrolyzable backbones are used to  
 CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This  
 CC sequence is melanogenesis associated oligonucleotide #3, a truncated  
 CC version of the oligonucleotide shown in AAS14906, one of the  
 CC oligonucleotides used to inhibit mammalian epithelial cell  
 CC proliferation, described in the method of the invention.

XX Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 7; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+08;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATGA 7

Db 1 AGTATGA 7

RESULT 3

AAS14911

ID AAS14911 standard; DNA; 7 BP.

XX AAS14911;

XX 14-FEB-2002 (first entry)

XX Melanogenesis associated oligonucleotide #7.

XX Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;  
 XX anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;  
 XX immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;  
 XX tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;  
 XX carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;  
 XX conjunctivitis; allergic rhinitis; vitiligo; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT modified\_base 1

FT /tag= a

FT /mod\_base= a

FT /note= "Phosphorylated"

XX WO200174342-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10162.

XX 31-MAR-2000; 2000US-0540843.

XX (UYBO-) UNIV BOSTON.

XX Gilchrist BA, Yaar M, Eller M;

XX WPI; 2001-626338/72.

XX Inhibiting proliferation of epithelial cells, useful e.g. for treating  
 PT carcinoma, using specific oligonucleotides that mimic the effects of  
 PT ultra-violet light -  
 XX Claim 1; Page 38; 74pp; English.

Result No.	Score	Query Length	ID	Description
1	7	100.0	7 20	Oligonucleotide se
2	7	100.0	7 23	Melanogenesis asso
3	7	100.0	7 23	Melanogenesis asso
4	7	100.0	9 20	Oligonucleotide se
5	7	100.0	9 23	Melanogenesis asso
6	7	100.0	10 21	Human dendritic ce
7	7	100.0	21	Metastatic breast
8	7	100.0	22	LPS activated huma

```

QY      1 GTATG 5
Db      |||||
        6 GTATG 2

RESULT 6
LOCUS   AX104946
DEFINITION
Sequence 1138 from Patent WO0122972.
ACCESSION
AX104946
VERSION
AX104946.1 GI:13921143
KEYWORDS
synthetic construct
SOURCE
artificial construct
ORGANISM
1 (bases 1 to 8)
REFERENCE
1 (bases 1 to 8)
AUTHORS
Krieg, A.M., Schetter, C. and Vollmer, J.C.
TITLE
Immunostimulatory nucleic acids
JOURNAL
Patent: WO 0122972-A 1138 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
Location/Qualifiers
1..8
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT      2 a 1 c 2 g 3 t
ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTATG 5
Db      |||||
        3 GTATG 7

RESULT 7
LOCUS   AX119567
DEFINITION
Sequence 224 from Patent WO0129251.
ACCESSION
AX119567
VERSION
AX119567.1 GI:14036486
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 8)
AUTHORS
Messiaen, L. and Callens, T.
TITLE
Improved mutation analysis of the nf1 gene
JOURNAL
Patent: WO 0129251-A 224 26-APR-2001;
UNIVERSITEIT GENT (BE)
FEATURES
Location/Qualifiers
1..8
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT      1 a 0 c 4 g 3 t
ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTATG 5
Db      |||||
        3 GTATG 7

RESULT 8
LOCUS   AX104946
DEFINITION
Sequence 1138 from Patent WO0122972.
ACCESSION
AX104946
VERSION
AX104946.1 GI:13921143
KEYWORDS
synthetic construct
SOURCE
artificial construct
ORGANISM
1 (bases 1 to 8)
REFERENCE
1 (bases 1 to 8)
AUTHORS
Krieg, A.M., Schetter, C. and Vollmer, J.C.
TITLE
Immunostimulatory nucleic acids
JOURNAL
Patent: WO 0122972-A 1138 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT      2 a 1 c 2 g 3 t
ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTATG 5
Db      |||||
        6 GTATG 2

RESULT 9
LOCUS   AX268753
DEFINITION
Sequence 1 from Patent WO0174342.
ACCESSION
AX268753
VERSION
AX268753.1 GI:16541825
KEYWORDS
synthetic construct
SOURCE
artificial construct
ORGANISM
1 (bases 1 to 8)
REFERENCE
1 (bases 1 to 8)
AUTHORS
Gilchrist, B.A., Yaar, M. and Eller, M.
TITLE
Use of locally applied dna fragments
JOURNAL
Patent: WO 0174342-A 1 11-OCT-2001;
TRUSTEES OF BOSTON UNIVERSITY (US)
FEATURES
Location/Qualifiers
1..9
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT      3 a 0 c 4 g 2 t
ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 9;

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Best Local Similarity 100.0%; Pred. No. 4.5e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTATG 5
    |||||
Db 3 GTATG 7

RESULT 10
AX667174/c
LOCUS AX667174
DEFINITION Sequence 623 from Patent WO0242459.
ACCESSION AX667174
VERSION AX667174.1 GI:29291326
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Liu, Q.
TITLE Position dependent recognition of gnn nucleotide triplets by zinc
JOURNAL Patent: WO 0242459-A 623 30-MAY-2002;
Sangamo Biosciences Inc. (US)
FEATURES
    source
        1..9
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
        /note="example target DNA"
BASE COUNT 2 a 2 c 3 g 2 t
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTATG 5
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Db 6 GTATG 2

RESULT 11
AX668771
LOCUS AX668771
DEFINITION Sequence 2220 from Patent WO0242459.
ACCESSION AX668771
VERSION AX668771.1 GI:29291746
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Liu, Q.
TITLE Position dependent recognition of gnn nucleotide triplets by zinc
JOURNAL Patent: WO 0242459-A 2220 30-MAY-2002;
Sangamo Biosciences Inc. (US)
FEATURES
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        /note="example target DNA"
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTATG 5
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Db 1 GTATG 5

Best Local Similarity 100.0%; Pred. No. 4.5e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTATG 5
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Db 4 GTATG 8

RESULT 12
AX668807
LOCUS AX668807
DEFINITION Sequence 2256 from Patent WO0242459.
ACCESSION AX668807
VERSION AX668807.1 GI:29291782
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Liu, Q.
TITLE Position dependent recognition of gnn nucleotide triplets by zinc
JOURNAL Patent: WO 0242459-A 2256 30-MAY-2002;
Sangamo Biosciences Inc. (US)
FEATURES
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        /note="example target DNA"
BASE COUNT 2 a 0 c 4 g 3 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 4.5e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTATG 5
    |||||
Db 4 GTATG 8

RESULT 13
S50583
LOCUS S50583
DEFINITION type I procollagen [human, mRNA Mutant, 9 nt].
ACCESSION S50583
VERSION S50583.1 GI:233928
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 9)
AUTHORS Tauneyoshi, T., Westerhausen, A., Constantinou, C.D. and Prockop, D.J.
TITLE Substitutions for glycine alpha 1-637 and glycine alpha 2-694 of
type I procollagen in lethal osteogenesis imperfecta. The
conformational strain on the triple helix introduced by a glycine
substitution can be transmitted along the helix
J. Biol. Chem. 266 (24), 15608-15613 (1991).
JOURNAL 91340689
MEDLINE 1874719
PUBMED
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibseq 50583] from the original journal article.
This sequence comes from Fig 5A.
FEATURES
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        /mol_type="mRNA"
        /db_xref="taxon:9606"
        1..9
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BASE COUNT 1 a 3 c 2 g 3 t
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Best Local Similarity 100.0%; Pred. No. 4.5e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTATG 5
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Db 1 GTATG 5
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Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5  
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Db 6 GTATG 10

Search completed: December 31, 2003, 17:09:45  
Job time : 462.316 secs

Qy 1 GTATG 5  
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Db 5 GTATG 9

RESULT 14  
S50585  
LOCUS S50585 9 bp DNA linear PRI 07-MAY-1993  
DEFINITION type I procollagen [human, Genomic Mutant, 9 nt].  
ACCESSION S50585  
VERSION S50585.1 GI:233929  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 9)  
Tauneyoshi,T., Westerhausen,A., Constantinou,C.D. and Prockop,D.J.  
Substitutions for glycine alpha 1-637 and glycine alpha 2-694 of  
type I procollagen in lethal osteogenesis imperfecta. The  
conformational strain on the triple helix introduced by a glycine  
substitution can be transmitted along the helix  
J. Biol. Chem. 266 (24), 15608-15613 (1991)  
91340689  
MEDLINE  
PUBMED 1874719  
REMARK GenBank staff at the National Library of Medicine created this  
entry [NCBI gibbsq 50585] from the original journal article.  
This sequence comes from Fig 5B.

FEATURES  
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Location/Qualifiers  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
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2 a 1 c 3 g 3 t

Query Match 100.0%; Score 5; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.5e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5  
|||||  
Db 5 GTATG 9

RESULT 15  
A18263  
LOCUS A18263 10 bp DNA linear PAT 12-APR-1994  
DEFINITION oligonucleotide.  
ACCESSION A18263  
VERSION A18263.1 GI:512254  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
1 (bases 1 to 10)  
Della Valle,F., Callegaro,L. and Negro,A.  
Process for the preparation of genetic vectors for the nerve growth  
factor expression in eukaryotic cells  
Patent: EP 0432510-A 12 19-JUN-1991;  
FIDIA S.p.A

FEATURES  
source 1..10  
Location/Qualifiers  
1..10  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
3 a 1 c 3 g 3 t

BASE COUNT 3 a 1 c 3 g 3 t  
ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 11:36:21 ; Search time 144.494 Seconds  
(without alignments)  
93.410 Million cell updates/sec

Title: US-09-540-843-4

Perfect score: 5  
Sequence: 1 gtagg 5

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 2101872

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	100.0	5	AAZ10695	Oligonucleotide se
2	5	100.0	5	AAZ10696	Oligonucleotide se
3	5	100.0	5	AAZ14908	Melanogenesis asso
4	5	100.0	5	AAZ14910	Melanogenesis asso
5	5	100.0	7	AAZ10694	Oligonucleotide se
6	5	100.0	7	AAZ14907	Melanogenesis asso
7	5	100.0	7	AAZ14911	Melanogenesis asso
8	5	100.0	8	AAZ02250	Direct repeat sequ

9	5	100.0	9	19	AAV22350	A promoter regulat
10	5	100.0	9	19	AAV22283	GAS complement gen
11	5	100.0	9	19	AAV15899	Cyclin D transcrip
12	5	100.0	9	20	AAZ10692	Oligonucleotide se
13	5	100.0	9	23	AAZ14905	Melanogenesis asso
14	5	100.0	9	24	ABX03786	Human DNA PCR prim
15	5	100.0	9	24	ABQ71504	Zinc finger protei
16	5	100.0	9	24	ABQ71922	Zinc finger protei
17	5	100.0	9	24	ABQ71958	Zinc finger protei
18	5	100.0	10	14	AAQ43164	Donor oligomer wit
19	5	100.0	10	15	AAQ71104	Merlin exon 14 spl
20	5	100.0	10	16	AAQ97224	Oligonucleotide Ec
21	5	100.0	10	16	AAZ32625	Anticancer duplex
22	5	100.0	10	17	AAZ35734	Primer E19 for V d
23	5	100.0	10	18	AAZ66073	(dG-da)n.(dG-dr)n
24	5	100.0	10	19	AAV50271	Yeast tag for addi
25	5	100.0	10	19	AAV50250	Yeast tag for addi
26	5	100.0	10	19	AAV50184	Yeast tag for addi
27	5	100.0	10	19	AAV50127	Yeast tag for NORF
28	5	100.0	10	19	AAV35934	Primer used in RAP
29	5	100.0	10	19	AAV35910	Primer used in RAP
30	5	100.0	10	20	AAZ18629	p53 serial analysi
31	5	100.0	10	20	AAV73806	Chromophore contai
32	5	100.0	10	21	AAZ73931	Human dendritic ce
33	5	100.0	10	21	AAZ74120	Human monocyte and
34	5	100.0	10	21	AAZ74154	Human monocyte and
35	5	100.0	10	21	AAZ93858	Oligonucleotide us
36	5	100.0	10	21	AAZ93865	Oligonucleotide us
37	5	100.0	10	21	AAZ53110	Mouse DNA adapter
38	5	100.0	10	21	AAZ15244	Primer MRI5 for mo
39	5	100.0	10	21	AAZ56166	Human monocyte gen
40	5	100.0	10	21	AAZ56218	Human macrophage g
41	5	100.0	10	21	AAZ56224	Human macrophage g
42	5	100.0	10	21	AAZ56294	Human macrophage g
43	5	100.0	10	21	AAZ56321	Human macrophage g
44	5	100.0	10	21	AAZ56331	Human macrophage g
45	5	100.0	10	21	AAZ56407	Human macrophage g

ALIGNMENTS

RESULT 1  
AAZ10695  
ID AAZ10695 standard; DNA; 5 BP.  
XX  
AC AAZ10695;  
XX  
DT 23-NOV-1999 (first entry)  
XX  
DE Oligonucleotide sequence that increases p53 activity in a cell.  
XX  
KW p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;  
KW UV-induced hyperproliferative disease; psoriasis; vitiligo;  
KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;  
KW skin cancer; ss.  
XX  
OS Synthetic.  
XX  
PN GB2336157-A.  
XX  
PD 13-OCT-1999.  
XX  
PF 24-MAR-1999; 99GB-0006758.  
XX  
PR 26-MAR-1998; 98US-0048927.  
XX  
PA (UYBO-) UNIV BOSTON.  
XX  
PI Gilchrist BA, Yaar M, Eller M;  
XX WPI; 1999-543520/46.  
XX

PT DNA fragments useful for increasing p53 activity in a cell and reducing  
 PT susceptibility to UV-induced hyperproliferative diseases -  
 XX  
 PS Claim 11; Page 30; 44pp; English.  
 XX  
 CC AA210692-97 represent DNA fragments that are used for increasing p53  
 CC activity in a cell. The oligonucleotides are UV mimetics and  
 CC protect cells against subsequent exposure to UV-irradiation or  
 CC chemicals. The oligonucleotides are useful for increasing p53 activity  
 CC in a cell, reducing the susceptibility to UV-induced hyperproliferative  
 CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic  
 CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging  
 CC and reducing susceptibility to skin cancer.  
 XX  
 SQ Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 other;  
 Query Match 100.0%; Score 5; DB 20; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GTATG 5  
 Db |||||  
 5 GTATG 1  
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 AA210696 standard; DNA; 5 BP.  
 AA210696;  
 23-NOV-1999 (first entry)  
 Oligonucleotide sequence that increases p53 activity in a cell.  
 p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;  
 UV-induced hyperproliferative disease; psoriasis; vitiligo;  
 atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;  
 skin cancer; ss.  
 Synthetic.  
 GB2336157-A.  
 13-OCT-1999.  
 24-MAR-1999; 99GB-0006758.  
 26-MAR-1998; 98US-0048927.  
 (UYBO-) UNIV BOSTON.  
 Gilchrest BA, Yaar M, Eller M;  
 WPI; 1999-543520/46.  
 DNA fragments useful for increasing p53 activity in a cell and reducing  
 PT susceptibility to UV-induced hyperproliferative diseases -  
 XX  
 PS Claim 11; Page 30; 44pp; English.  
 XX  
 CC AA210692-97 represent DNA fragments that are used for increasing p53  
 CC activity in a cell. The oligonucleotides are UV mimetics and  
 CC protect cells against subsequent exposure to UV-irradiation or  
 CC chemicals. The oligonucleotides are useful for increasing p53 activity  
 CC in a cell, reducing the susceptibility to UV-induced hyperproliferative  
 CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic  
 CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging  
 CC and reducing susceptibility to skin cancer.  
 XX  
 SQ Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other;  
 Query Match 100.0%; Score 5; DB 20; Length 5;

Best Local Similarity 100.0%; Pred. No. 5.2e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GTATG 5  
 Db |||||  
 5 GTATG 1  
 RESULT 3  
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 ID AA214908 standard; DNA; 5 BP.  
 XX  
 AC AA214908;  
 XX  
 DT 14-FEB-2002 (first entry)  
 XX  
 DE Melanogenesis associated oligonucleotide #4.  
 XX  
 KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;  
 KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;  
 KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;  
 KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;  
 KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;  
 KW conjunctivitis; allergic rhinitis; vitiligo; ss.  
 XX  
 OS Synthetic.  
 XX  
 FN WO200174342-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US10162.  
 XX  
 PR 31-MAR-2000; 2000US-0540843.  
 XX  
 PA (UYBO-) UNIV BOSTON.  
 XX  
 PI Gilchrest BA, Yaar M, Eller M;  
 XX  
 DR WPI; 2001-626338/72.  
 XX  
 XX Inhibiting proliferation of epithelial cells, useful e.g. for treating  
 PT carcinoma, using specific oligonucleotides that mimic the effects of  
 PT ultra-violet light -  
 PT  
 XX Claim 1; Page 36; 74pp; English.  
 XX  
 CC The invention describes inhibition of mammalian epithelial cell  
 CC proliferation by treating cells with at least one oligonucleotide, or  
 CC its fragment. The compounds, which have cytostatic, anti-allergic,  
 CC anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and  
 CC immunosuppressive activities, function as 'ultra-violet mimics' to induce  
 CC DNA repair processes (or a protective response to later exposure to  
 CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer  
 CC or a tumour necrosis factor inhibitor. Probably they mimic products of  
 CC DNA damage, or processed DNA-damage intermediates, by inducing the p53  
 CC pathway, resulting in transient arrest of cell growth, allowing more time  
 CC for DNA repair to occur before cell division takes place. The method is  
 CC especially used to treat carcinoma but may also be used to: treat other  
 CC hyperproliferative states (e.g. psoriasis or precancerous conditions);  
 CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat  
 CC allergic rhinitis and conjunctivitis; prevent or reduce dermatitis,  
 CC cells caused by radiation or chemicals; increase melanin production  
 CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to  
 CC promote apoptosis in epithelial cells that contain damaged DNA. Also  
 CC oligonucleotides that contain non-hydrolyzable backbones are used to  
 CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This  
 CC sequence is melanogenesis associated oligonucleotide #4, a truncated  
 CC version of the oligonucleotide shown in AA214906, one of the  
 CC oligonucleotides used to inhibit mammalian epithelial cell  
 CC proliferation, described in the method of the invention.  
 XX



SQ Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 other;  
 Query Match 100.0%; Score 5; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTATG 5  
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 Db 1 GTATG 5

RESULT 4  
 AAS14910/c  
 ID AAS14910 standard; DNA; 5 BP.  
 XX AC AAS14910;  
 14-FEB-2002 (first entry)  
 Melanogenesis associated oligonucleotide #6.

Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;  
 anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;  
 immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;  
 tumour necrosis factor inhibitor; phototaging; hyperproliferative disease;  
 carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;  
 conjunctivitis; allergic rhinitis; vitiligo; ss.

Synthetic.  
 WO200174342-A2.  
 11-OCT-2001.  
 30-MAR-2001; 2001WO-US10162.  
 31-MAR-2000; 2000US-0540843.  
 (UYBO-) UNIV BOSTON.  
 Gilchrest BA, Yaar M, Eller M;  
 WPI; 2001-626338/72.

Inhibiting proliferation of epithelial cells, useful e.g. for treating  
 carcinoma, using specific oligonucleotides that mimic the effects of  
 ultra-violet light -

Claim 1; Page 36; 74pp; English.

The invention describes inhibition of mammalian epithelial cell  
 proliferation by treating cells with at least one oligonucleotide, or  
 its fragment. The compounds, which have cytostatic, anti-allergic,  
 anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and  
 immunosuppressive activities, function as 'ultra-violet mimics' to induce  
 DNA repair processes (or a protective response to later exposure to  
 radiation or chemicals), as a proliferation inhibitor, apoptosis inducer  
 or a tumour necrosis factor inhibitor. Probably they mimic products of  
 DNA damage, or processed DNA-damage intermediates, by inducing the p53  
 pathway, resulting in transient arrest of cell growth, allowing more time  
 for DNA repair to occur before cell division takes place. The method is  
 especially used to treat carcinoma but may also be used to treat other  
 hyperproliferative states (e.g. psoriasis or precancerous conditions);  
 reduce phototaging, oxidative stress or damage; prevent skin cancer; treat  
 allergically mediated inflammation (atopic or contact dermatitis,  
 allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in  
 cells caused by radiation or chemicals; increase melanin production  
 (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to  
 promote apoptosis in epithelial cells that contain damaged DNA. Also  
 oligonucleotides that contain non-hydrolyzable backbones are used to  
 inhibit apoptosis, in response to DNA damage, in epithelial cell. This  
 sequence is melanogenesis associated oligonucleotide #6, one of the  
 oligonucleotides used to inhibit mammalian epithelial cell proliferation,

CC described in the method of the invention.  
 XX  
 SQ Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other;  
 Query Match 100.0%; Score 5; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTATG 5  
 |||||  
 Db 5 GTATG 1

RESULT 5  
 AAZ10694  
 ID AAZ10694 standard; DNA; 7 BP.  
 XX AC AAZ10694;  
 23-NOV-1999 (first entry)  
 Oligonucleotide sequence that increases p53 activity in a cell.  
 DE p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;  
 XX UV-induced hyperproliferative disease; psoriasis; vitiligo;  
 KW atopic dermatitis; allergic rhinitis; conjunctivitis; phototaging;  
 KW skin cancer; ss.  
 XX  
 OS Synthetic.  
 XX GB2336157-A.  
 PN 13-OCT-1999.  
 PD 24-MAR-1999; 99GB-0006758.  
 XX 26-MAR-1998; 98US-0048927.  
 PF (UYBO-) UNIV BOSTON.  
 PR Gilchrest BA, Yaar M, Eller M;  
 XX WPI; 1999-543520/46.  
 DR DNA fragments useful for increasing p53 activity in a cell and reducing  
 PT susceptibility to UV-induced hyperproliferative diseases -  
 XX Claim 11; Page 30; 44pp; English.

AAZ10692-97 represent DNA fragments that are used for increasing p53  
 activity in a cell. The oligonucleotides are UV mimetics and  
 protect cells against subsequent exposure to UV-irradiation or  
 chemicals. The oligonucleotides are useful for increasing p53 activity  
 in a cell, reducing the susceptibility to UV-induced hyperproliferative  
 diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic  
 rhinitis, conjunctivitis, and UV-induced dermatoses, reducing phototaging  
 and reducing susceptibility to skin cancer.

XX Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;  
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 Query Match 100.0%; Score 5; DB 20; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTATG 5  
 |||||  
 Db 2 GTATG 6

RESULT 6  
 AAS14907  
 ID AAS14907 standard; DNA; 7 BP.  
 XX

AC AAS14907;  
 DT 14-FEB-2002 (first entry)  
 XX  
 DE Melanogenesis associated oligonucleotide #3.  
 XX  
 KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;  
 KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;  
 KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;  
 KW tumour necrosis factor inhibitor; photoging; hyperproliferative disease;  
 KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;  
 KW conjunctivitis; allergic rhinitis; vitiligo; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200174342-A2.  
 XX  
 XX 11-OCT-2001.  
 XX  
 XX 30-MAR-2001; 2001WO-US10162.  
 XX  
 XX 31-MAR-2000; 2000US-0540843.  
 XX  
 XX (UYBO-) UNIV BOSTON.  
 XX  
 XX Gilchrest BA, Year M, Eller M;  
 XX  
 XX WPI; 2001-626338/72.  
 XX  
 XX Inhibiting proliferation of epithelial cells, useful e.g. for treating  
 XX carcinoma, using specific oligonucleotides that mimic the effects of  
 XX ultra-violet light -  
 XX  
 XX Claim 1; Page 36; 74pp; English.  
 XX  
 XX The invention describes inhibition of mammalian epithelial cell  
 XX proliferation by treating cells with at least one oligonucleotide, or  
 XX its fragment. The compounds, which have cytostatic, anti-allergic,  
 XX anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and  
 XX immunosuppressive activities, function as 'ultra-violet mimics' to induce  
 XX DNA repair processes (or a protective response to later exposure to  
 XX radiation or chemicals), as a proliferation inhibitor, apoptosis inducer  
 XX or a tumour necrosis factor inhibitor. Probably they mimic products of  
 XX DNA damage, or processed DNA-damage intermediates, by inducing the p53  
 XX pathway, resulting in transient arrest of cell growth, allowing more time  
 XX for DNA repair to occur before cell division takes place. The method is  
 XX especially used to treat carcinoma but may also be used to: treat other  
 XX hyperproliferative states (e.g. psoriasis or precancerous conditions);  
 XX reduce photoging, oxidative stress or damage; prevent skin cancer; treat  
 XX allergically mediated inflammation (atopic or contact dermatitis,  
 XX allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in  
 XX cells caused by radiation or chemicals; increase melanin production  
 XX (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to  
 XX promote apoptosis in epithelial cells that contain damaged DNA. Also  
 XX oligonucleotides that contain non-hydrolyzable backbones are used to  
 XX inhibit apoptosis, in response to DNA damage, in epithelial cell. This  
 XX sequence is melanogenesis associated oligonucleotide #3, a truncated  
 XX version of the oligonucleotide shown in AAS14906, one of the  
 XX oligonucleotides used to inhibit mammalian epithelial cell  
 XX proliferation, described in the method of the invention.  
 XX  
 XX Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 5; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATG 5  
 |||||  
 Db 2 GATG 6

RESULT 7

AAS14911  
 ID AAS14911 standard; DNA; 7 BP.  
 XX  
 AC AAS14911;  
 XX  
 DT 14-FEB-2002 (first entry)  
 XX  
 DE Melanogenesis associated oligonucleotide #7.  
 XX  
 KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;  
 KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;  
 KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;  
 KW tumour necrosis factor inhibitor; photoging; hyperproliferative disease;  
 KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;  
 KW conjunctivitis; allergic rhinitis; vitiligo; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 XX modified\_base 1  
 XX FT /\*tag= a  
 XX FT /mod\_base= a  
 XX FT /note= "Phosphorylated"  
 XX  
 XX WO200174342-A2.  
 XX  
 XX 11-OCT-2001.  
 XX  
 XX 30-MAR-2001; 2001WO-US10162.  
 XX  
 XX 31-MAR-2000; 2000US-0540843.  
 XX  
 XX (UYBO-) UNIV BOSTON.  
 XX  
 XX Gilchrest BA, Year M, Eller M;  
 XX  
 XX WPI; 2001-626338/72.  
 XX  
 XX Inhibiting proliferation of epithelial cells, useful e.g. for treating  
 XX carcinoma, using specific oligonucleotides that mimic the effects of  
 XX ultra-violet light -  
 XX  
 XX Claim 1; Page 38; 74pp; English.  
 XX  
 XX The invention describes inhibition of mammalian epithelial cell  
 XX proliferation by treating cells with at least one oligonucleotide, or  
 XX its fragment. The compounds, which have cytostatic, anti-allergic,  
 XX anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and  
 XX immunosuppressive activities, function as 'ultra-violet mimics' to induce  
 XX DNA repair processes (or a protective response to later exposure to  
 XX radiation or chemicals), as a proliferation inhibitor, apoptosis inducer  
 XX or a tumour necrosis factor inhibitor. Probably they mimic products of  
 XX DNA damage, or processed DNA-damage intermediates, by inducing the p53  
 XX pathway, resulting in transient arrest of cell growth, allowing more time  
 XX for DNA repair to occur before cell division takes place. The method is  
 XX especially used to treat carcinoma but may also be used to: treat other  
 XX hyperproliferative states (e.g. psoriasis or precancerous conditions);  
 XX reduce photoging, oxidative stress or damage; prevent skin cancer; treat  
 XX allergically mediated inflammation (atopic or contact dermatitis,  
 XX allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in  
 XX cells caused by radiation or chemicals; increase melanin production  
 XX (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to  
 XX promote apoptosis in epithelial cells that contain damaged DNA. Also  
 XX oligonucleotides that contain non-hydrolyzable backbones are used to  
 XX inhibit apoptosis, in response to DNA damage, in epithelial cell. This  
 XX sequence is melanogenesis associated oligonucleotide #7, one of the  
 XX oligonucleotides used to inhibit mammalian epithelial cell  
 XX proliferation, described in the method of the invention.  
 XX  
 XX Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;  
 XX  
 XX Query Match 100.0%; Score 5; DB 23; Length 7;  
 XX Best Local Similarity 100.0%; Pred. No. 3.7e+08;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5  
| | | | |  
Db 2 GTATG 6

RESULT 8  
AAD02250/c  
ID AAD02250 standard; DNA; 8 BP.

XX AC AAD02250;

XX DT 28-MAR-2001 (first entry)

XX DE Direct repeat sequence that binds to SB protein.

XX KW Sleeping Beauty; SB; AdSB10; adenovirus; transposase;  
XX KW non-integrating viral vector; cytosolic; anti-diabetic; cardiant;  
XX KW neuroprotective; genetic disease; gene therapy; cancer;  
XX KW cystic fibrosis; diabetes; cardiovascular disease; brain malfunction;  
XX KW genome analysis; chemotherapy; transgenic host cell; direct repeat; ds.

XX PS Unidentified.

XX OS WO200068399-A2.

XX PN 16-NOV-2000.

XX PD 11-MAY-2000; 2000WO-US12827.

XX PF 11-MAY-1999; 99US-0133569.

XX PR (MINU ) UNIV MINNESOTA.

XX RA (BAYU ) BAYLOR COLLEGE MEDICINE.

XX RA (NCIV/) MCIVOR R S.

XX RA (HACK/) HACKETT P B.

XX RA (AGUI/) AGUILAR-CORDOVA E.

XX PI Mcivor RS, Hackett PB, Aguilar-Cordova E;

XX PS WPI; 2001-024870/03.

XX PT Non-integrating (adenovirus-based) viral vectors useful in gene  
XX PT therapy, especially for treating patients suffering from a genetic  
XX PT disease, e.g. cystic fibrosis, diabetes, cardiovascular disease, cancer  
XX PT or brain malfunction -

XX PS Disclosure; Page 14; 62pp; English.

XX CC The patent discloses non-integrating viral vectors comprising a  
XX CC polynucleotide flanked by inverted repeats that bind a transposase, a  
XX CC transposase-encoding polynucleotide operably linked to a regulatory  
XX CC sequence comprising an operator, that alters expression of the  
XX CC transposase-encoding polynucleotide. Transposon sequences can integrate  
XX CC into genomic DNA whether or not the cell is dividing. AdSB10 is a SB  
XX CC (Sleeping Beauty) transposase-transducing adenoviral non-integrating  
XX CC vector. The non-integrating viral vectors are useful for treating  
XX CC genetic disease characterised by subnormal production of a polypeptide or  
XX CC RNA, e.g. for replacement of a defective gene, delivery of a polypeptide  
XX CC drug or supplementation of a metabolic activity. These genetic diseases  
XX CC include cystic fibrosis, diabetes, cardiovascular disease, cancer or  
XX CC brain malfunction. The non-integrating viral vectors are useful as  
XX CC nucleic acid delivery systems, e.g. for genome analysis or gene therapy  
XX CC and can also be used for applications that involve long-term production  
XX CC of a polypeptide. The non-integrating viral vectors are also useful for  
XX CC creating transgenic host cells that provide normal cells with protection  
XX CC against toxic side effects of chemotherapy.  
XX CC The sequence of the present invention is a direct repeat sequence that  
XX CC binds to SB protein.

XX SQ Sequence 8 BP; 4 A; 3 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 5; DB 22; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3.2e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5  
| | | | |  
Db 6 GTATG 2

RESULT 9

AAV22350

ID AAV22350 standard; RNA; 9 BP.

XX AC AAV22350;

XX DT 29-JUN-1998 (first entry)

XX DE A promoter regulatory motif found in the utrons of the invention.

XX KW 3' untranslated region; UTR; inhibition; gene expression; ICAM-7;  
XX KW interferon-gamma; IFN-gamma; major histocompatibility complex; MHC;  
XX KW antigen expression; gene promoter; utron; B7-1; B7-2; Fc gamma R;  
XX KW HIV gene expression; transplant rejection; treatment;  
XX KW autoimmune disease; inflammatory disease; ss.

XX OS Unidentified.

XX PN WO9744450-A1.

XX PD 27-NOV-1997.

XX PF 21-MAY-1997; 97WO-US09459.

XX PR 21-MAY-1996; 96US-0646789.

XX PA (UYVA ) UNIV YALE.

XX PI Peyman JA;

XX PS WPI; 1998-018505/02.

XX PT Utrons, RNA molecules containing promoter regulatory motifs -  
XX PT useful to suppress express expression from promoter of interest,  
XX PT specifically T5U nucleic acid suppression of MHC Class I and II gene  
XX PT expression

XX PS Claim 20; Page 20; 200pp; English.

XX CC The present sequence represents a promoter regulatory element,  
XX CC found in the utrons of the invention. Utrons are from, or are  
XX CC homologous to, the 3' untranslated region (UTR), of an mRNA that  
XX CC stimulates or inhibits a cellular response by sequence specific  
XX CC interactions. The utron is able to suppress constitutive and  
XX CC interferon-gamma (IFN-gamma) induced major histocompatibility complex  
XX CC (MHC) class I and class II antigen expression and expression of other  
XX CC antigens, the gene promoters of which contain related sequence motifs  
XX CC that are stimulated by the same factors which stimulate MHC class I and  
XX CC class II antigen expression. Such utrons can be used to regulate  
XX CC gene expression in a subject, e.g. a human or a cell in vitro,  
XX CC specifically inhibiting MHC class I or II, ICAM-7, B7-1, B7-2,  
XX CC Fc gamma R, IL-2 or HIV gene expression. They can be used to inhibit  
XX CC transplant rejection, or treat an autoimmune or inflammatory disease or  
XX CC disorder.

XX SQ Sequence 9 BP; 3 A; 0 C; 3 G; 3 U; 0 other;

Query Match 100.0%; Score 5; DB 19; Length 9;  
Best Local Similarity 60.0%; Pred. No. 2.9e+08;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5  
| | | | |  
Db 1 GUAUG 5

RESULT 10  
AAV22283  
ID AAV22283 standard; DNA; 9 BP.  
XX AC  
XX AC  
XX AAV22283;  
DT 29-JUN-1998 (first entry)  
XX  
XX GAS complement gene promoter motif found in a trophoblast STAT utron.  
DE  
XX Trophoblast STAT utron; TSU; 3' untranslated region; UTR; inhibition;  
XX interferon-gamma; IFN-gamma; major histocompatibility complex; MHC;  
KW antigen expression; gene promoter; class I; class II; IFN signalling;  
KW GAS; ISRE; interleukin-4 response element; gene expression; ICAM-7;  
KW B7-1; B7-2; Fc gamma R; HIV gene expression; transplant rejection;  
KW treatment; autoimmune disease; inflammatory disease; ss.  
XX Unidentified.  
XX WO9744450-A1.  
XX 27-NOV-1997.  
XX 21-MAY-1997; 97WO-US09459.  
XX 21-MAY-1996; 96US-0646789.  
XX (UYUA ) UNIV YALE.  
XX Peyman JA;  
XX WPI; 1998-018505/02.  
XX  
XX Utrons, RNA molecules containing promoter regulatory motifs -  
XX useful to suppress express expression from promoter of interest,  
XX specifically TSU nucleic acid suppression of MHC Class I and II gene  
XX expression  
XX  
XX Claim 22; Page 90; 200pp; English.  
XX  
XX The present sequence represents a GAS complement gene promoter motif  
XX found in a trophoblast STAT utron (TSU). TSUs be isolated from a CDNA  
XX library prepared from mRNA isolated from trophoblast cells. Utrons are  
XX from, or are homologous to, the 3' untranslated region (UTR), of an mRNA  
XX that stimulates or inhibits a cellular response by sequence specific  
XX interactions. The TSU is able to suppress constitutive and  
XX interferon-gamma (IFN-gamma) induced major histocompatibility complex  
XX (MHC) class I and class II antigen expression and expression of other  
XX antigens, the gene promoters of which contain related sequence motifs  
XX that are stimulated by the same factors which stimulate MHC class I and  
XX class II antigen expression. The TSU sequence contains motifs related to  
XX IFN signalling (GAS, ISRE and interleukin-4 response elements). The  
XX nucleic acid can be used to regulate gene expression in a subject, e.g. a  
XX human or a cell in vitro, specifically inhibiting MHC Class I or II,  
XX ICAM-7, B7-1, B7-2, Fc gamma R, IL-2 or HIV gene expression. It can be  
XX used to inhibit transplant rejection, or treat an autoimmune or  
XX inflammatory disease or disorder. It can also be used to inhibit the  
XX action of STAT1-6, or a cytokine.  
XX  
XX Sequence 9 BP; 3 A; 0 C; 3 G; 3 T; 0 other;

Query Match 100.0%; Score 5; DB 19; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.9e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5  
|  
|  
|  
|  
Db 1 GTATG 5

RESULT 11

AAV15899  
ID AAV15899 standard; DNA; 9 BP.  
XX AC  
XX AAV15899;  
DT 26-MAY-1998 (first entry)  
XX  
XX Cyclin D transcription factor DMP1 nonamer consensus sequence.  
DE  
XX cyclin D transcription factor; binding affinity; D-type cyclin; probe;  
KW cell cycle inhibitor; tumour; detection; cancer; DMP1; competitor;  
KW nonamer consensus sequence; ss.  
XX Mus musculus.  
OS Homo sapiens.  
XX WO9743415-A1.  
XX 20-NOV-1997.  
XX  
XX 16-MAY-1997; 97WO-US08480.  
XX 15-MAY-1997; 97US-0017815.  
XX 16-MAY-1996; 96US-0017815.  
XX 16-MAY-1996; 96US-0648837.  
XX (SUUD-) ST JUDE CHILDREN'S RES HOSPITAL.  
XX Hirai H, Inoue K, Sherr CJ;  
XX WPI; 1998-008884/01.  
XX  
XX Cyclin D transcription factor and related DNA - can be used to  
XX develop products for treatment of, e.g. cancer  
XX  
XX Claim 3; Page 99; 120pp; English.  
XX  
XX This is a nonamer consensus sequence of a cyclin D transcription factor  
XX DMP1. DMP1 is an amino acid polymer which has binding affinity for a  
XX D-type cyclin, in vitro, and for a specific DNA nucleotide sequence and  
XX is a transcription factor involved in the activation of genes that  
XX prevent cell proliferation. The DMP1 nucleic acid is operatively linked  
XX to an expression control sequence in an expression vector. The expression  
XX vector has a transcription control sequence comprising this nonamer  
XX sequence operably associated with a recombinant gene or a cassette  
XX insertion site for a recombinant gene. The vector is homologously  
XX recombined in a chromosome of a transgenic animal. A probe or a  
XX competitor in DMP1 transactivation assays is designed based on this  
XX nonamer sequence. The presence of activity of DMP1 can be determined by  
XX detecting binding of DMP1 and a probe by contacting a biological sample  
XX from a mammal with the probe under conditions that allow binding of the  
XX probe to DMP1, where the probe contains the core sequence GTA, and where  
XX the presence or activity of DMP1 is suspected in the sample. DMP1 can  
XX function as a cell cycle inhibitor when expressed in a tumour cell.  
XX Modulating the expression of DMP1 can be used to treat tumours and other  
XX cancers. DMP1 can also be used for controlling expression of heterologous  
XX proteins. Antisense sequences and ribozymes can be used to inhibit  
XX expression of the transcription factor. Detecting the level and activity  
XX of DMP1 in cells is useful for detection of cancer cells or  
XX dysproliferative cells.  
XX  
XX Sequence 9 BP; 1 A; 3 C; 2 G; 3 T; 0 other;

Query Match 100.0%; Score 5; DB 19; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.9e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5  
|  
|  
|  
|  
Db 4 GTATG 8

RESULT 12

```

AAZ10692
ID  AAZ10692 standard; DNA; 9 BP.
XX
AC  AAZ10692;
XX
DT  23-NOV-1999 (first entry)
XX
DE  Oligonucleotide sequence that increases p53 activity in a cell.
XX
XX  p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
XX  UV-induced hyperproliferative disease; psoriasis; vitiligo;
XX  atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
XX  skin cancer; ss.
XX
OS  Synthetic.
XX
NN  GB2336157-A.
XX
DD  13-OCT-1999.
XX
PF  24-MAR-1999; 99GB-0006758.
XX
PR  26-MAR-1998; 98US-0048927.
XX
PA  (UYBO-) UNIV BOSTON.
XX
PI  Gilchrist BA, Yaar M, Eller M;
XX
XX  WPI; 1999-543520/46.
XX
XX  DNA fragments useful for increasing p53 activity in a cell and reducing
XX  susceptibility to UV-induced hyperproliferative diseases -
XX
XX  Claim 11; Page 29; 44pp; English.
XX
XX  AAZ10692-97 represent DNA fragments that are used for increasing p53
XX  activity in a cell. The oligonucleotides are UV mimetics and
XX  protect cells against subsequent exposure to UV-irradiation or
XX  chemicals. The oligonucleotides are useful for increasing p53 activity
XX  in a cell, reducing the susceptibility to UV-induced hyperproliferative
XX  diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
XX  rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
XX  and reducing susceptibility to skin cancer.
XX
XX  Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;
XX
XX  Query Match 100.0%; Score 5; DB 20; Length 9;
XX  Best Local Similarity 100.0%; Pred. No. 2.9e+08;
XX  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  1 GTATG 5
XX  |||||
XX  3 GTATG 7
XX
XX  RESULT 13
XX  AAS14905
XX  ID  AAS14905 standard; DNA; 9 BP.
XX
XX  AC  AAS14905;
XX
XX  DT  14-FEB-2002 (first entry)
XX
XX  DE  Melanogenesis associated oligonucleotide #1.
XX
XX  KW  Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
XX  anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
XX  immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
XX  tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
XX  carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
XX  conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
XX  OS  Synthetic.
XX
AAZ10692
XX
FH  Key modified_base 1 Location/Qualifiers
XX
FT  /*tag= a
XX
FT  /mod_base=g
XX
FT  /note= "Optionally phosphorylated"
XX
XX  WO200174342-A2.
XX
XX  11-OCT-2001.
XX
XX  30-MAR-2001; 2001WO-US10162.
XX
XX  31-MAR-2000; 2000US-0540843.
XX
XX  (UYBO-) UNIV BOSTON.
XX
XX  Gilchrist BA, Yaar M, Eller M;
XX
XX  WPI; 2001-626338/72.
XX
XX  Inhibiting proliferation of epithelial cells, useful e.g. for treating
XX  carcinoma, using specific oligonucleotides that mimic the effects of
XX  ultra-violet light
XX
XX  Claim 1; Page 36; 74pp; English.
XX
XX  The invention describes inhibition of mammalian epithelial cell
XX  proliferation by treating cells with at least one oligonucleotide, or
XX  its fragment. The compounds, which have cytostatic, anti-allergic,
XX  anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and
XX  immunosuppressive activities, function as 'ultra-violet mimics' to induce
XX  DNA repair processes (or a protective response to later exposure to
XX  radiation or chemicals) as a proliferation inhibitor, apoptosis inducer
XX  or a tumour necrosis factor inhibitor. Probably they mimic products of
XX  DNA damage, or processed DNA-damage intermediates, by inducing the p53
XX  pathway, resulting in transient arrest of cell growth, allowing more time
XX  for DNA repair to occur before cell division takes place. The method is
XX  especially used to treat carcinoma but may also be used to treat other
XX  hyperproliferative states (e.g. psoriasis or precancerous conditions);
XX  reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
XX  allergic rhinitis and conjunctivitis; prevent or reduce DNA damage in
XX  cells caused by radiation or chemicals; increase melanin production
XX  (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
XX  promote apoptosis in epithelial cells that contain damaged DNA. Also
XX  oligonucleotides that contain non-hydrolyzable backbones are used to
XX  inhibit apoptosis, in response to DNA damage, in epithelial cell. This
XX  sequence is melanogenesis associated oligonucleotide #1, one of the
XX  oligonucleotides used to inhibit mammalian epithelial cell
XX  proliferation, described in the method of the invention.
XX
XX  Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;
XX
XX  Query Match 100.0%; Score 5; DB 23; Length 9;
XX  Best Local Similarity 100.0%; Pred. No. 2.9e+08;
XX  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  1 GTATG 5
XX  |||||
XX  3 GTATG 7
XX
XX  RESULT 14
XX  ABX03786
XX  ID  ABX03786 standard; DNA; 9 BP.
XX
XX  AC  ABX03786;
XX
XX  DT  09-JAN-2003 (first entry)
XX
XX  DE  Human DNA PCR primer #15.
XX
XX  OS  Synthetic.

```

Differential display method; leucine-rich motif; transmembrane protein; secreted protein; primer; PCR; ss; human.

Homo sapiens.  
Synthetic.

WO200259259-A2.

01-AUG-2002.

23-JAN-2002; 2002WO-IL00071.

23-JAN-2001; 2001US-263158P.

(UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.

Wreschner DH;

WPI; 2002-599769/64.

Differential display method for identifying secreted or transmembrane protein, comprises contacting a DNA with a first primer that hybridizes to a sequence coding for a leucine-rich motif and with a second oligonucleotide primer -

Claim 52; Page 17; 37pp; English.

The invention relates to a differential display comprising contacting cDNA with a first primer that hybridizes to an oligonucleotide sequence coding for a leucine-rich motif, and with a second oligonucleotide primer to form a cDNA-hybrid molecule. The method comprises obtaining mRNA from at least 2 samples, synthesizing cDNA from the RNA of each sample, contacting the cDNA with a first primer that hybridizes to an oligonucleotide sequence coding for a leucine-rich motif, and with a second oligonucleotide primer to form cDNA-hybrid molecules, amplifying the cDNA-hybrid molecules, detecting amplified products and comparing the amplified products from each sample to identify distinctive amplified products coding for at least one secreted or transmembrane protein. The method is useful for discovering novel secreted and/or transmembrane proteins which are important for cell processes and play an important role in determining its phenotype, and which act as mediators for the transfer of signals from external environment into the cell itself, thus modulating gene expression. Sequences ABX03772-ABX03790 represent PCR primers used in the differential display method of the invention.

Sequence 9 BP; 1 A; 0 C; 2 G; 2 T; 4 other;

Query Match 100.0%; Score 5; DB 24; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.9e+08;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTATG 5

|||||

5 GTATG 9

RESULT 15

ABQ71504/c

ID ABQ71504 standard; DNA; 9 BP.

AC ABQ71504;

28-AUG-2002 (first entry)

Zinc finger protein related oligonucleotide target SEQ ID NO:623.

Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.

Homo sapiens.

Synthetic.

WO200242459-A2.

PD

30-MAY-2002.

XX

20-NOV-2001; 2001WO-US43438.

XX

20-NOV-2000; 2000US-0716637.

XX

(SANG-) SANGAMO BIOSCIENCES INC.

XX

Liu Q;

XX

WPI; 2002-500284/53.

XX

New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus -

Example 1; Page 45; 81pp; English.

The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (3) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determine the phenotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention.

Sequence 9 BP; 2 A; 2 C; 3 G; 2 T; 0 other;

Query Match 100.0%; Score 5; DB 24; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.9e+08;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTATG 5

|||||

6 GTATG 2

Search completed: December 31, 2003, 15:08:14

Job time : 145.494 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 13:58:09 ; Search time 574.494 Seconds  
(without alignments)  
211.530 Million cell updates/sec

Title: US-09-540-843-4  
Perfect score: 5  
Sequence: 1 gratg 5

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 33330

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST.\*

1: em\_estba.\*

2: em\_esthum.\*

3: em\_estin.\*

4: em\_estmu.\*

5: em\_estov.\*

6: em\_estpl.\*

7: em\_estro.\*

8: em\_estc.\*

9: gb\_est1.\*

10: gb\_est2.\*

11: gb\_estc.\*

12: gb\_est3.\*

13: gb\_est4.\*

14: gb\_est5.\*

15: em\_estfun.\*

16: em\_estom.\*

17: em\_gss\_hum.\*

18: em\_gss\_inv.\*

19: em\_gss\_pln.\*

20: em\_gss\_vrt.\*

21: em\_gss\_fun.\*

22: em\_gss\_mam.\*

23: em\_gss\_mus.\*

24: em\_gss\_pro.\*

25: em\_gss\_rod.\*

26: em\_gss\_ptg.\*

27: em\_gss\_vrl.\*

28: gb\_gss1.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	5	100.0	14	12	BM398220 5009-0-42
C 2	5	100.0	16	9	AI424037 tF51H06.x
C 3	5	100.0	16	9	AI685758 tu37G09.x
C 4	5	100.0	16	9	AI721735 fc31G08.x

C 5	5	100.0	16	12	BG928185
C 6	5	100.0	17	12	BG929060
C 7	5	100.0	17	13	BQ595683
C 8	5	100.0	17	13	BQ595683 E012692-0
C 9	5	100.0	18	12	C21103 HUMGS000262
C 10	5	100.0	18	12	BM397954 5009-0-39
C 11	5	100.0	19	9	AA977115 OQ24C08.s
C 12	5	100.0	19	9	AI120725 ub72B11.x
C 13	5	100.0	19	9	AI747751 U121H05.x
C 14	5	100.0	19	14	C00646 HUMGS000819
C 15	5	100.0	19	28	AZ341880 1M0074O04
C 16	5	100.0	19	28	AZ345849 1M0080D16
C 17	5	100.0	19	28	AZ355195 1M0094G22
C 18	5	100.0	19	28	AZ406137 1M0175F16
C 19	5	100.0	19	28	AZ422163 1M0200B22
C 20	5	100.0	19	28	AZ434551 1M0221C12
C 21	5	100.0	19	28	AZ464990 1M0274G11
C 22	5	100.0	19	28	AZ486152 1M0314A04
C 23	5	100.0	19	28	AZ579566 1M0367L08
C 24	5	100.0	19	28	AZ614702 1M0443F10
C 25	5	100.0	19	28	AZ626685 1M0467M01
C 26	5	100.0	19	28	AZ645469 1M0510L24
C 27	5	100.0	19	28	AZ647364 1M0513O16
C 28	5	100.0	19	28	AZ759906 1M0553C10
C 29	5	100.0	19	28	AZ766086 1M0563G19
C 30	5	100.0	19	28	AZ799396 2M0056N18
C 31	5	100.0	19	28	AZ815067 2M0083P01
C 32	5	100.0	19	28	AZ817238 2M0086E01
C 33	5	100.0	19	28	AZ839614 2M0135N16
C 34	5	100.0	19	28	AZ864822 2M0174C08
C 35	5	100.0	19	28	AZ942806 2M0203F09
C 36	5	100.0	19	28	AZ948421 2M0211A01
C 37	5	100.0	19	28	AZ949895 2M0213N08
C 38	5	100.0	19	28	AZ953217 2M0218A23
C 39	5	100.0	19	28	AZ987324 2M0269B21
C 40	5	100.0	20	9	AB088508 2M0274F14
C 41	5	100.0	20	13	BQ593049 E012375-0
C 42	5	100.0	20	28	AZ336039 1M0066E09
C 43	5	100.0	20	28	AZ359199 1M0101M19
C 44	5	100.0	20	28	AZ369273 1M0119H13
C 45	5	100.0	20	28	AZ387347 1M0146K12

ALIGNMENTS

RESULT 1  
BM398220/c  
LOCUS  
DEFINITION  
5009-0-42-D11.t.1 Chilcoat/Turkewitz cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION  
BM398220  
VERSION  
BM398220.1 GI:18198273  
KEYWORDS  
EST.  
SOURCE  
Tetrahymena thermophila  
ORGANISM  
Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymena.  
REFERENCE  
1 (bases 1 to 14)  
AUTHORS  
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J., and Klobutcher, L.  
TITLE  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
JOURNAL  
Unpublished  
COMMENT  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkaw@midway.uchicago.edu  
Seq primer: T3.  
Location/Qualifiers  
1. .14

```

/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT      4 a 5 c 0 g 5 t
ORIGIN

Query Match      100.0%; Score 5; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTATG 5
|||||
5 GTATG 1

RESULT 2
AI424037/c
LOCUS      AI424037.1 16 bp mRNA linear EST 09-MAR-1999
DEFINITION ttf1h06.x1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:2102843 3'
similar to TR:Q69566 Q69566 ; mRNA sequence.
ACCESSION  AI424037
VERSION     AI424037.1 GI:42699968
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 16)
AUTHORS   NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGA), Tumor Gene Index
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2102843"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/clone_lib="NCI CGAP Brn23"
/note="Organ: brain; Vector: p7T3D-Pac (Pharmacia) with a modified polylinker; Site1: Not 1; Site2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAGTGGCGCGCATATCTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      8 a 6 c 1 g 1 t
ORIGIN

/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT      4 a 5 c 0 g 5 t
ORIGIN

Query Match      100.0%; Score 5; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTATG 5
|||||
6 GTATG 2

RESULT 3
AI685758/c
LOCUS      AI685758.1 16 bp mRNA linear EST 27-MAY-1999
DEFINITION t337909.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:2253280 3'
similar to TR:Q02393 Q02393 HUMAN PAPILLOMAVIRUS 18 E5 CENTRAL SEQUENCE MOTIF PROTEIN 1 ; contains element LTR4 repetitive element ; mRNA sequence.
ACCESSION  AI685758
VERSION     AI685758.1 GI:4897052
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 16)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2253280"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI CGAP Pr28"
/note="Organ: prostate; Vector: p7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      7 a 7 c 1 g 1 t
ORIGIN

Query Match      100.0%; Score 5; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTATG 5
|||||
9 GTATG 5

```



```

RESULT 4
AI721735/c
LOCUS
DEFINITION
fc31908.x1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone
IMAGE:3723038 3' similar to SW:YM14_PART2 P15615 HYPOTHETICAL 47.2
KD PROTEIN 1, mRNA sequence.

ACCESSION
AI721735
VERSION
AI721735.1 GI:5040064
KEYWORDS
EST.
SOURCE
Danio rerio (zebrafish)
ORGANISM
Danio rerio
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
1 (bases 1 to 16)
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy
, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood
, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,
Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,
Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
and Wilson, R.
WashU Zebrafish EST Project 1998
Unpublished
Other_ESTs: fc31908.y1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrfish@watson.wustl.edu
cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
ReSourceZentrumPrimaDatenbank, Berlin, Germany (web address:
www.rzpd.de)
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: T7 ET from Amersham
High quality sequence stop: 1.
FEATURES
Location/Qualifiers
1..16
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:3723038"
/sex="mixed"
/tissue_type="26 somite embryos, adult livers, shield
stage embryos"
/lab_host="X11-blue MRP"
/clone_lib="Zebrafish WashU MPIMG EST"
strand=vector; pSPORT1; Site 1: NotI; Site 2: SalI; 1st
strand cDNA was primed with a Not I - oligo(dT)15 primer
[5'PGACTAGTCTTAGATCCGAGCGGCCCTTTTCTTTTCTTTT3'];
double-stranded cDNA was ligated to Sal I adaptors (BRL),
digested with Not I and cloned into the Not I and Sal I
sites of the pSPORT1 vector (BRL). Library was constructed
by Matthew Clark (Lehrach lab; ICRF, London and Max Planck
Institut fuer Molekulare Genetik, Berlin). cDNAs for EST
analysis were selected following oligonucleotide
hybridization fingerprinting of arrayed clones from
zebrafish late somitogenesis (26 ss), adult liver or
embryonic shield stage (5.5 h) libraries. Fingerprint
data were used to computationally cluster cDNAs, and a
single cDNA from each cluster was chosen for sequencing.
In some cases multiple members of the same cluster were
sequenced to assess clustering parameters or single clones
were sequenced additional times to assess quality
control."
6 a 8 c 1 g 1 t

```

## ORIGIN

```

Query Match 100.0%; Score 5; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTATG 5
Db 13 GTATG 9

RESULT 5
BG928185/c
LOCUS
DEFINITION
HNC65-1-D12.R.R HNC (Human Normal Cartilage) Homo sapiens cDNA,
mRNA sequence.
ACCESSION
BG928185
VERSION
BG928185.1 GI:14322708
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16)
Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J.,
Sathe, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and
Lark, M.W.
Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
Osteoarthr. Cartil. 9 (7), 641-653 (2001)
21482651
11597177
Contact: Sanjay Kumar
UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@gsk.com
Seq primer: T7.
FEATURES
Location/Qualifiers
1..16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT 1; Site 1: SalI; Site 2: NotI;
Directional"
BASE COUNT 4 a 6 c 2 g 3 t 1 others

Query Match 100.0%; Score 5; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTATG 5
Db 12 GTATG 8

RESULT 6
BG929060/c
LOCUS
DEFINITION
HNC11-1-G8.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.
ACCESSION
BG929060
VERSION
BG929060.1 GI:14323583
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 17)  
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W.

IDENTIFICATION AND INITIAL CHARACTERIZATION OF 5000 EXPRESSED SEQUENCED TAGS (ESTs) EACH FROM ADULT HUMAN NORMAL AND OSTEOARTHRITIC CARTILAGE cDNA LIBRARIES  
Osteoarthritis. Cartil. 9 (7), 641-653 (2001)

JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Contact: Sanjay Kumar  
11597177  
UW2109  
GlaxoSmithKline  
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
Tel: 610-270-7245  
Fax: 610-270-5598  
Email: sanjay.kumar-1@gsk.com  
Seq primer: 17.

FEATURES  
source  
1..17 Location/Qualifiers

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="cartilage"  
/lab\_host="E.coli DH10 B"  
/clone\_lib="HNC (Human Normal Cartilage)"  
/note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI;  
Directional"

BASE COUNT 5 a 8 c 2 g 2 t

ORIGIN

Query Match 100.0%; Score 5; DB 12; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTATG 5  
|||||  
10 GTATG 6

RESULT 7

LOCUS BQ595683 17 bp mRNA linear EST 06-DEC-2002  
DEFINITION E012692-024-022-H17-SP6 MP1Z-ADIS-024-developing root Beta vulgaris cDNA clone 024-022-H17 5-PRIME, mRNA sequence.

ACCESSION BQ595683  
VERSION BQ595683.1 GI:26125266  
KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE

1 (bases 1 to 17)  
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Leirach,H. and Radelof,U.

Construction of a 'unigenes' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)

JOURNAL

COMMENT ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weissshaar@piz-koeln.mpg.de

Insert Length: 17 Std Error: 0.00  
Plate: 22 row: H column: 17  
Seq primer: SP6; CATACGATTGATGACACTATAG.

FEATURES  
source  
1..17 Location/Qualifiers

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/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line)"  
/db\_xref="GABI:191174"  
/db\_xref="taxon:161934"  
/clone="024-022-H17"  
/tissue\_type="developing root"  
/lab\_host="EMDH10B"  
/clone\_lib="MP1Z-ADIS-024-developing root"  
/note="Vector: pCMVSPORT6; Site\_1: SalI; Site\_2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
orientation:  
SP6-Sali-CCAGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet project.  
Local PI: Dr. Katharina Schneider, coordinator: Prof.  
Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

BASE COUNT 4 a 8 c 2 g 3 t

Query Match 100.0%; Score 5; DB 13; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5  
|||||  
Db 7 GTATG 3

RESULT 8

C21103/c  
LOCUS C21103 17 bp mRNA linear EST 31-DEC-2002  
DEFINITION HUMGS0002626 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA sequence.

ACCESSION C21103

VERSION C21103.1 GI:1622213

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 17)

REFERENCE Okubo,K.

BodyMap; human gene expression database

TITLE Unpublished

JOURNAL

COMMENT

Contact: Okubo,K.

Institute for Molecular and Cellular Biol

Osaka University

1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan

Tel: 06-877-5111(ex.3315)

Email: kousaku@imcb.osaka-u.ac.jp

We are not submitting the same cDNA sequence redundantly to DDBJ since 1993. For the abundance information of clones with this sequence in this library and as well as in other 3'-directed libraries, see: http://www.imcb.osaka-u.ac.jp/bodymap/. The sequences of the clones represented by this GS sequences is also found there.

FEATURES  
source  
1..17 Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev\_stage="adult"

/clone\_lib="Human adult (K.Okubo)"

/note="One or more human adult tissue"

BASE COUNT 5 a 5 c 2 g 5 t

Query Match 100.0%; Score 5; DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5  
|||||

Db 13 GTATG 9

RESULT 9  
BM397954/c  
LOCUS  
DEFINITION  
Tetrahymena thermophila cDNA (large fraction)

ACCESSION  
BM397954  
VERSION  
BM397954.1 GI:18198022  
KEYWORDS  
EST.

ORGANISM  
Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymena.

REFERENCE  
1 (bases 1 to 18)  
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel  
J. and Klobutcher, L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells

TITLE  
Unpublished

JOURNAL  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.

FEATURES  
source  
1. .18  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/notes="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT  
3 a 7 c 5 g 3 t

Query Match 100.0%; Score 5; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5  
|||||

Db 5 GTATG 1

RESULT 10  
AA977115  
LOCUS  
DEFINITION  
Oq24c08.s1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1587278 3'  
similar to TR:Q69566 Q69566 ; mRNA sequence.

ACCESSION  
AA977115  
VERSION  
AA977115.1 GI:3154561  
KEYWORDS  
EST.

SOURCE  
Homo sapiens (human)

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1 (bases 1 to 19)  
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

TITLE  
Unpublished

JOURNAL  
Contact: Robert Strausberg, Ph.D.  
Email: cgapsb@mail.nih.gov

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5  
|||||

Db 13 GTATG 9

RESULT 9  
BM397954  
LOCUS  
DEFINITION  
Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION  
BM397954  
VERSION  
BM397954.1 GI:18198022  
KEYWORDS  
EST.

ORGANISM  
Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymena.

REFERENCE  
1 (bases 1 to 18)  
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel  
J. and Klobutcher, L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells

TITLE  
Unpublished

JOURNAL  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.

FEATURES  
source  
1. .18  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/notes="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT  
3 a 7 c 5 g 3 t

Query Match 100.0%; Score 5; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5  
|||||

Db 5 GTATG 1

RESULT 10  
AA977115  
LOCUS  
DEFINITION  
Oq24c08.s1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1587278 3'  
similar to TR:Q69566 Q69566 ; mRNA sequence.

ACCESSION  
AA977115  
VERSION  
AA977115.1 GI:3154561  
KEYWORDS  
EST.

SOURCE  
Homo sapiens (human)

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1 (bases 1 to 19)  
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

TITLE  
Unpublished

JOURNAL  
Contact: Robert Strausberg, Ph.D.  
Email: cgapsb@mail.nih.gov

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5  
|||||

Db 13 GTATG 9

RESULT 9  
BM397954  
LOCUS  
DEFINITION  
Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION  
BM397954  
VERSION  
BM397954.1 GI:18198022  
KEYWORDS  
EST.

ORGANISM  
Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymena.

REFERENCE  
1 (bases 1 to 18)  
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel  
J. and Klobutcher, L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells

TITLE  
Unpublished

JOURNAL  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.

FEATURES  
source  
1. .18  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/notes="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT  
3 a 7 c 5 g 3 t

Query Match 100.0%; Score 5; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5  
|||||

Db 5 GTATG 1

RESULT 10  
AA977115  
LOCUS  
DEFINITION  
Oq24c08.s1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1587278 3'  
similar to TR:Q69566 Q69566 ; mRNA sequence.

ACCESSION  
AA977115  
VERSION  
AA977115.1 GI:3154561  
KEYWORDS  
EST.

SOURCE  
Homo sapiens (human)

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1 (bases 1 to 19)  
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

TITLE  
Unpublished

JOURNAL  
Contact: Robert Strausberg, Ph.D.  
Email: cgapsb@mail.nih.gov

FEATURES  
source

1. .19  
Location/Qualifiers

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1587278"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP GC4"  
/note="Vector: pT773D-Pac (Pharmacia) with a modified  
polylinker; 1st strand cDNA was prepared from 3 pooled  
germ cell tumors, and was then primed with a Not I -  
oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
RI adaptors (Pharmacia), digested with Not I and cloned  
into the Not I and Eco RI sites of the modified pT773  
vector. Library is normalized. Library was constructed by  
Bento Soares and M. Fatima Bonaldo."

BASE COUNT 2 a 0 c 7 g 10 t

Query Match 100.0%; Score 5; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5  
|||||

Db 3 GTATG 7

RESULT 11  
LOCUS

DEFINITION  
A1120725 19 bp mRNA linear EST 02-SEP-1998  
ub72b1.r1 Soares mammary gland NMLMG Mus musculus cDNA clone  
IMAGE:1383261 5' similar to TR:Q15009 Q15009 ORF, COMPLETE CDS. ;  
mRNA sequence.

ACCESSION  
A1120725  
VERSION  
A1120725.1 GI:3521049  
KEYWORDS  
EST.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus

REFERENCE  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
Theising, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterston, R.

TITLE  
The WashU-HHMI Mouse EST Project  
JOURNAL  
Unpublished

COMMENT  
Contact: Marra M/Mouse EST Project  
WashU-HHMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu

This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:905729  
Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand  
Seq primer: -28m13 rev2 ET from Amerisham  
High quality sequence stop: 1.

#### FEATURES

source  
1..19  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1383261"  
/sex="female (lactating)"  
/tissue\_type="mammary gland"  
/lab\_host="DH10B"  
/clone\_lib="Soares mammary gland NLMG"

/note="Vector: pT73D-PAC (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

#### BASE COUNT

9 a 3 c 4 g 3 t

#### ORIGIN

Query Match 100.0%; Score 5; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred.No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTATG 5  
|||||  
11 GTATG 7

#### RESULT 12

##### LOCUS

##### DEFINITION

AI747751 19 bp mRNA linear EST 22-JUN-1999  
ul21h05.xl Sugano mouse embryo mewa Mus musculus cDNA clone  
IMAGE:208249 3' similar to TR:P79101 P79101 CLEAVAGE AND  
POLYADENYLATION SPECIFICITY FACTOR PROTEIN. ; mRNA sequence.

##### ACCESSION

##### VERSION

##### KEYWORDS

##### SOURCE

##### ORGANISM

##### REFERENCE

##### AUTHORS

##### TITLE

##### JOURNAL

##### COMMENT

Unpublished  
Contact: Marra M/WashU-NCI Mouse EST Project 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
MGI:95933  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: custom primer used  
High quality sequence stop: 1.

#### FEATURES

source  
1..19  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL"  
/db\_xref="taxon:10090"

/clone="IMAGE:208249"  
/dev\_stage="embryo, 14 dpc"  
/lab\_host="DH10B"  
/clone\_lib="Sugano mouse embryo mewa"

/note="Vector: pME18S-FL3; Site\_1: DralII (CACTGTGTG); Site\_2: DralII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer (ATGTGGCTTTTTTTTTTTTTTTT); double-stranded cDNA was ligated to a DralII adaptor (TGTGGCTTACTGG), digested and cloned into distinct DralII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTCTCTCTAAAAGCTGGC and 3' end primer CGACCTCGACCTCGACCA."

BASE COUNT 6 a 2 c 8 g 3 t

#### ORIGIN

Query Match 100.0%; Score 5; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred.No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5  
|||||  
Db 13 GTATG 17

#### RESULT 13

##### LOCUS

##### DEFINITION

C00646 19 bp mRNA linear EST 31-DEC-2002  
HUMGS0008192 Human adult (K.Okubo) Homo sapiens cDNA, mRNA  
sequence.

##### ACCESSION

##### VERSION

##### KEYWORDS

##### SOURCE

##### ORGANISM

##### REFERENCE

##### AUTHORS

##### TITLE

##### JOURNAL

##### COMMENT

Unpublished  
Contact: Okubo,K.  
Institute for Molecular and Cellular Biol  
Osaka University  
1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan  
Tel: 06-877-5111(ex.3315)  
Email: kousaku@imcb.osaka-u.ac.jp  
We are not submitting the same cDNA sequence redundantly to DBJ since 1993. For the abundance information of clones with this sequence in this library and as well as in other 3'-directed libraries, see <http://www.imcb.osaka-u.ac.jp/bodymap/>. The sequences of the clones represented by this GS sequences is also found there.

#### FEATURES

##### Location/Qualifiers

1..19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="adult"  
/clone\_lib="Human adult (K.Okubo)"  
/note="One or more human adult tissue"

BASE COUNT 4 a 1 c 8 g 6 t

Query Match 100.0%; Score 5; DB 14; Length 19;  
Best Local Similarity 100.0%; Pred.No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5

Db 14 GTATG 18  
|||||

RESULT 14  
AZ341880  
LOCUS  
DEFINITION  
1M0074004R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0074004 R, genomic survey sequence.

ACCESSION  
AZ341880  
VERSION  
AZ341880.1 GI:10418570  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
Unpublished  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0074 row: 0 column: 04  
Seq primer: CACACGGAACACGATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
source  
1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0074004"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: FWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 4 a 4 c 6 g 5 t  
ORIGIN

Query Match 100.0%; Score 5; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTATG 5  
|||||  
Db 8 GTATG 12

RESULT 15  
AZ345849/c  
LOCUS  
DEFINITION  
1M0080D16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0080D16 R, genomic survey sequence.

ACCESSION  
AZ345849  
VERSION  
AZ345849.1 GI:10425086  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
Unpublished  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0080 row: D column: 16  
Seq primer: CACACGGAACACGATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
Location/Qualifiers  
1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0080D16"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 9 a 4 c 0 g 6 t  
ORIGIN

Query Match 100.0%; Score 5; DB 28; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5  
| | | | |  
Db 13 GTATG 9

Search completed: December 31, 2003, 19:41:20  
Job time : 578.494 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 17:10:00 ; Search time 58.2911 Seconds  
(without alignments)  
296.896 Million cell updates/sec

Title: US-09-540-843-4

Perfect score: 5

Sequence: 1 gtag5

Scoring table:

IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2263443 seqs, 1730637950 residues

Total number of hits satisfying chosen parameters: 998502

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications NA:
- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq\*
  - 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq\*
  - 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq\*
  - 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq\*
  - 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq\*
  - 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq\*
  - 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq\*
  - 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq\*
  - 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq\*
  - 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq\*
  - 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq\*
  - 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq\*
  - 13: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq\*
  - 14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq\*
  - 15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq\*
  - 16: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq\*
  - 17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq\*
  - 18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	5	100.0	5	15	US-10-122-630-4
2	5	100.0	5	15	US-10-122-630-6
3	5	100.0	5	15	US-10-122-633-4
4	5	100.0	5	15	US-10-122-633-6
5	5	100.0	5	13	US-10-027-633-178029
6	5	100.0	7	13	US-10-027-632-178043
7	5	100.0	7	14	US-10-027-632-178029
8	5	100.0	7	14	US-10-027-632-178043
9	5	100.0	7	15	US-10-122-630-3
10	5	100.0	7	15	US-10-122-630-7
11	5	100.0	7	15	US-10-122-633-3
12	5	100.0	7	15	US-10-122-633-7
13	5	100.0	8	9	US-09-142-593-11
14	5	100.0	8	10	US-09-927-886-17
15	5	100.0	8	10	US-09-861-014-6

16	5	100.0	8	13	US-10-128-560-224	Sequence 224, App
17	5	100.0	8	13	US-10-191-698-11	Sequence 11, Appl
18	5	100.0	8	15	US-10-263-159-11	Sequence 11, Appl
19	5	100.0	9	9	US-09-989-789-2220	Sequence 623, App
20	5	100.0	9	9	US-09-989-789-2220	Sequence 2220, Ap
21	5	100.0	9	9	US-09-989-789-2256	Sequence 2256, Ap
22	5	100.0	9	11	US-09-990-186-623	Sequence 623, App
23	5	100.0	9	11	US-09-990-186-2220	Sequence 2220, Ap
24	5	100.0	9	11	US-09-990-186-2256	Sequence 2256, Ap
25	5	100.0	9	11	US-09-989-994-623	Sequence 623, App
26	5	100.0	9	11	US-09-989-994-2220	Sequence 2220, Ap
27	5	100.0	9	11	US-09-989-994-2256	Sequence 2256, Ap
28	5	100.0	9	15	US-10-122-630-1	Sequence 1, Appli
29	5	100.0	9	15	US-10-122-633-1	Sequence 1, Appli
30	5	100.0	9	15	US-10-096-596-32	Sequence 32, Appl
31	5	100.0	10	7	US-08-935-177-16	Sequence 16, Appl
32	5	100.0	10	9	US-09-822-250-16	Sequence 16, Appl
33	5	100.0	10	9	US-09-398-399-31	Sequence 31, Appl
34	5	100.0	10	9	US-09-989-789-622	Sequence 622, App
35	5	100.0	10	9	US-09-989-789-636	Sequence 636, App
36	5	100.0	10	9	US-09-989-789-1338	Sequence 1338, Ap
37	5	100.0	10	9	US-09-989-789-1341	Sequence 1341, Ap
38	5	100.0	10	9	US-09-989-789-1342	Sequence 1342, Ap
39	5	100.0	10	9	US-09-989-789-1343	Sequence 1343, Ap
40	5	100.0	10	9	US-09-899-381-31	Sequence 31, Appl
41	5	100.0	10	11	US-09-962-602-7	Sequence 7, Appli
42	5	100.0	10	11	US-09-962-602-8	Sequence 8, Appli
43	5	100.0	10	11	US-09-990-186-622	Sequence 622, App
44	5	100.0	10	11	US-09-990-186-636	Sequence 636, App
45	5	100.0	10	11	US-09-990-186-1338	Sequence 1338, Ap

## ALIGNMENTS

RESULT 1  
US-10-122-630-4  
; Sequence 4, Application US/10122630  
; Publication No. US20030032610A1  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrist, Barbara A.  
; APPLICANT: Eller, Mark S.  
; APPLICANT: Yaar, Mina  
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
; TITLE OF INVENTION: Oligonucleotides  
; FILE REFERENCE: 0054, 1088-018  
; CURRENT APPLICATION NUMBER: US/10/122,630  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US 08/467,012  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: PCT/US96/08386  
; PRIOR FILING DATE: 1996-06-03  
; PRIOR APPLICATION NUMBER: US 09/048,927  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: US 09/540,843  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: PCT/US01/10162  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 5  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA Fragment  
US-10-122-630-4

Query Match 100.0%; Score 5; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6.7e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTATG 5

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Db          1 GTATG 5
|||||
Query Match 100.0%; Score 5; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
US-10-122-630-6/c
; Sequence 6, Application US/10122630
; Publication No. US2003032610A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE REFERENCE: 0054.1088-018
; CURRENT APPLICATION NUMBER: US/10/122,630
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US96/08386
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: US 09/048,927
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-6

Query Match 100.0%; Score 5; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db          1 GTATG 5
|||||
Query Match 100.0%; Score 5; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
US-10-122-633-4
; Sequence 4, Application US/10122633
; Publication No. US2003032611A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE REFERENCE: 0054.1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-4

Query Match 100.0%; Score 5; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db          1 GTATG 5
|||||
Query Match 100.0%; Score 5; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
US-10-122-633-6/c
; Sequence 6, Application US/10122633
; Publication No. US2003032611A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE REFERENCE: 0054.1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-6

Query Match 100.0%; Score 5; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db          1 GTATG 5
|||||
Query Match 100.0%; Score 5; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
US-10-027-632-178029/c
; Sequence 178029, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178029
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; LENGTH: 7
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178029

Query Match      100.0%; Score 5; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.8e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTATG 5
Db      |||||
        5 GTATG 1

RESULT 6
US-10-027-632-178043/c
Sequence 178043, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 178043
LENGTH: 7
TYPE: DNA
ORGANISM: Human
US-10-027-632-178043

Query Match      100.0%; Score 5; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.8e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTATG 5
Db      |||||
        5 GTATG 1

RESULT 7
US-10-027-632-178029/c
Sequence 178029, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 178043
LENGTH: 7
TYPE: DNA
ORGANISM: Human
US-10-027-632-178043

Query Match      100.0%; Score 5; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.8e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTATG 5
Db      |||||
        5 GTATG 1

RESULT 8
US-10-027-632-178043/c
Sequence 178043, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 178043
LENGTH: 7
TYPE: DNA
ORGANISM: Human
US-10-027-632-178043

Query Match      100.0%; Score 5; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.8e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTATG 5
Db      |||||
        5 GTATG 1

RESULT 9
US-10-122-630-3
Sequence 3, Application US/10122630
Publication No. US20030032610A1
GENERAL INFORMATION:
APPLICANT: Gilchrist, Barbara A.
PRIOR FILING DATE: 2000-03-29
APPLICANT: Eller, Mark S.
APPLICANT: Yaar, Mina

```

; TITLE OF INVENTION: Method to Inhibit Cell Growth Using

; FILE REFERENCE: 0054.1088-018  
; CURRENT APPLICATION NUMBER: US/10/122,630  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US 08/467,012  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: PCT/US96/08386  
; PRIOR FILING DATE: 1996-06-03  
; PRIOR APPLICATION NUMBER: US 09/048,927  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: US 09/540,843  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: PCT/US01/10162  
; PRIOR FILING DATE: 2001-03-30

; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 7

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic DNA Fragment

US-10-122-630-3

Query Match 100.0%; Score 5; DB 15; Length 7;

Best Local Similarity 100.0%; Pred. No. 4.8e+08;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTATG 5

|||||

2 GTATG 6

RESULT 10

US-10-122-630-7

Sequence 7, Application US/10122630

Publication No. US20030032610A1

GENERAL INFORMATION:

APPLICANT: Gilchrest, Barbara A.

APPLICANT: Eller, Mark S.

; TITLE OF INVENTION: Method to Inhibit Cell Growth Using

; FILE REFERENCE: 0054.1088-018

; CURRENT APPLICATION NUMBER: US/10/122,630

; CURRENT FILING DATE: 2002-04-12

; PRIOR APPLICATION NUMBER: US 08/467,012

; PRIOR FILING DATE: 1995-06-06

; PRIOR APPLICATION NUMBER: PCT/US96/08386

; PRIOR FILING DATE: 1996-06-03

; PRIOR APPLICATION NUMBER: US 09/048,927

; PRIOR FILING DATE: 1998-03-26

; PRIOR APPLICATION NUMBER: US 09/540,843

; PRIOR FILING DATE: 2000-03-31

; PRIOR APPLICATION NUMBER: PCT/US01/10162

; PRIOR FILING DATE: 2001-03-30

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 7

LENGTH: 7

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic DNA Fragment

US-10-122-630-7

Query Match 100.0%; Score 5; DB 15; Length 7;

Best Local Similarity 100.0%; Pred. No. 4.8e+08;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTATG 5

|||||

Db 2 GTATG 6

RESULT 11

US-10-122-633-3

Sequence 3, Application US/10122633

Publication No. US20030032611A1

GENERAL INFORMATION:

APPLICANT: Gilchrest, Barbara A.

APPLICANT: Eller, Mark S.

APPLICANT: Yaar, Mina

; TITLE OF INVENTION: Method to Inhibit Cell Growth Using

; FILE REFERENCE: 0054.1088-019

; CURRENT APPLICATION NUMBER: US/10/122,633

; CURRENT FILING DATE: 2002-04-12

; PRIOR APPLICATION NUMBER: US 09/540,843

; PRIOR FILING DATE: 2000-03-31

; PRIOR APPLICATION NUMBER: PCT/US01/10162

; PRIOR FILING DATE: 2001-03-30

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 7

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic DNA Fragment

US-10-122-633-3

Query Match 100.0%; Score 5; DB 15; Length 7;

Best Local Similarity 100.0%; Pred. No. 4.8e+08;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTATG 5

|||||

2 GTATG 6

RESULT 12

US-10-122-633-7

Sequence 7, Application US/10122633

Publication No. US20030032611A1

GENERAL INFORMATION:

APPLICANT: Gilchrest, Barbara A.

APPLICANT: Eller, Mark S.

APPLICANT: Yaar, Mina

; TITLE OF INVENTION: Method to Inhibit Cell Growth Using

; FILE REFERENCE: 0054.1088-019

; CURRENT APPLICATION NUMBER: US/10/122,633

; CURRENT FILING DATE: 2002-04-12

; PRIOR APPLICATION NUMBER: US 09/540,843

; PRIOR FILING DATE: 2000-03-31

; PRIOR APPLICATION NUMBER: PCT/US01/10162

; PRIOR FILING DATE: 2001-03-30

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 7

LENGTH: 7

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic DNA Fragment

US-10-122-633-7

Query Match 100.0%; Score 5; DB 15; Length 7;

Best Local Similarity 100.0%; Pred. No. 4.8e+08;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTATG 5

|||||

2 GTATG 6

RESULT 13  
US-09-142-593-11/c  
; Sequence 11, Application US/09142593  
; Patent No. US20020016975A1  
; GENERAL INFORMATION:  
; APPLICANT: HACKETT ET AL.  
; TITLE OF INVENTION: DNA-BASED TRANSPOSON SYSTEM FOR THE  
; INTRODUCTION OF NUCLEIC ACID INTO DNA OF A CELL  
; NUMBER OF SEQUENCES: 63  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.  
; STREET: 119 NORTH FOURTH STREET, SUITE 203  
; CITY: MINNEAPOLIS  
; STATE: MINNESOTA  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/142,593  
; FILING DATE: 10-SEP-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/040,664  
; FILING DATE: 11-MAR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/053,868  
; FILING DATE: 28-JUL-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/065,303  
; FILING DATE: 13-NOV-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US98/04687  
; FILING DATE: 11-MAR-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SANDBERG, VICTORIA A.  
; REGISTRATION NUMBER: 41,287  
; REFERENCE/DOCKET NUMBER: 110.00450101  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-305-1226  
; TELEFAX: 612-305-1228  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-09-142-593-11

Query Match 100.0%; Score 5; DB 9; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.2e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTATG 5  
DB 6 GTATG 2

RESULT 14  
US-09-927-886-17/c  
; Sequence 17, Application US/09927886  
; Patent No. US20020103152A1  
; GENERAL INFORMATION:  
; APPLICANT: Kay, Mark A.  
; APPLICANT: Yant, Stephen  
; TITLE OF INVENTION: Methods of In Vivo Gene Transfer Using a  
; Sleeping Beauty Transposon System

FILE REFERENCE: STAN-160CIP  
; CURRENT APPLICATION NUMBER: US/09/927,886  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/162,279  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: 09/440,301  
; PRIOR FILING DATE: 1999-11-17  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 8  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: transposon repeat sequence  
US-09-927-886-17

Query Match 100.0%; Score 5; DB 10; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.2e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTATG 5  
DB 6 GTATG 2

RESULT 15  
US-09-861-014-6/c  
; Sequence 6, Application US/09861014  
; Patent No. US20020115216A1  
; GENERAL INFORMATION:  
; APPLICANT: Steer, Clifford  
; APPLICANT: Kren, Betsy  
; APPLICANT: Linehan-Stieers, Cheryl  
; APPLICANT: McIvor, R.  
; APPLICANT: Hackett, Perry  
; TITLE OF INVENTION: Composition for Delivery of Compounds to Cells  
; FILE REFERENCE: 110.01330101  
; CURRENT APPLICATION NUMBER: US/09/861,014  
; CURRENT FILING DATE: 2001-05-19  
; PRIOR APPLICATION NUMBER: US 60/206,002  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: US 60/285,121  
; PRIOR FILING DATE: 2001-04-20  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6  
; LENGTH: 8  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Direct repeat sequence  
US-09-861-014-6

Query Match 100.0%; Score 5; DB 10; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.2e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTATG 5  
DB 6 GTATG 2

Search completed: January 1, 2004, 01:10:36  
Job time : 58.2911 secs



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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 11:36:21 ; Search time 1012.7 Seconds  
(without alignments)  
444.364 Million cell updates/sec

Title: US-09-540-843-5  
Perfect score: 11  
Sequence: 1 gttagggttag 11

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 1010434

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
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- 17: em\_hum.\*
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- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	11	100.0	11	6	AR026486	Sequence
C 3	11	100.0	11	6	AR026487	Sequence
C 4	11	100.0	11	6	AR059195	Sequence
C 5	11	100.0	11	6	AR075506	Sequence
C 6	11	100.0	11	6	AR161904	Sequence
C 7	11	100.0	11	6	AR306454	Sequence
C 8	11	100.0	11	6	AX033373	Sequence
C 9	11	100.0	11	6	AX268757	Sequence
C 10	11	100.0	11	6	AX268761	Sequence
C 11	11	100.0	11	6	AX283296	Sequence
C 12	11	100.0	11	6	BD071047	Modulatio
C 13	11	100.0	11	6	BD071064	Modulatio
C 14	11	100.0	11	6	BD071077	Modulatio
C 15	11	100.0	11	6	BD176143	Mammalian
C 16	11	100.0	11	6	I31749	Sequence 2
C 17	11	100.0	12	6	BD071042	Modulatio
C 18	11	100.0	13	6	BD071035	Modulatio
C 19	11	100.0	13	6	BD071046	Modulatio
C 20	11	100.0	15	6	AR026479	Sequence
C 21	11	100.0	15	6	BD071036	Modulatio
C 22	11	100.0	15	6	BD071039	Modulatio
C 23	11	100.0	15	6	BD071078	Modulatio
C 24	11	100.0	16	6	AR050942	Sequence
C 25	11	100.0	16	6	AR204610	Sequence
C 26	11	100.0	16	6	AR307264	Sequence
C 27	11	100.0	16	6	I51743	Sequence 11
C 28	11	100.0	17	6	A84605	Sequence 15
C 29	11	100.0	17	6	AR026488	Sequence
C 30	11	100.0	17	6	AR145675	Sequence
C 31	11	100.0	17	6	AR145676	Sequence
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C 33	11	100.0	18	6	A79654	Sequence 3
C 34	11	100.0	18	6	A79665	Sequence 14
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ALIGNMENTS

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ACCESSION AR016034  
VERSION AR016034.1 GI:3972311  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 11)  
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.  
TITLE Assays for the DNA component of human telomerase  
JOURNAL Patent: US 5776679-A 2 07-JUL-1998;  
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DEFINITION Sequence 11 from patent US 5856096.
ACCESSION AR026486
VERSION AR026486.1 GI:5937326
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Windle,B.E., Qiu,M., Chen,S.-F., Fletcher,T.M. and Maine,I.
TITLE Rapid and sensitive assays for detecting and distinguishing between
processive and non-processive telomerase activities
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ACCESSION AR026487
VERSION AR026487.1 GI:5937327
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
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AUTHORS Windle,B.E., Qiu,M., Chen,S.-F., Fletcher,T.M. and Maine,I.
TITLE Rapid and sensitive assays for detecting and distinguishing between
processive and non-processive telomerase activities
JOURNAL Patent: US 5856096-A 12 05-JAN-1999;
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ACCESSION AR059195
VERSION AR059195.1 GI:5984772
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5837857-A 2 17-NOV-1998;
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ACCESSION AR075506
VERSION AR075506.1 GI:10002256
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5958680-A 3 28-SEP-1999;
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DEFINITION Sequence 2 from patent US 6258535.
ACCESSION AR161904
VERSION AR161904.1 GI:16228913
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 6258535-A 2 10-JUL-2001;

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KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 11)  
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.  
TITLE Mammalian telomerase  
JOURNAL Patent: US 6548298-A 2 15-APR-2003;  
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ACCESSION AX033373  
VERSION AX033373.1 GI:10280147  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Larsen,F. and Skaanseng,M.  
TITLE Detecting telomerase activity  
JOURNAL Patent: WO 0046601-A 5 10-AUG-2000;  
LARSSEN FRANK (NO) ; SKAANSENG MARIANNE (NO)  
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ACCESSION AX268757  
VERSION AX268757.1 GI:16541829  
KEYWORDS  
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ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1  
AUTHORS Gilchrest,B.A., Yaar,M. and Eller,M.  
TITLE Use of locally applied dna fragments  
JOURNAL Patent: WO 0174342-A 5 11-OCT-2001;  
TRUSTEES OF BOSTON UNIVERSITY (US)  
FEATURES Location/Qualifiers  
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VERSION AX268761.1 GI:16541833  
KEYWORDS  
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ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1  
AUTHORS Gilchrest,B.A., Yaar,M. and Eller,M.  
TITLE Use of locally applied dna fragments  
JOURNAL Patent: WO 0174342-A 9 11-OCT-2001;  
TRUSTEES OF BOSTON UNIVERSITY (US)  
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ACCESSION AX283296  
VERSION AX283296.1 GI:16541833  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
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REFERENCE 1  
AUTHORS Gilchrest,B.A., Yaar,M. and Eller,M.  
TITLE Use of locally applied dna fragments  
JOURNAL Patent: WO 0174342-A 9 11-OCT-2001;  
TRUSTEES OF BOSTON UNIVERSITY (US)  
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VERSION AX283296.1 GI:17044177
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Uhlmann,E., Breipohl,G. and Will,D.W.
TITLE Polyamide nucleic acid derivatives, agents and methods for
JOURNAL producing the same
Patent: WO 0179249-A 60 25-OCT-2001;
Aventis Pharma Deutschland GmbH (DE)
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DEFINITION Modulation of mammalian telomerase by peptide nucleic acids.
ACCESSION BD071047
VERSION BD071047.1 GI:22616650
KEYWORDS JP 2001517929-A/13.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Shay,J.W., Wright,W.E., Piatyszek,M.A., Corey,D. and Norton,J.C.
TITLE Modulation of mammalian telomerase by peptide nucleic acids
JOURNAL Patent: JP 2001517929-A 13 09-OCT-2001;
GERON CORP
COMMENT OS Unidentified
PN JP 2001517929-A/13
PD 09-OCT-2001
PF 09-APR-1997 JP 1997536487
PR 09-APR-1996 US 08/630019
PI JERRY W SHAY,WOODRING E WRIGHT,MIECZYSLAW A PIATYSZEK,DAVID
PI COREY,
PI JAMES C NORTON
PC C07K14/00,A61K38/16,C12Q1/68
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CC /desc = 'peptide nucleic acid (PNA), where (deoxy(ribose- CC
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DEFINITION Modulation of mammalian telomerase by peptide nucleic acids.
ACCESSION BD071077
VERSION BD071077.1 GI:22616680
KEYWORDS JP 2001517929-A/43.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Shay,J.W., Wright,W.E., Piatyszek,M.A., Corey,D. and Norton,J.C.
TITLE Modulation of mammalian telomerase by peptide nucleic acids
JOURNAL Patent: JP 2001517929-A 13 09-OCT-2001;
GERON CORP
COMMENT OS Unidentified
PN JP 2001517929-A/13
PD 09-OCT-2001
PF 09-APR-1997 JP 1997536487
PR 09-APR-1996 US 08/630019
PI JERRY W SHAY,WOODRING E WRIGHT,MIECZYSLAW A PIATYSZEK,DAVID
PI COREY,
PI JAMES C NORTON
PC C07K14/00,A61K38/16,C12Q1/68
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Shay,J.W., Wright,W.E., Piatyszek,M.A., Corey,D. and Norton,J.C.
Modulation of mammalian telomerase by peptide nucleic acids
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GERON CORP
OS Unidentified
PN JP 2001517929-A/43
PD 09-OCT-2001
PP 09-APR-1997 JP 1997536487
PR 09-APR-1996 US 08/630019
PI JERRY W SHAY,WOODRING E WRIGHT,MIECZYSLAW A PIATYSZEK, DAVID
PI COREY, C
PI JAMES C NORTON
PC C07K14/00,A61K38/16,C12Q1/68
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DEFINITION Mammalian telomerase.
ACCESSION BD176143
VERSION BD176143.1 GI:29121847
KEYWORDS JP 2002272489-A/2.
SOURCE unclassified
ORGANISM unclassified.
1 (bases 1 to 11)
Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
Mammalian telomerase
Patent: JP 2002272489-A 2 24-SEP-2002;
GERON CORP
OS Unidentified
PN JP 2002272489-A/2
PD 24-SEP-2002
PP 06-MAR-2002 JP 2002061125
PR 07-JUL-1994 US 08/272102,27-OCT-1994 US 08/330123 PR
07-JUN-1995 US 09/472802,07-JUN-1995 US 08/482115 PI BRYANT
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GenCore version 5.1.6  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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3	11	100.0	11	18	AAAT89237
4	11	100.0	11	18	AAAT90060
5	11	100.0	11	21	AAAT37556
6	11	100.0	11	21	AAAT37561
7	11	100.0	11	21	AAAT37562
8	11	100.0	11	21	AAAT37573
-----					
1	11	100.0	11	18	AAV07769
2	11	100.0	11	18	AAAT89250
3	11	100.0	11	18	AAAT89237
4	11	100.0	11	18	AAAT90060
5	11	100.0	11	21	AAAT37556
6	11	100.0	11	21	AAAT37561
7	11	100.0	11	21	AAAT37562
8	11	100.0	11	21	AAAT37573

9	11	100.0	11	21	AAA37586	Antisense sequence
10	11	100.0	11	22	AAF81185	Oligonucleotide th
11	11	100.0	11	22	AAH26728	Phosphoramidate-11
12	11	100.0	11	22	AAH26732	Phosphoramidate-11
13	11	100.0	11	23	AAH14909	Melanogenesis asso
14	11	100.0	11	23	AAH14913	Melanogenesis asso
15	11	100.0	11	23	AAH14913	Melanogenesis asso
16	11	100.0	11	23	AAH14913	Melanogenesis asso
17	11	100.0	11	23	AAH14913	Melanogenesis asso
18	11	100.0	11	24	AAK98619	Modified peptide n
19	11	100.0	11	24	AAK98619	Modified peptide n
20	11	100.0	11	24	AAK98619	Modified peptide n
21	11	100.0	11	25	AAH26728	Human telomerase t
22	11	100.0	11	25	AAH26728	Oligonucleotide #2
23	11	100.0	11	25	AAH26728	Oligonucleotide #1
24	11	100.0	11	25	AAH26728	Oligonucleotide #1
25	11	100.0	11	25	AAH26728	Oligonucleotide #1
26	11	100.0	11	25	AAH26728	Oligonucleotide #1
27	11	100.0	11	25	AAH26728	Oligonucleotide #1
28	11	100.0	11	25	AAH26728	Oligonucleotide #1
29	11	100.0	11	25	AAH26728	Oligonucleotide #1
30	11	100.0	11	25	AAH26728	Oligonucleotide #1
31	11	100.0	11	25	AAH26728	Oligonucleotide #1
32	11	100.0	11	25	AAH26728	Oligonucleotide #1
33	11	100.0	11	25	AAH26728	Oligonucleotide #1
34	11	100.0	11	25	AAH26728	Oligonucleotide #1
35	11	100.0	11	25	AAH26728	Oligonucleotide #1
36	11	100.0	11	25	AAH26728	Oligonucleotide #1
37	11	100.0	11	25	AAH26728	Oligonucleotide #1
38	11	100.0	11	25	AAH26728	Oligonucleotide #1
39	11	100.0	11	25	AAH26728	Oligonucleotide #1
40	11	100.0	11	25	AAH26728	Oligonucleotide #1
41	11	100.0	11	25	AAH26728	Oligonucleotide #1
42	11	100.0	11	25	AAH26728	Oligonucleotide #1
43	11	100.0	11	25	AAH26728	Oligonucleotide #1
44	11	100.0	11	25	AAH26728	Oligonucleotide #1
45	11	100.0	11	25	AAH26728	Oligonucleotide #1

## ALIGNMENTS

RESULT 1	AAV07769	standard; DNA; 11 BP.
ID	AAV07769	standard; DNA; 11 BP.
XX	AAV07769	
AC	AAV07769	
XX	AAV07769	
DT	07-DEC-1998	(first entry)
XX	07-DEC-1998	(first entry)
DE	N3 to P5 oligonucleotide phosphoramidate useful as telomerase inhibitor.	
XX	N3 to P5 oligonucleotide phosphoramidate useful as telomerase inhibitor.	
XX	telomerase inhibitor; phosphoramidate; telomerase-binding region; TBR;	
KW	cell proliferation; tumour; lukaemia; duplex; ss.	
XX	Synthetic.	
OS	Synthetic.	
XX	Synthetic.	
PH	Key	Location/Qualifiers
FT	misc_feature	1..11
FT	FT	/*tag= a
FT	FT	/note= "each linkage is a phosphoramidate linkage"
XX	XX	
PN	WO9737691-A1.	
XX	WO9737691-A1.	
PD	16-OCT-1997.	
XX	16-OCT-1997.	
PF	08-APR-1997;	97WO-US05773.
XX	08-APR-1997;	97WO-US05773.
PR	10-APR-1996;	96US-0630242.
XX	10-APR-1996;	96US-0630242.
PA	(LYNX-) LYNX THERAPEUTICS INC.	
XX	(LYNX-) LYNX THERAPEUTICS INC.	
PI	Lloyd DH;	



Query Match 100.0%; Score 11; DB 18; Length 11;  
 Best Local Similarity 100.0%; Pred. NO. 2.1e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGGGTTAG 11  
 |||||  
 Db 1 GTTAGGGTTAG 11

## RESULT 4

AAT90060

ID AAT90060 standard; DNA; 11 BP.

XX AC

AC AAT90060;

XX DT

24-NOV-1997 (first entry)

XX DE

Telomerase primer.

Detection; telomerase; amplification; polymerase chain reaction;  
 PCR; primer; cancer; carcinoma; sarcoma; leukaemia; leukemia;  
 myeloma; lymphoma; neuroblastoma; astrocytoma; glioma;  
 glioblastoma; retinoblastoma; melanoma; screen; drug;  
 determination; telomere length; ss.

XX OS

OS Synthetic.

XX NN

NN WO9711198-A1.

XX DD

DD 27-MAR-1997.

XX PP

PP 20-SEP-1996; 96WO-US15162.

XX RR

RR 20-SEP-1995; 95US-0531743.

XX PA

PA (CTRC-) CTCR RES FOUND.

XX PI

PI Chen S, Fletcher TM, Maine I, Qiu M, Windle BE;

XX DR

DR WPI; 1997-202904/18.

XX PT

PT Detecting telomerase activity by ligation sequential reaction -

XX PS

PS useful for diagnosis of cancer or to screen for telomerase

XX SS

SS inhibitors

XX CC

CC Claim 40; Page 27; 71pp; English.

XX CC

CC A novel method of detecting telomerase activity in a sample,

XX CC

CC comprises amplifying a sample with a telomerase primer, e.g. the

XX CC

CC present sequence, and contacting the product with 1st and 2nd

XX CC

CC oligonucleotides, which hybridise to the product so that no single

XX CC

CC stranded region intervenes between them. The hybridised product and

XX CC

CC oligonucleotides are then contacted with ligase and the ligated

XX CC

CC form of the oligonucleotides detected.

XX CC

CC The method can be used to detect cancer, e.g. carcinomas of the

XX CC

CC breast, colon, oesophagus, kidney, liver, lung, ovaries, prostate,

XX CC

CC stomach, uterus, pancreas and head and neck, sarcomas of bone and

XX CC

CC muscle, leukaemias, myelomas, lymphomas, neuroblastomas, and

XX CC

CC astrocytomas, gliomas, glioblastomas, retinoblastomas and

XX CC

CC melanomas. The method can also be used to screen for

XX CC

CC anti-telomerase activity in candidate drugs and to determine

XX CC

CC telomere length.

XX CC

CC Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

XX CC

CC Query Match 100.0%; Score 11; DB 18; Length 11;

XX CC

CC Best Local Similarity 100.0%; Pred. NO. 2.1e+03;

XX CC

CC Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX CC

CC QY 1 GTTAGGGTTAG 11

XX CC

CC |||||

XX CC

CC Db 1 GTTAGGGTTAG 11

## RESULT 5

AAA37556

ID AAA37556 standard; DNA; 11 BP.

XX AC

AC AAA37556;

XX DT

DT 15-AUG-2000 (first entry)

XX DE

DE PNA sequence #13 used to inhibit telomerase activity.

XX KW

KW Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;

XX KW

KW inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;

XX KW

KW AIDS; HIV; fungal infection; forensic identification; detect; tumour;

XX KW

KW paternity testing; ss.

XX OS

OS Synthetic.

XX FH

FH Key

XX FT

FT misc\_feature

XX FT

FT 1..11

XX FT

FT /tag= a

XX FT

FT /note= "Peptide nucleic acid molecule, where

XX FT

FT N-(2-aminoethyl)glycine units are linked to

XX FT

FT nucleotide bases via glycine amino N through a

XX FT

FT methylenecarbonyl linker"

XX PN

PN US6046307-A.

XX PD

PD 04-APR-2000.

XX PF

PF 09-APR-1997; 97US-0838545.

XX PR

PR 09-APR-1996; 96US-0630019.

XX PA

PA (TEXA ) UNIV TEXAS SYSTEM.

XX PI

PI Wright WE, Piatyszek MA, Shay JW, Norton JC, Corey DR;

XX DR

DR WPI; 2000-292432/25.

XX CC

CC New peptide nucleic acid (PNA) compounds that inhibit telomerase

XX CC

CC activity in mammalian cells is useful as probes to detect the RNA

XX CC

CC component of a mammalian telomerase

XX PS

PS Claim 6; Column 71; 45pp; English.

XX CC

CC The present sequence represents a peptide nucleic acid molecule which

XX CC

CC hybridises to the mRNA component of mammalian telomerase, and inhibits

XX CC

CC telomerase activity. Telomerase is a ribonucleoprotein enzyme that

XX CC

CC synthesizes one strand of the telomeric DNA, using as a template an 11

XX CC

CC nucleotide sequence contained within the RNA component of the enzyme. The

XX CC

CC invention relates to PNA molecules having a sequence of no more than 25

XX CC

CC bases, which include the sequence GTTAGG. The uncharged nature of the PNA

XX CC

CC backbone increases the melting temperature of associating strands,

XX CC

CC affords greater resistance of degradation by proteases or nucleases. The

XX CC

CC therapeutic PNAs may be used for treating disease conditions such as

XX CC

CC immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency

XX CC

CC syndrome) and associated pathologies, fungal infections, and other

XX CC

CC diseases characterized by abnormal telomere metabolism or telomerase

XX CC

CC activity, in combination with antineoplastic and other cytotoxic or

XX CC

CC cytostatic agents, antifungal agents, and other nucleotides. PNAs may be

XX CC

CC used for molecular diagnostics, labelled PNAs are used as hybridization

XX CC

CC probes to detect or quantitate polynucleotides having a human telomerase

XX CC

CC RNA (htr) sequence. PNA probes are also used for forensic identification

XX CC

CC of individuals, e.g. paternity testing, based on htr gene restriction

XX CC

CC fragment length polymorphism (RFLP) pattern. PNAs are also useful as

XX CC

CC probes to detect the RNA component of a mammalian telomerase and as

XX CC

CC inhibitors of telomerase activity. The method of the present invention

XX CC

CC allows cancerous conditions to be detected with increased confidence and

XX CC

CC possibly at an earlier stage, before cells are detected as cancerous

CC based on pathological characteristics. The diagnostic and prognostic  
 CC methods of the present invention can be used to detect an immortal or  
 CC neoplastic cell or tumour tissue or cancer of any origin, provided the  
 CC cell expresses telomerase activity and its RNA component.

XX SQ Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;  
 Query Match 100.0%; Score 11; DB 21; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTTAGGGTTAG 11  
 |||||  
 Db 1 GTTAGGGTTAG 11

## RESULT 6

AAA37561  
 AAA37561 standard; DNA; 11 BP.

AAA37561;

15-AUG-2000 (first entry)

PNA sequence #18 used to inhibit telomerase activity.

Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;  
 inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;  
 AIDS; HIV; fungal infection; forensic identification; detect; tumour;  
 paternity testing; ss.

Synthetic.

Key Location/Qualifiers  
 misc\_feature 1..11

/\*tag= a  
 /note= "Peptide nucleic acid molecule, where  
 N-(2-aminoethyl)glycine units are linked to  
 nucleotide bases via glycine amino N through a  
 methylenecarbonyl linker"

misc\_feature 1  
 /\*tag= b  
 /note= "G residue is linked to the carboxy end of the  
 peptide GGRQIKIWQNNMKWK"

US6046307-A.

04-APR-2000.

09-APR-1997; 97US-0838545.

09-APR-1996; 96US-0630019.

(TEXA ) UNIV TEXAS SYSTEM.

Wright WE, Platyszek MA, Shay JW, Norton JC, Corey DR;

WPI; 2000-292432/25.

New peptide nucleic acid (PNA) compounds that inhibit telomerase  
 activity in mammalian cells is useful as probes to detect the RNA  
 component of a mammalian telomerase

Claim 9; Column 71-72; 45pp; English.

The present sequence represents a peptide nucleic acid molecule which  
 hybridizes to the mRNA component of mammalian telomerase, and inhibits  
 telomerase activity. Telomerase is a ribonucleoprotein enzyme that  
 synthesizes one strand of the telomeric DNA, using as a template an 11  
 nucleotide sequence contained within the RNA component of the enzyme. The  
 invention relates to PNA molecules having a sequence of no more than 25  
 bases, which include the sequence GTTAGG. The uncharged nature of the PNA  
 backbone increases the melting temperature of associating strands,

CC increases the rate of association with targeted nucleic acids, and  
 CC affords greater resistance of degradation by proteases or nucleases. The  
 CC therapeutic PNAs may be used for treating disease conditions such as  
 CC cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human  
 CC immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency  
 CC syndrome) and associated pathologies, fungal infections, and other  
 CC diseases characterized by abnormal telomere metabolism and other  
 CC activity in combination with antineoplastic and other cytotoxic or  
 CC cytostatic agents, antifungal agents, and other nucleotides. PNAs may be  
 CC used for molecular diagnostics, labelled PNAs are used as hybridization  
 CC probes to detect or quantitate polynucleotides having a human telomerase  
 CC RNA (HTR) sequence. PNA probes are also used for forensic identification  
 CC of individuals, e.g. paternity testing, based on HTR gene restriction  
 CC fragment length polymorphism (RFLP) pattern. PNAs are also useful as  
 CC probes to detect the RNA component of a mammalian telomerase and as  
 CC inhibitors of telomerase activity. The method of the present invention  
 CC allows cancerous conditions to be detected with increased confidence and  
 CC possibly at an earlier stage, before cells are detected as cancerous  
 CC based on pathological characteristics. The diagnostic and prognostic  
 CC methods of the present invention can be used to detect an immortal or  
 CC neoplastic cell or tumour tissue or cancer of any origin, provided the  
 CC cell expresses telomerase activity and its RNA component.

XX SQ Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 11; DB 21; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTTAGGGTTAG 11  
 |||||  
 Db 1 GTTAGGGTTAG 11

## RESULT 7

AAA37562

AAA37562 standard; DNA; 11 BP.

AAA37562;

15-AUG-2000 (first entry)

PNA sequence #19 used to inhibit telomerase activity.

Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;  
 inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;  
 AIDS; HIV; fungal infection; forensic identification; detect; tumour;  
 paternity testing; ss.

Synthetic.

Key Location/Qualifiers  
 misc\_feature 1..11

/\*tag= a  
 /note= "Peptide nucleic acid molecule, where  
 N-(2-aminoethyl)glycine units are linked to  
 nucleotide bases via glycine amino N through a  
 methylenecarbonyl linker"

misc\_feature 11  
 /\*tag= b  
 /note= "G residue is linked to the amino end of the  
 peptide GGRQIKIWQNNMKWK"

US6046307-A.

04-APR-2000.

09-APR-1997; 97US-0838545.

09-APR-1996; 96US-0630019.

(TEXA ) UNIV TEXAS SYSTEM.

PI Wright WE, Piatyszek MA, Shay JW, Norton JC, Corey DR;  
 XX WPI; 2000-292432/25.  
 XX  
 XX New peptide nucleic acid (PNA) compounds that inhibit telomerase  
 PT activity in mammalian cells is useful as probes to detect the RNA  
 PT component of a mammalian telomerase -  
 XX  
 XX Claim 9; Column 71-72; 45pp; English.  
 PS  
 XX The present sequence represents a peptide nucleic acid molecule which  
 CC hybridizes to the mRNA component of mammalian telomerase, and inhibits  
 CC telomerase activity. Telomerase is a ribonucleoprotein enzyme that  
 CC synthesizes one strand of the telomeric DNA, using as a template an 11  
 CC nucleotide sequence contained within the RNA component of the enzyme. The  
 CC invention relates to PNA molecules having a sequence of no more than 25  
 CC bases, which include the sequence GTTAGG. The uncharged nature of the PNA  
 CC backbone increases the melting temperature of associating strands,  
 CC increases the rate of association with targeted nucleic acids, and  
 CC affords greater resistance of degradation by proteases or nucleases. The  
 CC therapeutic PNAs may be used for treating disease conditions such as  
 CC cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human  
 CC immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency  
 CC syndrome) and associated pathologies, fungal infections, and other  
 CC diseases characterized by abnormal telomere metabolism or telomerase  
 CC activity, in combination with antineoplastic and other cytotoxic or  
 CC cytostatic agents, antifungal agents, and other nucleotides. PNAs may be  
 CC used for molecular diagnostics, labelled PNAs are used as hybridization  
 CC probes to detect or quantitate polynucleotides having a human telomerase  
 CC RNA (hTR) sequence. PNA probes are also used for forensic identification  
 CC of individuals, e.g. paternity testing, based on hTR gene restriction  
 CC fragment length polymorphism (RFLP) pattern. PNAs are also useful as  
 CC probes to detect the RNA component of a mammalian telomerase and as  
 CC inhibitors of telomerase activity. The method of the present invention  
 CC allows cancerous conditions to be detected with increased confidence and  
 CC possibly at an earlier stage, before cells are detected as cancerous  
 CC based on pathological characteristics. The diagnostic and prognostic  
 CC methods of the present invention can be used to detect an immortal or  
 CC neoplastic cell or tumour tissue or cancer of any origin, provided the  
 CC cell expresses telomerase activity and its RNA component.  
 XX  
 XX Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;  
 XX  
 XX Query Match 100.0%; Score 11; DB 21; Length 11;  
 XX Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 1 GTTAGGGTTAG 11  
 XX |||||  
 XX 1 GTTAGGGTTAG 11  
 XX  
 XX RESULT 8  
 XX AAA37573/c  
 XX ID AAA37573 standard; DNA; 11 BP.  
 XX  
 XX AAA37573;  
 XX  
 XX 15-AUG-2000 (first entry)  
 XX  
 XX PNA sequence #31 used to inhibit telomerase activity.  
 XX  
 XX Peptide nucleic acid; PNA; Telomerase; ribonucleoprotein enzyme; cancer;  
 XX inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;  
 XX AIDS; HIV; fungal infection; forensic identification; detect; tumour;  
 XX paternity testing; ss.  
 XX  
 XX Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 XX misc\_feature 1..11  
 XX /\*tag= a  
 XX /note= "Peptide nucleic acid molecule, where

US6046307-A.  
 04-APR-2000.  
 09-APR-1997; 97US-0838545.  
 09-APR-1996; 96US-0630019.  
 (TEXA ) UNIV TEXAS SYSTEM.  
 Wright WE, Piatyszek MA, Shay JW, Norton JC, Corey DR;  
 WPI; 2000-292432/25.  
 New peptide nucleic acid (PNA) compounds that inhibit telomerase  
 activity in mammalian cells is useful as probes to detect the RNA  
 component of a mammalian telomerase -  
 XX  
 XX Example 2; Column 33; 45pp; English.  
 XX  
 XX The present sequence represents a peptide nucleic acid molecule which  
 CC hybridizes to the mRNA component of mammalian telomerase, and inhibits  
 CC telomerase activity. Telomerase is a ribonucleoprotein enzyme that  
 CC synthesizes one strand of the telomeric DNA, using as a template an 11  
 CC nucleotide sequence contained within the RNA component of the enzyme. The  
 CC invention relates to PNA molecules having a sequence of no more than 25  
 CC bases, which include the sequence GTTAGG. The uncharged nature of the PNA  
 CC backbone increases the melting temperature of associating strands,  
 CC increases the rate of association with targeted nucleic acids, and  
 CC affords greater resistance of degradation by proteases or nucleases. The  
 CC therapeutic PNAs may be used for treating disease conditions such as  
 CC cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human  
 CC immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency  
 CC syndrome) and associated pathologies, fungal infections, and other  
 CC diseases characterized by abnormal telomere metabolism or telomerase  
 CC activity, in combination with antineoplastic and other cytotoxic or  
 CC cytostatic agents, antifungal agents, and other nucleotides. PNAs may be  
 CC used for molecular diagnostics, labelled PNAs are used as hybridization  
 CC probes to detect or quantitate polynucleotides having a human telomerase  
 CC RNA (hTR) sequence. PNA probes are also used for forensic identification  
 CC of individuals, e.g. paternity testing, based on hTR gene restriction  
 CC fragment length polymorphism (RFLP) pattern. PNAs are also useful as  
 CC probes to detect the RNA component of a mammalian telomerase and as  
 CC inhibitors of telomerase activity. The method of the present invention  
 CC allows cancerous conditions to be detected with increased confidence and  
 CC possibly at an earlier stage, before cells are detected as cancerous  
 CC based on pathological characteristics. The diagnostic and prognostic  
 CC methods of the present invention can be used to detect an immortal or  
 CC neoplastic cell or tumour tissue or cancer of any origin, provided the  
 CC cell expresses telomerase activity and its RNA component.  
 XX  
 XX Sequence 11 BP; 4 A; 5 C; 0 G; 2 T; 0 other;  
 XX  
 XX Query Match 100.0%; Score 11; DB 21; Length 11;  
 XX Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 1 GTTAGGGTTAG 11  
 XX |||||  
 XX 11 GTTAGGGTTAG 1  
 XX  
 XX RESULT 9  
 XX AAA37586  
 XX ID AAA37586 standard; DNA; 11 BP.  
 XX  
 XX AAA37586;  
 XX  
 XX 15-AUG-2000 (first entry)

N-(2-aminoethyl)glycine units are linked to  
 nucleotide bases via glycine amino N through a  
 methylenecarbonyl linker"

Antisense sequence #44 used to inhibit telomerase activity.

Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer; inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia; AIDS; HIV; fungal infection; forensic identification; detect; tumour; paternity testing; ss.

Synthetic.

Key Location/Qualifiers  
misc\_feature 1..11  
/\*tag= a  
/note= "Phosphorothioate internucleotide linkages"

US6046307-A.  
04-APR-2000.  
09-APR-1997; 97US-0838545.  
09-APR-1996; 96US-0630019.  
(TEXA ) UNIV TEXAS SYSTEM.

Wright WE, Piatyszek MA, Shay JW, Norton JC, Corey DR;  
WPI; 2000-292432/25.

New peptide nucleic acid (PNA) compounds that inhibit telomerase activity in mammalian cells is useful as probes to detect the RNA component of a mammalian telomerase

Example 1; Column 27-28; 45pp; English.

The present sequence represents an antisense oligonucleotide used as a control sequence alongside a peptide nucleic acid molecule which hybridizes to the mRNA component of mammalian telomerase, and inhibits telomerase activity. Telomerase is a ribonucleoprotein enzyme that synthesizes one strand of the telomeric DNA, using as a template an 11 nucleotide sequence contained within the RNA component of the enzyme. The invention relates to PNA molecules having a sequence of no more than 25 bases, which include the sequence GTTAGG. The uncharged nature of the PNA backbone increases the melting temperature of associating strands, increases the rate of association with targeted nucleic acids, and affords greater resistance of degradation by proteases or nucleases. The therapeutic PNAs may be used for treating disease conditions such as cancer, neoplasia, hyperplasia, neurodegenerative diseases, aging, human immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency syndrome) and associated pathologies, fungal infections, and other diseases characterized by abnormal telomere metabolism or telomerase activity, in combination with antineoplastic and other cytotoxic or cytostatic agents, antifungal agents, and other nucleotides. PNAs may be used for molecular diagnostics, labelled PNAs are used as hybridization probes to detect or quantitate polynucleotides having a human telomerase RNA (hTR) sequence. PNA probes are also used for forensic identification of individuals, e.g. paternity testing, based on hTR gene restriction fragment length polymorphism (RFLP) pattern. PNAs are also useful as probes to detect the RNA component of a mammalian telomerase and as inhibitors of telomerase activity. The method of the present invention allows cancerous conditions to be detected with increased confidence and possibly at an earlier stage, before cells are detected as cancerous based on pathological characteristics. The diagnostic and prognostic methods of the present invention can be used to detect an immortal or neoplastic cell or tumour tissue or cancer of any origin, provided the cell expresses telomerase activity and its RNA component.

Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;  
Query Match 100.0%; Score 11; DB 21; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTAGGCTTAG 11  
| | | | | | | | | |  
Db 1 GTTAGGCTTAG 11

RESULT 10  
AAF81185  
ID AAF81185 standard; DNA; 11 BP.  
XX  
XX AAF81185;  
AC AAF81185;  
XX  
XX 30-MAY-2001 (first entry)  
DT  
XX  
DE Oligonucleotide thiophosphoramidate, SEQ ID NO: 1.  
XX  
KW Thiophosphoramidate oligonucleotide; virucide; cytostatic;  
KW immunosuppressive; contraceptive; RNA inhibitor; telomerase inhibitor;  
KW antisense therapy; viral infection; cancer; hyperproliferative disorder;  
KW autoimmune disorder; ss.  
XX  
OS Synthetic.  
XX  
XX WO200118015-A1.  
XX  
XX 15-MAR-2001.  
XX  
XX 08-SEP-2000; 2000WO-US24688.  
XX  
XX 10-SEP-1999; 99US-0153201.  
PR 19-OCT-1999; 99US-0160444.  
XX  
XX (GERO-) GERON CORP.  
XX  
XX Gryaznov S, Pomgracz K, Matray T;  
PI  
XX  
XX WPI; 2001-265967/27.  
XX  
PT Novel thiophosphoramidate polynucleotide useful for detection of RNA or  
PT DNA having a given target sequence, for inhibiting RNA function in a  
PT cell, and for treating cancer and viral infection  
XX  
XX Example 3; Page 39; 68pp; English.  
XX  
CC The present sequence was synthesised in an example illustrating an  
CC invention relating to polynucleotides comprising a non-homopolymetric  
CC sequence of nucleoside subunits joined by at least one inter-subunit  
CC linkage that is a N3'-P5', thiophosphoramidate. The thiophosphoramidate  
CC oligonucleotides retain a high RNA binding affinity and exhibit a much  
CC higher acid stability. They are useful for detecting a specific sequence  
CC in a sample, by forming a hybridisation complex with the sequence. They  
CC are useful for inhibiting function of an RNA in a cell (for inhibiting  
CC translation of a mRNA or for inhibiting telomerase enzyme in a cell).  
CC They are also useful in the preparation of a medicament for treatment of  
CC viral infection or cancer. The oligonucleotides are useful for anti-sense  
CC and anti-gene diagnostic or therapeutic applications and may be used for  
CC treating telomerase-mediated conditions or diseases, such as  
CC hyperproliferative and autoimmune disorders, and for contraceptive  
CC purposes.  
XX  
SQ Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;  
Query Match 100.0%; Score 11; DB 22; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTAGGCTTAG 11  
| | | | | | | | | |  
Db 1 GTTAGGCTTAG 11

RESULT 11  
AAH26728  
ID AAH26728 standard; DNA; 11 BP.



```
XX AC AAH26728;
XX DT 26-NOV-2001 (first entry)
XX DE Phosphoramidate-linked 2'-arabino-fluorooligonucleotide.
XX KW 2'-arabino-fluorooligonucleotide; phosphoramidate; telomerase;
XX KW inhibitor; infection; cancer; diagnosis; therapy; cytostatic;
XX KW virucide; antisense; antigene; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 2..11
XX FT /*tag= a
XX FT /mod_base= "OTHER"
XX FT /note= "2'-arabino-fluoronucleosides"
XX FT modified_base 2..11
XX FT /*tag= b
XX FT /mod_base= "OTHER"
XX FT /note= "phosphoramidate linkage"
XX PN WO200153307-A1.
XX PD 26-JUL-2001.
XX PD 19-JAN-2001; 2001WO-US01918.
XX PD 21-JAN-2000; 2000US-178248P.
XX PA (GERO-) GERON CORP.
XX PI Gryaznov S, Schultz RG;
XX PI WPI; 2001-589652/66.
XX DR Polynucleotides, used to detect and isolate nucleic acids, inhibit
XX PT function of RNA and telomerase enzymes and to treat e.g. viral
XX PT infections, contain 2'-arabino-fluoronucleoside(s) linked to
XX PT nucleoside(s) -
XX PS Example 6; Page 46; 61pp; English.
XX CC The present sequence is that of a N3'-P5' 2'-arabino-fluoro
XX CC phosphoramidate oligonucleotide that is complementary to
XX CC telomerase RNA. The oligonucleotide was used to assess the
XX CC relative efficacy of novel 2'-arabino-fluoro phosphoramidate
XX CC oligonucleotides and their 2'-ribo fluorooligonucleotide
XX CC counterparts (see AAH26728-35) for the inhibition of telomerase
XX CC activity. Novel phosphoramidate 2'-arabino-fluorooligonucleotides
XX CC are generally more acid stable, more resistant to cellular
XX CC proteases, and also show greater telomerase inhibition activity
XX CC than 2'-ribose-fluoro phosphoramidates. They are therefore useful
XX CC for treating cancer (claimed) and other diseases in which telomerase
XX CC activity is present at abnormal levels, such as hyperproliferative
XX CC or autoimmune diseases e.g. psoriasis, rheumatoid arthritis,
XX CC immune system disorders requiring immunosuppression, and in the
XX CC treatment of viral infection (claimed).
XX SQ Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;
Query Match 100.0%; Score 11; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTAGGGTTAG 11
Db 1 GTTAGGGTTAG 11
RESULT 12
AAH26732
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ID AAH26732 standard; DNA; 11 BP.
XX AC AAH26732;
XX DT 26-NOV-2001 (first entry)
XX DE Phosphoramidate-linked 2'-ribose-fluorooligonucleotide.
XX KW 2'-ribose-fluorooligonucleotide; phosphoramidate; telomerase;
XX KW inhibitor; infection; cancer; diagnosis; therapy; cytostatic;
XX KW virucide; antisense; antigene; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 2..11
XX FT /*tag= a
XX FT /mod_base= "OTHER"
XX FT /note= "2'-ribose-fluoronucleosides"
XX FT modified_base 2..11
XX FT /*tag= b
XX FT /mod_base= "OTHER"
XX FT /note= "phosphoramidate linkage"
XX PN WO200153307-A1.
XX PD 26-JUL-2001.
XX PD 19-JAN-2001; 2001WO-US01918.
XX PD 21-JAN-2000; 2000US-178248P.
XX PA (GERO-) GERON CORP.
XX PI Gryaznov S, Schultz RG;
XX PI WPI; 2001-589652/66.
XX DR Polynucleotides, used to detect and isolate nucleic acids, inhibit
XX PT function of RNA and telomerase enzymes and to treat e.g. viral
XX PT infections, contain 2'-arabino-fluoronucleoside(s) linked to
XX PT nucleoside(s) -
XX PS Example 6; Page 46; 61pp; English.
XX CC The present sequence is that of a 2'-ribose-fluoro
XX CC phosphoramidate oligonucleotide that is complementary to
XX CC telomerase RNA. The oligonucleotide was used to assess the
XX CC relative efficacy of novel 2'-arabino-fluoro phosphoramidate
XX CC oligonucleotides and their 2'-ribose fluorooligonucleotide
XX CC counterparts (see AAH26728-35) for the inhibition of telomerase
XX CC activity. Novel phosphoramidate 2'-arabino-fluorooligonucleotides
XX CC are generally more acid stable, more resistant to cellular
XX CC proteases, and also show greater telomerase inhibition activity
XX CC than 2'-ribose-fluoro phosphoramidates. They are therefore useful
XX CC for treating cancer (claimed) and other diseases in which telomerase
XX CC activity is present at abnormal levels, such as hyperproliferative
XX CC or autoimmune diseases e.g. psoriasis, rheumatoid arthritis,
XX CC immune system disorders requiring immunosuppression, and in the
XX CC treatment of viral infection (claimed).
XX SQ Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;
Query Match 100.0%; Score 11; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTAGGGTTAG 11
Db 1 GTTAGGGTTAG 11
RESULT 13
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AAS14909  
 ID AAS14909 standard; DNA; 11 BP.  
 AC AAS14909;  
 XX  
 DT 14-FEB-2002 (first entry)  
 XX  
 DE Melanogenesis associated oligonucleotide #5.  
 XX  
 KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;  
 KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;  
 KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;  
 KW tumour necrosis factor inhibitor; photoging; hyperproliferative disease;  
 KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;  
 KW conjunctivitis; allergic rhinitis; vitiligo; ss.  
 XX  
 OS Synthetic.  
 XX  
 Key Location/Qualifiers  
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 /tag= a  
 /mod\_base= g  
 /note= "Optionally phosphorylated"  
 modified\_base 1..11  
 /tag= b  
 /mod\_base= OTHER  
 /note= "OTHER= Optionally phosphorothiolate linkages"  
 WO200174342-A2.  
 11-OCT-2001.  
 30-MAR-2001; 2001WO-US10162.  
 31-MAR-2000; 2000US-0540843.  
 (UYBO-) UNIV BOSTON.  
 Gilchrest BA, Yaar M, Eller M;  
 WPI; 2001-626338/72.  
 Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonucleotides that mimic the effects of ultra-violet light -  
 Claim 1; Page 37; 74pp; English.  
 The invention describes inhibition of mammalian epithelial cell proliferation by treating cells with at least one oligonucleotide, or its fragment. The compounds, which have cytostatic, anti-allergic, anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and immunosuppressive activities, function as 'ultra-violet mimics' to induce DNA repair processes (or a protective response to later exposure to radiation or chemicals), as a proliferation inhibitor, apoptosis inducer or a tumour necrosis factor inhibitor. Probably they mimic products of DNA damage, or processed DNA-damage intermediates, by inducing the p53 pathway, resulting in transient arrest of cell growth, allowing more time for DNA repair to occur before cell division takes place. The method is especially used to treat carcinoma but may also be used to: treat other hyperproliferative states (e.g. psoriasis or precancerous conditions); reduce photoging, oxidative stress or damage; prevent skin cancer; treat allergically mediated inflammation (atopic or contact dermatitis; allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in cells caused by radiation or chemicals; increase melanin production (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to promote apoptosis in epithelial cells that contain damaged DNA. Also oligonucleotides that contain non-hydrolyzable backbones are used to inhibit apoptosis, in response to DNA damage, in epithelial cell. This sequence is melanogenesis associated oligonucleotide #5, representative of the telomere over-hang sequence and one of the oligonucleotides used to inhibit mammalian epithelial cell proliferation, described in the method of the invention.

XX  
 SQ Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;  
 Query Match 100.0%; Score 11; DB 23; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.le+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GTTAGGCTTAG 11  
 Db 1 GTTAGGCTTAG 11  
 RESULT 14  
 AAS14913/c  
 ID AAS14913 standard; DNA; 11 BP.  
 XX  
 AC AAS14913;  
 XX  
 DT 14-FEB-2002 (first entry)  
 XX  
 DE Melanogenesis associated oligonucleotide #9.  
 XX  
 KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;  
 KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;  
 KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;  
 KW tumour necrosis factor inhibitor; photoging; hyperproliferative disease;  
 KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;  
 KW conjunctivitis; allergic rhinitis; vitiligo; ss.  
 XX  
 OS Synthetic.  
 XX  
 Key Location/Qualifiers  
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 /tag= a  
 /mod\_base= c  
 /note= "Phosphorylated"  
 WO200174342-A2.  
 11-OCT-2001.  
 30-MAR-2001; 2001WO-US10162.  
 31-MAR-2000; 2000US-0540843.  
 (UYBO-) UNIV BOSTON.  
 Gilchrest BA, Yaar M, Eller M;  
 WPI; 2001-626338/72.  
 Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonucleotides that mimic the effects of ultra-violet light -  
 Example 12; Page 37; 74pp; English.  
 The invention describes inhibition of mammalian epithelial cell proliferation by treating cells with at least one oligonucleotide, or its fragment. The compounds, which have cytostatic, anti-allergic, anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and immunosuppressive activities, function as 'ultra-violet mimics' to induce DNA repair processes (or a protective response to later exposure to radiation or chemicals), as a proliferation inhibitor, apoptosis inducer or a tumour necrosis factor inhibitor. Probably they mimic products of DNA damage, or processed DNA-damage intermediates, by inducing the p53 pathway, resulting in transient arrest of cell growth, allowing more time for DNA repair to occur before cell division takes place. The method is especially used to treat carcinoma but may also be used to: treat other hyperproliferative states (e.g. psoriasis or precancerous conditions); reduce photoging, oxidative stress or damage; prevent skin cancer; treat allergically mediated inflammation (atopic or contact dermatitis; allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in

CC cells caused by radiation or chemicals; increase melanin production  
 CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to  
 CC promote apoptosis in epithelial cells that contain damaged DNA. Also  
 CC oligonucleotides that contain non-hydrolyzable backbones are used to  
 CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This  
 CC sequence is melanogenesis, associated oligonucleotide #9, one of the  
 CC oligonucleotides used to inhibit mammalian epithelial cell proliferation,  
 CC described in the method of the invention.  
 XX  
 SQ Sequence 11 BP; 4 A; 5 C; 0 G; 2 T; 0 other;  
 Query Match 100.0%; Score 11; DB 23; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTTAGGGTTAG 11  
 DB 11 GTTAGGGTTAG 1  
 RESULT 15  
 AAS15434  
 AAS15434 standard; DNA; 11 BP.  
 AAS15434;  
 14-FEB-2002 (first entry)  
 PNA 7/IV inhibiting human and mammalian telomerase activity.  
 Mammalian; peptide nucleic acid; probe; forensic; paternity testing;  
 human telomerase RNA component; hTR gene RFLP pattern; cancer;  
 inflammation; lymphoproliferative disease; autoimmune disease;  
 neurodegenerative disease; neoplasia; hyperplasia; HIV; AIDS;  
 human immunodeficiency virus; acquired immunodeficiency syndrome;  
 telomere metabolism; mutant; cytostatic; anti-inflammatory;  
 immunosuppressive; polyamide backbone; ss.  
 Homo sapiens.  
 Synthetic.  
 Key Location/Qualifiers  
 modified\_base 1..11  
 /tag= a  
 /note= "This sequence is a peptide nucleic acid, i.e. it  
 contains a polyamide backbone instead of a  
 deoxyribose backbone"  
 US6294650-B1.  
 25-SEP-2001.  
 08-JUL-1999; 99US-0349532.  
 09-APR-1997; 97US-0838545.  
 09-APR-1996; 96US-0630019.  
 (TEXA ) UNIV TEXAS SYSTEM.  
 Shay JW, Wright WE, Piatyszek MA, Corey DR, Norton JC;  
 WPI; 2001-638024/73.  
 New peptide nucleic acids that hybridizes to the RNA component of  
 mammalian telomerase, useful for treating or preventing cancer,  
 inflammation, lymphoproliferative diseases, autoimmune disease, or  
 neurodegenerative diseases -  
 Claim 7; Column 73; 46pp; English.  
 The present invention relates to peptide nucleic acids (PNAs), comprising  
 a sequence of 6-25 nucleobases, that inhibit telomerase activity in  
 mammalian cells by hybridising to the RNA component of mammalian

CC telomerase. The PNAs are useful as probes to detect the RNA component  
 CC of mammalian telomerase and as inhibitors of telomerase activity, or to  
 CC detect and/or quantitate polynucleotide having the human telomerase  
 CC RNA component (hTR) sequence, as well as in forensic identification of  
 CC individuals, such as paternity testing or identification of criminal  
 CC suspects or unknown descendants based on the hTR gene RFLP pattern. The  
 CC PNA can be further used for treating or preventing cancer, inflammation,  
 CC lymphoproliferative diseases, autoimmune disease, or neurodegenerative  
 CC diseases. The PNAs in combination with other pharmaceuticals (such as  
 CC antineoplastic or cytostatic agents) can be used for treating neoplasia,  
 CC hyperplasia, human immunodeficiency virus (HIV) infections, acquired  
 CC immunodeficiency syndrome (AIDS) and associated pathologies, and other  
 CC diseases characterised by abnormal telomere metabolism or telomerase  
 CC activity. The present sequence represents one of the PNA sequences  
 CC of the invention.  
 XX  
 SQ Sequence 11 BP; 2 A; 0 C; 5 G; 4 T; 0 other;  
 Query Match 100.0%; Score 11; DB 23; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTTAGGGTTAG 11  
 DB 1 GTTAGGGTTAG 11  
 Search completed: December 31, 2003, 15:08:14  
 Job time : 317.886 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 13:58:09 ; Search time 1263.89 Seconds  
(without alignments)  
211.530 Million cell updates/sec

Title: US-09-540-843-5  
Perfect score: 11  
Sequence: 1 gttagggttag 11

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues  
Total number of hits satisfying chosen parameters: 33330

Minimum DB seq length: 0  
Maximum DB seq length: 30  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:

- 1: em\_estba.\*
- 2: em\_esthum.\*
- 3: em\_estin.\*
- 4: em\_estnu.\*
- 5: em\_estov.\*
- 6: em\_estpl.\*
- 7: em\_estro.\*
- 8: em\_htc.\*
- 9: gb\_est1.\*
- 10: gb\_est2.\*
- 11: gb\_htc.\*
- 12: gb\_est3.\*
- 13: gb\_est4.\*
- 14: gb\_est5.\*
- 15: em\_estfun.\*
- 16: em\_estom.\*
- 17: em\_gss\_hum.\*
- 18: em\_gss\_inv.\*
- 19: em\_gss\_pln.\*
- 20: em\_gss\_vrt.\*
- 21: em\_gss\_fun.\*
- 22: em\_gss\_man.\*
- 23: em\_gss\_mus.\*
- 24: em\_gss\_pro.\*
- 25: em\_gss\_rod.\*
- 26: em\_gss\_phg.\*
- 27: em\_gss\_vri.\*
- 28: gb\_gss1.\*
- 29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	100.0	19	28	AZ614760
2	11	100.0	20	29	TA158A03P
3	11	100.0	25	29	TA84A06P
4	11	100.0	27	28	AZ803795

5	9.4	85.5	22	28	AZ666649
6	9.4	85.5	29	28	AZ514597
7	9	81.8	22	14	D18745
8	9	81.8	24	28	BH907981
9	8.4	76.4	21	28	AZ766315
10	8.4	76.4	23	29	TA139C11P
11	8.4	76.4	24	9	AU256889
12	8.4	76.4	25	9	AU544203
13	8.4	76.4	25	29	TA274G11Q
14	8.4	76.4	27	9	AU255344
15	8.4	76.4	27	14	L32043
16	8.4	76.4	27	28	AZ789654
17	8.4	76.4	29	28	BH901129
18	8.4	76.4	30	10	BE385567
19	8.4	76.4	30	28	AZ761166
20	8	72.7	19	28	AZ778302
21	8	72.7	20	28	BH000596
22	8	72.7	21	28	AZ770857
23	8	72.7	22	28	AZ483833
24	8	72.7	23	28	AZ623979
25	8	72.7	24	28	AZ785628
26	8	72.7	25	28	AZ339860
27	8	72.7	25	28	AZ759615
28	8	72.7	25	28	AZ759793
29	8	72.7	25	29	TA11D05P
30	8	72.7	25	29	TA187A12Q
31	8	72.7	27	28	AZ785654
32	8	72.7	28	28	AQ107735
33	8	72.7	28	28	AZ644025
34	8	72.7	28	29	TA290C11Q
35	8	72.7	29	28	AZ331636
36	8	72.7	30	28	AZ796681
37	7.8	70.9	19	28	AZ830578
38	7.8	70.9	20	28	AZ307088
39	7.8	70.9	20	28	AZ784073
40	7.8	70.9	21	28	AZ662703
41	7.8	70.9	21	28	AZ760907
42	7.8	70.9	21	28	AZ833982
43	7.8	70.9	22	28	AZ868780
44	7.8	70.9	23	28	AZ462640
45	7.8	70.9	23	28	AZ827252

ALIGNMENTS

RESULT 1  
AZ614760  
LOCUS  
DEFINITION  
1M0443A17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0443A17 R, genomic survey sequence.

ACCESSION  
AZ614760

VERSION  
GSS.

SOURCE  
Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0413 row: A column: 17  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers  
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#### FEATURES

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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M043A17"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: FWD42HV; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnates/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 3 a 0 c 10 g 6 t  
 ORIGIN

Query Match 100.0%; Score 11; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTTAGGGTTAG 11  
 |||||  
 3 GTTAGGGTTAG 13

#### RESULT 2

TA158A03P/c  
 LOCUS  
 DEFINITION  
 T. brucei sheared genomic DNA clone 158a03, forward sequence,  
 genomic survey sequence.  
 ACCESSION  
 AL472050  
 VERSION  
 AL472050.1 GI:11837404  
 KEYWORDS  
 GSS.  
 SOURCE  
 Trypanosoma brucei  
 ORGANISM  
 Trypanosoma brucei  
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
 Trypanosoma.

REFERENCE 1 (bases 1 to 20)

AUTHORS  
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE  
 JOURNAL  
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
 nh@sanger.ac.uk

COMMENT  
 Constructed at the Institute for Genomic Research (TIGR),  
 Rockville, MD. Genomic DNA isolated from a cloned population of  
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
 to give a tight size distribution (4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small  
 insert libraries for whole genome shotgun sequencing projects. In  
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
 Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org  
 Details of T. brucei sequencing at the Sanger Centre are available  
 at http://www.sanger.ac.uk/Projects/T\_brucei/.

#### FEATURES

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 1. .20  
 /organism="Trypanosoma brucei"  
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 /db\_xref="taxon:5691"  
 /clone="158a03"

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 ORIGIN

Query Match 100.0%; Score 11; DB 29; Length 20;  
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 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTAGGGTTAG 11  
 |||||  
 Db 20 GTTAGGGTTAG 10

#### RESULT 3

TA84A06P  
 LOCUS  
 DEFINITION  
 T. brucei sheared genomic DNA clone 84a06, forward sequence,  
 genomic survey sequence.  
 ACCESSION  
 AL462065  
 VERSION  
 AL462065.1 GI:11860923  
 KEYWORDS  
 GSS.  
 SOURCE  
 Trypanosoma brucei  
 ORGANISM  
 Trypanosoma brucei  
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
 Trypanosoma.

25 bp DNA linear GSS 13-DEC-2000

REFERENCE 1 (bases 1 to 25)

AUTHORS  
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE  
 JOURNAL  
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
 nh@sanger.ac.uk

#### COMMENT

Constructed at the Institute for Genomic Research (TIGR),  
 Rockville, MD. Genomic DNA isolated from a cloned population of  
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
 to give a tight size distribution (4 kb). The v + i method used for the library construction is  
 described in detail in Smith, H. and Venter, J.C. (Making small  
 insert libraries for whole genome shotgun sequencing projects. In  
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
 Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org  
 Details of T. brucei sequencing at the Sanger Centre are available  
 at http://www.sanger.ac.uk/Projects/T\_brucei/.

#### FEATURES

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 1. .25  
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 /strain="TREU927"  
 /db\_xref="taxon:5691"  
 /clone="84a06"

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 ORIGIN

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 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 GTTAGGTTAG 11
Db      6 GTTAGGTTAG 16

RESULT 4
AZ803795/c
LOCUS   27 bp      DNA      linear      GSS 16-FEB-2001
DEFINITION
clone UUGC2M0064D22 F, genomic survey sequence.
ACCESSION
AZ803795
VERSION
AZ803795.1 GI:12956118
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0064 row: D column: 22
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers
1..27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0064D22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      9 a      11 c      2 g      5 t
ORIGIN

Query Match      100.0%; Score 11; DB 28; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTTAGGTTAG 11
Db      26 GTTAGGTTAG 16

RESULT 5
AZ666649
LOCUS   22 bp      DNA      linear      GSS 14-DEC-2000
DEFINITION
clone UUGC1M0548M19 R, genomic survey sequence.
ACCESSION
AZ666649
VERSION
AZ666649.1 GI:11803795
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0548 row: M column: 19
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0548M19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      3 a      0 c      14 g      5 t
ORIGIN

Query Match      85.5%; Score 9.4; DB 28; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.4e+05;

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Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTAGGGTTAG 11
   |||||
Db 4 GTTAGGGTTAG 14

RESULT 6
LOCUS AZ514597/c
DEFINITION IM0361E14F Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0361E14 F, genomic survey sequence.
ACCESSION AZ514597
VERSION AZ514597.1 GI:10695829
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 29)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0361 row: E column: 14
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers
1. .29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0361E14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
6 a 9 c 6 g 8 t

BASE COUNT
ORIGIN
Query Match 85.5%; Score 9.4; DB 28; Length 29;

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```

Best Local Similarity 90.9%; Pred. No. 1.4e+05;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTAGGGTTAG 11
   |||||
Db 12 GTTAGGGTTAG 2

RESULT 7
LOCUS D18745/c
DEFINITION MUSGS01807 Mouse 3'-directed Mus musculus domesticus cDNA clone md1403 3', mRNA sequence.
ACCESSION D18745
VERSION D18745.1 GI:1100714
KEYWORDS EST.
SOURCE Mus musculus domesticus (western European house mouse)
ORGANISM Mus musculus domesticus
REFERENCE 1 (bases 1 to 22)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Kawamoto, S., Okubo, K., Yoshii, J., Katsuki, M. and Matsubara, K.
TITLE Analysis of gene expression in mouse embryogenesis by 3'-directed cDNA sequencing
JOURNAL Unpublished
COMMENT Contact: Kawamoto, S., Okubo, K., Yoshii, J., Katsuki, M. and Matsubara, K.
Institute for Cellular and Molecular Biology
Osaka University
3-1 Yamada-Oka, Suita, Osaka 565, Japan.
Location/Qualifiers
1. .22
/organism="Mus musculus domesticus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10092"
/clone="md1403"
/tissue_type="decidual tissue (day 6.5-8.5 of gestation)"
/clone_lib="Mouse 3'-directed"
7 a 5 c 1 g 9 t

BASE COUNT
ORIGIN
Query Match 81.8%; Score 9; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTAGGGTTA 10
   |||||
Db 21 TTAGGGTTA 13

RESULT 8
LOCUS BH907981/c
DEFINITION SALK_045087.34.20.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_045087.34.20.x, genomic survey sequence.
ACCESSION BH907981
VERSION BH907981.1 GI:22720914
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 24)
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J., and Ecker, J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished
COMMENT Contact: Joseph R. Ecker

```



Salk Institute Genomic Analysis Laboratory (SIGnAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@alk.edu  
This is single pass sequence recovered from the left border of  
TDNA. This sequence lies within an annotated intron of Atlg44820.  
Class: TDNA tagged.

## FEATURES

source

1. 24

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SALK\_045087.34.20.x"

/clone.lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

## BASE COUNT

ORIGIN

Query Match 81.8%; Score 9; DB 28; Length 24;

Best Local Similarity 100.0%; Pred. No. 2.4e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 TTAGGGTTA 10

|||||

12 TTAGGGTTA 4

## RESULT 9

LOCUS

A2766315 21 bp DNA linear GSS 16-FEB-2001

IM0563K14R Mouse 10kb plasmid UGCGIM library Mus musculus genomic

clone UGCGIM0563K14 R, genomic survey sequence.

## ACCESSION

A2766315

GSS.

## KEYWORDS

Mus musculus

Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly

, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0563 row: K column: 14

Seq primer: CACACGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. 21

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGCGIM0563K14"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone.lib="Mouse 10kb plasmid UGCGIM library"

/notes="Vector: FWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pW42 (G14732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

2 a 3 c 7 g 9 t

## BASE COUNT

ORIGIN

Query Match 76.4%; Score 8.4; DB 28; Length 21;

Best Local Similarity 90.0%; Pred. No. 5.2e+05;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2 TTAGGGTTAG 11

|||||

10 TTAGGGTTGG 19

## RESULT 10

LOCUS

TA319C11P/c

T. brucei sheared genomic DNA clone 319c11, forward sequence,

genomic survey sequence.

ACCESSION

AL492458

VERSION

AL492458.1

GI:11867402

GSS.

KEYWORDS

Trypanosoma brucei

Trypanosoma brucei

Trypanosoma brucei

Eukaryota; Eukaryota; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

1 (bases 1 to 23)

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Melville, S.E., Rajandream, M.A. and Barrell, B.G.

Direct Submission

Submitted (10-DEC-2000)

Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

nh@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTAT 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available

at [http://www.sanger.ac.uk/projects/T\\_brucei/](http://www.sanger.ac.uk/projects/T_brucei/).

## FEATURES

source

1. 23

/organism="Trypanosoma brucei"

/mol\_type="genomic DNA"

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/strain="TREU927"
/db_xref="taxon:5691"
/clone="319c11"
6 a 7 c 3 g 7 t
BASE COUNT
ORIGIN
Query Match 76.4%; Score 8.4; DB 29; Length 23;
Best Local Similarity 90.0%; Pred. No. 5.3e+05;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTAGGGTTA 10
|||||
Db 23 GTTAAGGTTA 14

RESULT 11
LOCUS AU256889 24 bp mRNA linear EST 25-APR-2002
DEFINITION AU256889 3'-directed mouse cDNA library Mus musculus cDNA clone
BED0009219 3', mRNA sequence.
ACCESSION AU256889
VERSION AU256889.1 GI:20320970
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Kato, K. and Matoba, R.
Generation of expressed sequence tags from mouse brain
Unpublished
Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: kkatob@ns.aist-nara.ac.jp,
URL: http://love2.aist-nara.ac.jp/BED/index.html.
Location/Qualifiers
1..24
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="BED0009219"
/tissue_type="brain"
/clone_lib="3'-directed mouse cDNA library"
BASE COUNT 10 a 6 c 3 g
ORIGIN
Query Match 76.4%; Score 8.4; DB 9; Length 24;
Best Local Similarity 90.0%; Pred. No. 5.4e+05;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTAGGGTTAG 11
|||||
Db 15 TTAAAGTTAG 6

RESULT 12
LOCUS AV544203 25 bp mRNA linear EST 07-SEP-2000
DEFINITION AV544203 Arabidopsis thaliana roots Columbia Arabidopsis thaliana
cDNA clone R236allf 3', mRNA sequence.
ACCESSION AV544203
VERSION AV544203.1 GI:8715617
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 25)
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="R236allf"
/tissue_type="roots"
/clone_lib="Arabidopsis thaliana roots Columbia"
/notes="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 9 a 2 c 8 g 6 t
ORIGIN
Query Match 76.4%; Score 8.4; DB 9; Length 25;
Best Local Similarity 90.0%; Pred. No. 5.4e+05;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTAGGGTTAG 11
|||||
Db 14 TTAAAGTTAG 23

RESULT 13
LOCUS TA274G11Q 25 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 274g11, reverse sequence,
genomic survey sequence.
ACCESSION AL485967
VERSION AL485967.1 GI:11851842
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 25)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 Gutat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
1..25
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
FEATURES
source

```

RESULT 11

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

GRADUATE

NARA

TEL

FAX

EMAIL

URL

LOCATION

QUALIFIERS

BASE

COUNT

ORIGIN

QUERY

MATCHES

CONSERVATIVE

MISMATCHES

INDELS

GAPS

QY

DB

RESULT

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

GRADUATE

NARA

TEL

FAX

EMAIL

URL

LOCATION

QUALIFIERS

BASE

COUNT

ORIGIN

QUERY

MATCHES

CONSERVATIVE

MISMATCHES

INDELS

GAPS

QY

DB

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/db_xref="taxon:5691"
/clone="274911"
5 a 6 c 10 g 4 t
BASE COUNT
ORIGIN
Query Match 76.4%; Score 8.4; DB 29; Length 25;
Best Local Similarity 90.0%; Pred. No. 5.4e+05;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTAGGGTTAG 11
|||||
Db 18 TTAGGGTCAG 9

RESULT 14
AU255344/c
LOCUS
DEFINITION AU255344 3'-directed mouse cDNA library Mus musculus cDNA clone
BED0005210 3', mRNA sequence.
ACCESSION AU255344
VERSION AU255344.1 GI:20317995
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 27) Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Kato,K. and Matoba,R.
TITLE Generation of expressed sequence tags from mouse brain
JOURNAL Unpublished
COMMENT Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: kkatob@bs.aist-nara.ac.jp,
URL: http://love2.aist-nara.ac.jp/BED/index.html.
FEATURES
source
1..27
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="BED0005210"
/tissue_type="brain"
/clone_lib="3'-directed mouse cDNA library"
11 a 5 c 3 g 8 t
BASE COUNT
ORIGIN
Query Match 76.4%; Score 8.4; DB 9; Length 27;
Best Local Similarity 90.0%; Pred. No. 5.5e+05;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTAGGGTTAG 11
|||||
Db 19 TTAGGATTAG 10

RESULT 15
L32043/c
LOCUS
DEFINITION L32043 HUMXP2G6A Human placenta Homo sapiens cDNA clone XP2G6A, mRNA
sequence.
ACCESSION L32043
VERSION L32043.1 GI:557155
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 27) Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Lee,C.-C., Yazdani,A., Wehnert,M., Bailey,J., Couch,L., Xiong,M.,
Coolbaugh,M.I., Chinault,C.A., Baldini,A., Lindeay,E.A., Zhao,Z.-Y.

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and Caskey, C.T.H.
Isolation of chromosome-specific genes by reciprocal probing of
arrayed cDNAs and cosmid libraries
Hum. Mol. Genet. 4, 1373-1380 (1995)
96090257
PUBMED 7581376
COMMENT Contact: Caskey, C.T.H.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/map="Xq21.3; Xq21.3, Yp11.3"
/clone="XP2G6A"
/clone_lib="Human placenta"
/note="Arrayed cDNAs and cosmid libraries from human
placental tissue"
BASE COUNT 13 a 7 c 6 g 1 t
ORIGIN
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Best Local Similarity 90.0%; Pred. No. 5.5e+05;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTAGGGTTAG 11
|||||
Db 19 TTGGGGTTAG 10

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Search completed: December 31, 2003, 19:41:24  
Job time : 1267.89 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 14:40:05 ; Search time 42.7468 Seconds  
(without alignments)  
113.581 Million cell updates/sec

Title: US-09-540-843-5  
Perfect score: 11  
Sequence: 1 gttagggttag 11

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 547746

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
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2: /cgn2\_6/ptodata/1/ina/5B COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PTUS COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	11	100.0	11	1	US-08-482-115B-2
3	11	100.0	11	2	US-08-660-678A-2
4	11	100.0	11	2	US-08-531-743-11
5	11	100.0	11	2	US-08-531-743-12
6	11	100.0	11	2	US-08-485-778-36
7	11	100.0	11	2	US-08-472-802C-3
8	11	100.0	11	3	US-08-520-550A-36
9	11	100.0	11	3	US-08-630-019A-9
10	11	100.0	11	3	US-08-630-019A-30
11	11	100.0	11	3	US-08-630-019A-39
12	11	100.0	11	3	US-08-838-545-13
13	11	100.0	11	3	US-08-838-545-31
14	11	100.0	11	3	US-08-838-545-44
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16	11	100.0	11	3	US-09-060-523-2
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18	11	100.0	11	3	US-09-349-532-31
19	11	100.0	11	3	US-09-349-532-44
20	11	100.0	11	4	US-09-580-517-2
21	11	100.0	11	4	US-09-057-351-2
22	11	100.0	12	3	US-08-630-019A-10
23	11	100.0	12	3	US-08-838-545-8
24	11	100.0	12	3	US-09-349-532-8
25	11	100.0	13	3	US-08-630-019A-11
26	11	100.0	13	3	US-08-630-019A-15
27	11	100.0	13	3	US-08-838-545-1

28	11	100.0	13	3	US-08-838-545-12	Sequence 12, Appl
29	11	100.0	13	3	US-09-349-532-1	Sequence 1, Appl
30	11	100.0	13	3	US-09-349-532-12	Sequence 12, Appl
c 31	11	100.0	15	2	US-08-531-743-4	Sequence 4, Appl
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33	11	100.0	15	3	US-08-630-019A-18	Sequence 18, Appl
34	11	100.0	15	3	US-08-630-019A-40	Sequence 40, Appl
35	11	100.0	15	3	US-08-838-545-2	Sequence 2, Appl
36	11	100.0	15	3	US-08-838-545-5	Sequence 5, Appl
37	11	100.0	15	3	US-08-838-545-45	Sequence 45, Appl
38	11	100.0	15	3	US-09-349-532-2	Sequence 2, Appl
39	11	100.0	15	3	US-09-349-532-5	Sequence 5, Appl
40	11	100.0	15	3	US-09-349-532-45	Sequence 45, Appl
c 41	11	100.0	16	1	US-08-153-051B-11	Sequence 11, Appl
c 42	11	100.0	16	2	US-08-151-477A-11	Sequence 11, Appl
c 43	11	100.0	16	3	US-08-819-867-20	Sequence 20, Appl
c 44	11	100.0	16	4	US-08-464-011B-60	Sequence 60, Appl
c 45	11	100.0	16	4	US-09-378-535-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1  
US-08-330-123A-2/c  
; Sequence 2, Application US/08330123A  
; Patent No. 5583016  
; GENERAL INFORMATION:  
; APPLICANT: VILLEPONTEAU, Bryant  
; APPLICANT: FENG, Junli  
; APPLICANT: FUNK, Walter  
; APPLICANT: ANDREWS, William H.  
; TITLE OF INVENTION: HUMAN TELOMERASE  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/330,123A  
; FILING DATE: 27-OCT-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/272,102  
; FILING DATE: 07-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 15389-000810  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA  
US-08-330-123A-2

Query Match 100.0%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GTTAGGGTTAG 11
Db 11 GTTAGGGTTAG 1

RESULT 2
US-08-482-115B-2/c
; Sequence 2, Application US/08482115B
; Patent No. 5776679
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Assays for the RNA Component of Human
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; APPLICATION NUMBER: US/08/482,115B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000830US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; US-08-482-115B-2

Query Match 100.0%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTAGGGTTAG 11
Db 11 GTTAGGGTTAG 1

RESULT 3
US-08-660-678A-2/c
; Sequence 2, Application US/08660678A
; Patent No. 5837857
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.

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; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,678A
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000811US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; US-08-660-678A-2

Query Match 100.0%; Score 11; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 11 GTTAGGGTTAG 1

RESULT 4
US-08-531-743-11
; Sequence 11, Application US/08531743
; Patent No. 5856096
; GENERAL INFORMATION:
; APPLICANT: Windle, Bradford E.
; APPLICANT: Qiu, Ming
; APPLICANT: Chen, Shi-fong
; APPLICANT: Fletcher, Terace M.
; APPLICANT: Maine, Ira
; TITLE OF INVENTION: Rapid and Sensitive Assays for Detecting and
; TITLE OF INVENTION: Distinguishing Between Processive and
; TITLE OF INVENTION: No. 5856096-Processive Telomerase Activities
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/531,743
; FILING DATE: 20-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: CTCR:026/HYL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-531-743-11

Query Match          100.0%; Score 11; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CG      1 GTTAGGGTTAG 11
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db       1 GTTAGGGTTAG 11

RESULT 5
US-08-531-743-12/c
Sequence 12, Application US/08531743
Patent No. 5856096
GENERAL INFORMATION:
APPLICANT: Windle, Bradford E.
APPLICANT: Qiu, Ming
APPLICANT: Chen, Shi-fong
APPLICANT: Fletcher, Terace M.
APPLICANT: Maine, Ira
TITLE OF INVENTION: Rapid and Sensitive Assays for Detecting and
TITLE OF INVENTION: Distinguishing Between Processive and
TITLE OF INVENTION: No. 5856096-Processive Telomerase Activities
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,743
FILING DATE: 20-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: CTCR:026/HYL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

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US-08-531-743-12
Query Match          100.0%; Score 11; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels

QY      1 GTTAGGGTTAG 11
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DB      11 GTTAGGGTTAG 1
      |||||

RESULT 6
US-08-485-778-36/c
; Sequence 36, Application US/08485778
; Patent No. 5876979
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel Athena
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria Antonia Blasco
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-JE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05A4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

US-08-485-778-36
Query Match          100.0%; Score 11; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels

QY      1 GTTAGGGTTAG 11
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DB      11 GTTAGGGTTAG 1
      |||||

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Query Match      100.0%; Score 11; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels
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Db 11 GTTAGGGTTAG 1
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RESULT 7  
US-08-472-802C-3/c  
; Sequence 3, Application US/08472802C  
; Patent No. 5958680  
; GENERAL INFORMATION:  
; APPLICANT: Villegonteau, Bryant  
; APPLICANT: Feng, Junli  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Mammalian Telomerase  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,802C  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15389-000820  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
-08-472-802C-3

Query Match 100.0%; Score 11; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTAGGGTTAG 11  
Db 11 GTTAGGGTTAG 1

RESULT 8  
US-08-520-550A-36/c  
; Sequence 36, Application US/08520550A  
; Patent No. 6013468  
; GENERAL INFORMATION:  
; APPLICANT: Andrews, William H.  
; APPLICANT: Avillion, Ariel A.  
; APPLICANT: Feng, Junli  
; APPLICANT: Funk, Walter  
; APPLICANT: Greider, Carol  
; APPLICANT: Marhuenda, Maria A. B.  
; APPLICANT: Villegonteau, Bryant  
; TITLE OF INVENTION: RNA Component of Telomerase  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/520,550A  
FILING DATE: 29-AUG-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/387,524  
FILING DATE: 13-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL94-05A3B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-9540  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-520-550A-36

Query Match 100.0%; Score 11; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTAGGGTTAG 11  
Db 11 GTTAGGGTTAG 1

RESULT 9  
US-08-630-019A-9  
; Sequence 9, Application US/08630019A  
; Patent No. 6015710  
; GENERAL INFORMATION:  
; APPLICANT: Shay, Jerry W.  
; APPLICANT: Wright, Woodring E.  
; APPLICANT: Piatyszek, Mieczyslaw A.  
; APPLICANT: Corey, David  
; APPLICANT: No. 6015710ton, James C.  
; TITLE OF INVENTION: Modulation of Mammalian Telomerase by  
; TITLE OF INVENTION: Peptide Nucleic Acids  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30



; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/630,019A  
 ; FILING DATE: 09-JUN-1996  
 ; CLASSIFICATION: 536  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Storella, John R.  
 ; REGISTRATION NUMBER: 32,944  
 ; REFERENCE/DOCKET NUMBER: 015389-001600US  
 ; TELEPHONE: (415) 576-0200  
 ; TELEFAX: (415) 576-0300  
 ; INFORMATION FOR SEQ ID NO: 9:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 11 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; DESCRIPTION: /desc = "peptide nucleic acid (PNA),  
 ; DESCRIPTION: where (deoxy)ribose-phosphate linkages are replaced by  
 ; DESCRIPTION: N-(2-aminoethyl)glycine units linked to nucleotide bases via  
 ; DESCRIPTION: glycine amino nitrogen through a methylenecarbonyl linker"  
 ; US-08-630-019A-9

Query Match 100.0%; Score 11; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTAGGGTTAG 11  
 Db 1 GTTAGGGTTAG 11

RESULT 10  
 US-08-630-019A-30/c  
 Sequence 30, Application US/08630019A  
 Patent No. 6015710  
 GENERAL INFORMATION:  
 APPLICANT: Shay, Jerry W.  
 APPLICANT: Wright, Woodring E.  
 APPLICANT: Piatyszek, Mieczyslaw A.  
 APPLICANT: Corey, David  
 APPLICANT: No. 6015710ton, James C.  
 TITLE OF INVENTION: Modulation of Mammalian Telomerase by  
 TITLE OF INVENTION: Peptide Nucleic Acids  
 NUMBER OF SEQUENCES: 46  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-3834

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/630,019A  
 FILING DATE: 09-JUN-1996  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Storella, John R.  
 REGISTRATION NUMBER: 32,944  
 REFERENCE/DOCKET NUMBER: 015389-001600US  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 30:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 11 base pairs  
 TYPE: nucleic acid

Query Match 100.0%; Score 11; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTAGGGTTAG 11  
 Db 1 GTTAGGGTTAG 11

; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: RNA  
 ; US-08-630-019A-30

Query Match 100.0%; Score 11; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTAGGGTTAG 11  
 Db 1 GTTAGGGTTAG 11

RESULT 11  
 US-08-630-019A-39  
 Sequence 39, Application US/08630019A  
 Patent No. 6015710  
 GENERAL INFORMATION:  
 APPLICANT: Shay, Jerry W.  
 APPLICANT: Wright, Woodring E.  
 APPLICANT: Piatyszek, Mieczyslaw A.  
 APPLICANT: Corey, David  
 APPLICANT: No. 6015710ton, James C.  
 TITLE OF INVENTION: Modulation of Mammalian Telomerase by  
 TITLE OF INVENTION: Peptide Nucleic Acids  
 NUMBER OF SEQUENCES: 46  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-3834

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/630,019A  
 FILING DATE: 09-JUN-1996  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Storella, John R.  
 REGISTRATION NUMBER: 32,944  
 REFERENCE/DOCKET NUMBER: 015389-001600US  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 39:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 11 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 DESCRIPTION: /desc = "phosphorothioate (PS) nucleic acid"

Query Match 100.0%; Score 11; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTAGGGTTAG 11  
 Db 1 GTTAGGGTTAG 11

RESULT 12  
 US-08-838-545-13  
 Sequence 13, Application US/08838545  
 Patent No. 6046307

GENERAL INFORMATION:  
APPLICANT: Shay, Jerry W.  
APPLICANT: Wright, Woodring E.  
APPLICANT: Piatyszek, Mieczyslaw A.  
APPLICANT: Corey, David R.  
APPLICANT: No. 6046307ton, James C.  
TITLE OF INVENTION: Modulation of Mammalian Telomerase by Peptide Nucleic Acids  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/838,545  
FILING DATE: 09-APR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,019  
FILING DATE: 09-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-001610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "peptide nucleic acid (PNA), where (deoxy(ribose-phosphate) linkages are replaced by N-(2-aminoethyl)glycine units linked to nucleotide bases via glycine amino N through a methylenecarbonyl linker"  
US-08-838-545-13

Query Match 100.0%; Score 11; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 GTTAGGGTTAG 11

RESULT 13  
US-08-838-545-31/c  
Sequence 31, Application US/08838545  
Patent No. 6046307  
GENERAL INFORMATION:  
APPLICANT: Shay, Jerry W.  
APPLICANT: Wright, Woodring E.  
APPLICANT: Piatyszek, Mieczyslaw A.  
APPLICANT: Corey, David R.  
APPLICANT: No. 6046307ton, James C.  
TITLE OF INVENTION: Modulation of Mammalian Telomerase by Peptide Nucleic Acids  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/838,545  
FILING DATE: 09-APR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,019  
FILING DATE: 09-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-001610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "peptide nucleic acid (PNA), where (deoxy(ribose-phosphate) linkages are replaced by N-(2-aminoethyl)glycine units linked to nucleotide bases via glycine amino N through a methylenecarbonyl linker"  
US-08-838-545-31

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Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 GTTAGGGTTAG 11

RESULT 14  
US-08-838-545-44  
Sequence 44, Application US/08838545  
Patent No. 6046307  
GENERAL INFORMATION:  
APPLICANT: Shay, Jerry W.  
APPLICANT: Wright, Woodring E.  
APPLICANT: Piatyszek, Mieczyslaw A.  
APPLICANT: Corey, David R.  
APPLICANT: No. 6046307ton, James C.  
TITLE OF INVENTION: Modulation of Mammalian Telomerase by Peptide Nucleic Acids  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/838,545  
FILING DATE: 09-APR-1997

Search completed: January 1, 2004, 00:32:18  
Job time : 42.8579 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 11:36:21 ; Search time 460.316 Seconds  
(without alignments)  
444.364 Million cell updates/sec

Title: US-09-540-843-6  
Perfect score: 5  
Sequence: 1 catcac 5

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 2888711 seqs, 20454813386 residues  
Total number of hits satisfying chosen parameters: 1010434

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: gb\_htg:\*
- 3: gb\_in:\*
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- 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	5	100.0	5	6	AX268758	AX268758 Sequence
C 3	5	100.0	7	6	AX268755	AX268755 Sequence
C 4	5	100.0	7	6	AX268759	AX268759 Sequence
C 5	5	100.0	8	6	AX047565	AX047565 Sequence
C 6	5	100.0	8	6	AX104946	AX104946 Sequence
C 7	5	100.0	8	6	AX119567	AX119567 Sequence
C 8	5	100.0	8	6	BD085298	BD085298 DNA-based
C 9	5	100.0	9	6	AX268753	AX268753 Sequence
C 10	5	100.0	9	6	AX667174	AX667174 Sequence
C 11	5	100.0	9	6	AX668771	AX668771 Sequence
C 12	5	100.0	9	6	AX668807	AX668807 Sequence
C 13	5	100.0	9	9	S50583	S50583 type I proc
C 14	5	100.0	9	9	S50585	S50585 type I proc
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C 16	5	100.0	10	6	AR065157	AR065157 Sequence
C 17	5	100.0	10	6	AR079101	AR079101 Sequence
C 18	5	100.0	10	6	AR079103	AR079103 Sequence
C 19	5	100.0	10	6	AR098909	AR098909 Sequence
C 20	5	100.0	10	6	AR107335	AR107335 Sequence
C 21	5	100.0	10	6	AR107344	AR107344 Sequence
C 22	5	100.0	10	6	AR123039	AR123039 Sequence
C 23	5	100.0	10	6	AR136787	AR136787 Sequence
C 24	5	100.0	10	6	AR160130	AR160130 Sequence
C 25	5	100.0	10	6	AR202278	AR202278 Sequence
C 26	5	100.0	10	6	AR217382	AR217382 Sequence
C 27	5	100.0	10	6	AR223280	AR223280 Sequence
C 28	5	100.0	10	6	AR241735	AR241735 Sequence
C 29	5	100.0	10	6	AR254391	AR254391 Sequence
C 30	5	100.0	10	6	AR287776	AR287776 Sequence
C 31	5	100.0	10	6	AR303527	AR303527 Sequence
C 32	5	100.0	10	6	AR303540	AR303540 Sequence
C 33	5	100.0	10	6	AR303548	AR303548 Sequence
C 34	5	100.0	10	6	AR303553	AR303553 Sequence
C 35	5	100.0	10	6	AR303569	AR303569 Sequence
C 36	5	100.0	10	6	AR303578	AR303578 Sequence
C 37	5	100.0	10	6	AR303617	AR303617 Sequence
C 38	5	100.0	10	6	AR303671	AR303671 Sequence
C 39	5	100.0	10	6	AR303680	AR303680 Sequence
C 40	5	100.0	10	6	AR303681	AR303681 Sequence
C 41	5	100.0	10	6	AR303690	AR303690 Sequence
C 42	5	100.0	10	6	AR303694	AR303694 Sequence
C 43	5	100.0	10	6	AR303720	AR303720 Sequence
C 44	5	100.0	10	6	AR303722	AR303722 Sequence
C 45	5	100.0	10	6	AR303730	AR303730 Sequence

ALIGNMENTS

RESULT 1  
AX268756/c  
LOCUS AX268756  
DEFINITION Sequence 4 from Patent WO0174342.  
ACCESSION AX268756  
VERSION AX268756.1 GI:16541828  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Gilchrist, B. A., Yaar, M. and Eller, M.  
TITLE Use of locally applied dna fragments  
JOURNAL Patent: WO 0174342-A 4 11-OCT-2001;  
TRUSTEES OF BOSTON UNIVERSITY (US)

AX268756 5 bp DNA linear PAT 29-OCT-2001

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LOCUS
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  Sequence 3 from Patent WO0174342.
  5 bp DNA linear PAT 29-OCT-2001
ACCESSION
  AX268758
VERSION
  AX268758.1 GI:16541830
KEYWORDS
  synthetic construct
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ORIGIN
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  Best Local Similarity 100.0%; Pred. No. 8.2e+09;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

REFERENCE
  1
  Gilchrest,B.A., Yaar,M. and Eller,M.
  Use of locally applied dna fragments
  Patent: WO 0174342-A 6 11-OCT-2001;
  TRUSTEES OF BOSTON UNIVERSITY (US)
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ACCESSION
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VERSION
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KEYWORDS
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  artificial sequences.
ORIGIN
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  Best Local Similarity 100.0%; Pred. No. 8.2e+09;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

REFERENCE
  1
  Gilchrest,B.A., Yaar,M. and Eller,M.
  Use of locally applied dna fragments
  Patent: WO 0174342-A 6 11-OCT-2001;
  TRUSTEES OF BOSTON UNIVERSITY (US)
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Query Match
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  Best Local Similarity 100.0%; Pred. No. 5.8e+09;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
LOCUS
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  Sequence 7 from Patent WO0174342.
  7 bp DNA linear PAT 29-OCT-2001
ACCESSION
  AX268759
VERSION
  AX268759.1 GI:16541831
KEYWORDS
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  artificial sequences.
ORIGIN
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  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

REFERENCE
  1
  Gilchrest,B.A., Yaar,M. and Eller,M.
  Use of locally applied dna fragments
  Patent: WO 0174342-A 7 11-OCT-2001;
  TRUSTEES OF BOSTON UNIVERSITY (US)
  LOCATION/Qualifiers
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RESULT 5
LOCUS
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  8 bp DNA linear PAT 15-DEC-2000
ACCESSION
  AX047565
VERSION
  AX047565.1 GI:11876656
KEYWORDS
  synthetic construct
  artificial sequences.
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  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

REFERENCE
  1 (bases 1 to 8)
  Mcivor,R.S., Hackett,P.B. and Aguilar-Cordova,E.
  Vector-mediated delivery of integrating transposon sequences
  Patent: WO 0068399-A 6 16-NOV-2000;
  REGENTS OF THE UNIVERSITY OF MINNESOTA (US) ; BAYLOR COLLEGE OF
  MEDICINE (US) ; Mcivor, R. Scott (US) ; Hackett, Perry B. (US) ;
  Aguilar-Cordova, Estuardo (US)
  LOCATION/Qualifiers
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  /note="Direct Repeat Sequence"
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Db      |||||
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RESULT 6
AX104946/c
LOCUS   AX104946 8 bp DNA linear PAT 30-APR-2001
DEFINITION
Sequence 1138 from Patent WO0122972.
ACCESSION
AX104946.1 GI:13921143
KEYWORDS
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 8)
AUTHORS
Krieg, A.M., Schetter, C. and Vollmer, J.C.
TITLE
Immunostimulatory nucleic acids
JOURNAL
Patent: WO 0122972-A 1138 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
Location/Qualifiers
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/db_xref="taxon:32630"
BASE COUNT 2 a 1 c 2 g 3 t
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Query Match 100.0%; Score 5; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+09;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      |||||
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RESULT 7
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LOCUS   AX119567 8 bp DNA linear PAT 11-MAY-2001
DEFINITION
Sequence 224 from Patent WO0129251.
ACCESSION
AX119567.1 GI:14036486
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 8)
AUTHORS
Messiaen, L. and Callens, T.
TITLE
Improved mutation analysis of the nf1 gene
JOURNAL
Patent: WO 0129251-A 224 26-APR-2001;
UNIVERSITEIT GENT (BE)
FEATURES
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      |||||
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RESULT 8
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LOCUS   AX268753 9 bp DNA linear PAT 29-OCT-2001
DEFINITION
Sequence 1 from Patent WO0174342.
ACCESSION
AX268753.1 GI:16541825
KEYWORDS
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1
AUTHORS
Gilchrest, B.A., Yaar, M. and Eller, M.
TITLE
Use of locally applied dna fragments
JOURNAL
Patent: WO 0174342-A 1 11-OCT-2001;
TRUSTEES OF BOSTON UNIVERSITY (US)
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
| | | | |  
Db 10 CATAC 6

Search completed: December 31, 2003, 17:09:47  
Job time : 460.316 secs

Qy 1 CATAC 5  
| | | | |  
Db 9 CATAC 5

RESULT 14  
S50585/c  
LOCUS  
DEFINITION type I procollagen [human, Genomic Mutant, 9 nt].  
ACCESSION S50585  
VERSION S50585.1 GI:233929  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 9)  
Tsuneyoshi, T., Westerhausen, A., Constantinou, C.D. and Prockop, D.J.  
Substitutions for glycine alpha 1-637 and glycine alpha 2-694 of  
type I procollagen in lethal osteogenesis imperfecta. The  
conformational strain on the triple helix introduced by a glycine  
substitution can be transmitted along the helix  
J. Biol. Chem. 266 (24), 15608-15613 (1991)  
91340689  
MEDLINE  
PUBMED 1874719  
REMARK GenBank staff at the National Library of Medicine created this  
entry [NCBI gibbsq 50585] from the original journal article.  
This sequence comes from Fig 5B.

FEATURES  
source 1..9  
Location/Qualifiers  
1..9  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
1..9  
/gene="type I procollagen"  
2 a 1 c 3 g 3 t

Query Match 100.0%; Score 5; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.5e+09;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
| | | | |  
Db 9 CATAC 5

RESULT 15  
A18263/c  
LOCUS  
DEFINITION oligonucleotide.  
ACCESSION A18263  
VERSION A18263.1 GI:512254  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
1 (bases 1 to 10)  
Della Valle, F., Callegaro, L. and Negro, A.  
Process for the preparation of genetic vectors for the nerve growth  
factor expression in eukaryotic cells  
Patent: Ep 0432510-A 12 19-JUN-1991;  
FIDIA S.p.A

FEATURES  
source 1..10  
Location/Qualifiers  
1..10  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
3 a 1 c 3 g 3 t

Query Match 100.0%; Score 5; DB 6; Length 10;



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 11:36:21 ; Search time 144.494 Seconds  
(without alignments)  
93.410 Million cell updates/sec

Title: US-09-540-843-6  
Perfect score: 5  
Sequence: 1 catcac 5

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 2101872

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq 19Jun03:\*

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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:\*

3: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:\*

4: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:\*

5: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:\*

6: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:\*

7: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:\*

8: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:\*

9: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:\*

10: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1989.DAT:\*

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21: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:\*

22: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:\*

23: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:\*

24: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:\*

25: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	5	100.0	5	20	AAZ10695
C 2	5	100.0	5	20	AAZ10696
C 3	5	100.0	5	23	AAZ14908
C 4	5	100.0	5	23	AAZ14910
C 5	5	100.0	7	20	AAZ10694
C 6	5	100.0	7	23	AAZ14907
C 7	5	100.0	7	23	AAZ14911
C 8	5	100.0	8	22	AAZ02250

C 9	5	100.0	9	19	AAV22350	A promoter regulat
C 10	5	100.0	9	19	AAV22283	GAS complement gen
C 11	5	100.0	9	19	AAV15899	Cyclin D transcript
C 12	5	100.0	9	20	AAZ10692	Oligonucleotide se
C 13	5	100.0	9	23	AAZ14905	Melanogenesis asso
C 14	5	100.0	9	24	ABX03786	Human DNA PCR prim
C 15	5	100.0	9	24	ABQ71504	zinc finger protei
C 16	5	100.0	9	24	ABQ71922	zinc finger protei
C 17	5	100.0	9	24	ABQ71958	zinc finger protei
C 18	5	100.0	10	14	AAQ43164	Donor oligomer wit
C 19	5	100.0	10	15	AAQ71104	Merlin exon 14 spl
C 20	5	100.0	10	16	AAQ97224	Oligonucleotide Ec
C 21	5	100.0	10	16	AAZ32625	Anticancer duplex
C 22	5	100.0	10	17	AAZ35734	Primer E19 for V.d
C 23	5	100.0	10	18	AAZ66073	(dC-dA)n.(dG-dT)n
C 24	5	100.0	10	19	AAV50271	Yeast tag for addi
C 25	5	100.0	10	19	AAV50250	Yeast tag for addi
C 26	5	100.0	10	19	AAV50184	Yeast tag for addi
C 27	5	100.0	10	19	AAV50127	Yeast tag for NORP
C 28	5	100.0	10	19	AAV35934	Primer used in RAP
C 29	5	100.0	10	19	AAV35910	Primer used in RAP
C 30	5	100.0	10	20	AAZ18629	p53 serial analysi
C 31	5	100.0	10	20	AAV73806	Chromophore contai
C 32	5	100.0	10	21	AAZ73931	Human dendritic ce
C 33	5	100.0	10	21	AAZ74120	Human monocyte and
C 34	5	100.0	10	21	AAZ74154	Human monocyte and
C 35	5	100.0	10	21	AAZ93858	Oligonucleotide us
C 36	5	100.0	10	21	AAZ93865	Oligonucleotide us
C 37	5	100.0	10	21	AAZ53110	Mouse DNA adapter
C 38	5	100.0	10	21	AAZ15244	Primer MR15 for mo
C 39	5	100.0	10	21	AAZ56166	Human monocyte gen
C 40	5	100.0	10	21	AAZ56218	Human macrophage g
C 41	5	100.0	10	21	AAZ56224	Human macrophage g
C 42	5	100.0	10	21	AAZ56294	Human macrophage g
C 43	5	100.0	10	21	AAZ56321	Human macrophage g
C 44	5	100.0	10	21	AAZ56331	Human macrophage g
C 45	5	100.0	10	21	AAZ56407	Human macrophage g

ALIGNMENTS

RESULT 1

AAZ10695/c

ID AAZ10695 standard; DNA; 5 BP.

XX AAZ10695;

AC AAZ10695;

XX 23-NOV-1999 (first entry)

DT

DE Oligonucleotide sequence that increases p53 activity in a cell.

XX p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;

KW UV-induced hyperproliferative disease; psoriasis; vitiligo;

KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;

KW skin cancer; ss.

XX Synthetic.

OS

XX GE2336157-A.

PN

XX 13-OCT-1999.

PD

XX 24-MAR-1999; 99GB-0006758.

PF

XX 26-MAR-1998; 98US-0048927.

PR

XX (UYBO-) UNIV BOSTON.

PA

XX Gilchrest BA, Yaar M, Eller M;

PI

XX WPI; 1999-543520/46.

DR

XX

PT DNA fragments useful for increasing p53 activity in a cell and reducing  
 XX susceptibility to UV-induced hyperproliferative diseases -  
 XX Claim 11; Page 30; 44pp; English.

CC AA210692-97 represent DNA fragments that are used for increasing p53  
 CC activity in a cell. The oligonucleotides are UV mimetics and  
 CC protect cells against subsequent exposure to UV-irradiation or  
 CC chemicals. The oligonucleotides are useful for increasing p53 activity  
 CC in a cell, reducing the susceptibility to UV-induced hyperproliferative  
 CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic  
 CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging  
 CC and reducing susceptibility to skin cancer.

SQ Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 5; DB 20; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATAC 5  
 |||||  
 5 CATAC 1

RESULT 2  
 AA210696  
 AA210696 standard; DNA; 5 BP.

AA210696;

23-NOV-1999 (first entry)

Oligonucleotide sequence that increases p53 activity in a cell.

p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;  
 UV-induced hyperproliferative disease; psoriasis; vitiligo;  
 atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;  
 skin cancer; ss.

Synthetic.

GB2336157-A.

13-OCT-1999.

24-MAR-1999; 99GB-0006758.

26-MAR-1998; 98US-0048927.

(UYBO-) UNIV BOSTON.

Gilchrest BA, Yaar M, Eller M;

WPI; 1999-543520/46.

PT DNA fragments useful for increasing p53 activity in a cell and reducing  
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Claim 11; Page 30; 44pp; English.

CC AA210692-97 represent DNA fragments that are used for increasing p53  
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 CC chemicals. The oligonucleotides are useful for increasing p53 activity  
 CC in a cell, reducing the susceptibility to UV-induced hyperproliferative  
 CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic  
 CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging  
 CC and reducing susceptibility to skin cancer.

SQ Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 5; DB 20; Length 5;

Best Local Similarity 100.0%; Pred. No. 5.2e+08;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5  
 |||||  
 DB 1 CATAC 5

RESULT 3  
 AAS14908/c  
 ID AAS14908 standard; DNA; 5 BP.

XX AAS14908;

XX 14-FEB-2002 (first entry)

XX Melanogenesis associated oligonucleotide #4.

XX Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;  
 KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;  
 KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;  
 KW tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;  
 KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;  
 KW conjunctivitis; allergic rhinitis; vitiligo; ss.

OS Synthetic.

XX WO200174342-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10162.

XX 31-MAR-2000; 2000US-0540843.

XX (UYBO-) UNIV BOSTON.

XX Gilchrest BA, Yaar M, Eller M;

XX WPI; 2001-626338/72.

PT Inhibiting proliferation of epithelial cells, useful e.g. for treating  
 PT carcinoma, using specific oligonucleotides that mimic the effects of  
 PT ultra-violet light

XX Claim 1; Page 36; 74pp; English.

XX The invention describes inhibition of mammalian epithelial cell  
 CC proliferation by treating cells with at least one oligonucleotide, or  
 CC its fragment. The compounds, which have cytostatic, anti-allergic,  
 CC anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and  
 CC immunosuppressive activities, function as 'ultra-violet mimics' to induce  
 CC DNA repair processes (or a protective response to later exposure to  
 CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer  
 CC or a tumour necrosis factor inhibitor. Probably they mimic products of  
 CC DNA damage, or processed DNA-damage intermediates, by inducing the p53  
 CC pathway, resulting in transient arrest of cell growth, allowing more time  
 CC for DNA repair to occur before cell division takes place. The method is  
 CC especially used to treat carcinoma but may also be used to: treat other  
 CC hyperproliferative states (e.g. psoriasis or precancerous conditions);  
 CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat  
 CC allergically mediated inflammation (atopic or contact dermatitis, treat  
 CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in  
 CC cells caused by radiation or chemicals; increase melanin production  
 CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to  
 CC promote apoptosis in epithelial cells that contain damaged DNA. Also  
 CC oligonucleotides that contain non-hydrolyzable backbones are used to  
 CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This  
 CC sequence is melanogenesis associated oligonucleotide #4, a truncated  
 CC version of the oligonucleotide shown in AAS14906, one of the  
 CC oligonucleotides used to inhibit mammalian epithelial cell  
 CC proliferation, described in the method of the invention.

SQ Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 5; DB 23; Length 5;  
Best Local Similarity 100.0%; Pred. No. 5.2e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5  
|||||  
Db 5 CATAC 1

RESULT 4  
AAS14910  
ID AAS14910 standard; DNA; 5 BP.  
XX AC AAS14910;  
XX DT 14-FEB-2002 (first entry)  
XX DE Melanogenesis associated oligonucleotide #6.  
XX KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;  
XX KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;  
XX KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;  
XX KW tumour necrosis factor inhibitor; phototaging; hyperproliferative disease;  
XX KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;  
XX KW conjunctivitis; allergic rhinitis; vitiligo; ss.  
XX OS Synthetic.  
XX WO200174342-A2.  
XX 11-OCT-2001.  
XX 30-MAR-2001; 2001WO-US10162.  
XX 31-MAR-2000; 2000US-0540843.  
XX (UYBO-) UNIV BOSTON.  
XX Gilchrest BA, Yaar M, Eller M;  
XX WPI; 2001-626338/72.  
XX  
XX Inhibiting proliferation of epithelial cells, useful e.g. for treating  
XX carcinoma, using specific oligonucleotides that mimic the effects of  
XX ultra-violet light -  
XX  
XX Claim 1; Page 36; 74pp; English.  
XX  
XX The invention describes inhibition of mammalian epithelial cell  
XX proliferation by treating cells with at least one oligonucleotide, or  
XX its fragment. The compounds, which have cytostatic, anti-allergic,  
XX anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and  
XX immunosuppressive activities, function as 'ultra-violet mimics' to induce  
XX DNA repair processes (or a protective response to later exposure to  
XX radiation or chemicals), as a proliferation inhibitor, apoptosis inducer  
XX or a tumour necrosis factor inhibitor. Probably they mimic products of  
XX DNA damage, or processed DNA-damage intermediates, by inducing the p53  
XX pathway, resulting in transient arrest of cell growth, allowing more time  
XX for DNA repair to occur before cell division takes place. The method is  
XX especially used to treat carcinoma but may also be used to: treat other  
XX hyperproliferative states (e.g. psoriasis or precancerous conditions);  
XX reduce phototaging, oxidative stress or damage; prevent skin cancer; treat  
XX allergically mediated inflammation (atopic or contact dermatitis,  
XX allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in  
XX cells caused by radiation or chemicals; increase melanin production  
XX (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to  
XX promote apoptosis in epithelial cells that contain damaged DNA. Also  
XX oligonucleotides that contain non-hydrolyzable backbones are used to  
XX inhibit apoptosis, in response to DNA damage, in epithelial cell. This  
XX sequence is melanogenesis associated oligonucleotide #6, one of the  
XX oligonucleotides used to inhibit mammalian epithelial cell proliferation,

CC described in the method of the invention.

XX  
SQ Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 5; DB 23; Length 5;  
Best Local Similarity 100.0%; Pred. No. 5.2e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5  
|||||  
Db 1 CATAC 5

RESULT 5  
AAZ10694/C  
ID AAZ10694 standard; DNA; 7 BP.  
XX AC AAZ10694;  
XX DT 23-NOV-1999 (first entry)  
XX DE Oligonucleotide sequence that increases p53 activity in a cell.  
XX KW p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;  
XX KW UV-induced hyperproliferative disease; psoriasis; vitiligo;  
XX KW atopic dermatitis; allergic rhinitis; conjunctivitis; phototaging;  
XX KW skin cancer; ss.  
XX OS Synthetic.  
XX GB2336157-A.  
XX 13-OCT-1999.  
XX 24-MAR-1999; 99GB-0006758.  
XX 26-MAR-1998; 98US-0048927.  
XX (UYBO-) UNIV BOSTON.  
XX Gilchrest BA, Yaar M, Eller M;  
XX WPI; 1999-543520/46.  
XX  
XX DNA fragments useful for increasing p53 activity in a cell and reducing  
XX susceptibility to UV-induced hyperproliferative diseases -  
XX  
XX Claim 1; Page 30; 44pp; English.  
XX  
XX AAZ10692-97 represent DNA fragments that are used for increasing p53  
XX activity in a cell. The oligonucleotides are UV mimetics and  
XX protect cells against subsequent exposure to UV-irradiation or  
XX chemicals. The oligonucleotides are useful for increasing p53 activity  
XX in a cell, reducing the susceptibility to UV-induced hyperproliferative  
XX diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic  
XX rhinitis, conjunctivitis, and UV-induced dermatoses, reducing phototaging  
XX and reducing susceptibility to skin cancer.  
XX  
SQ Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 5; DB 20; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.7e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5  
|||||  
Db 6 CATAC 2

RESULT 6  
AAS14907/c  
ID AAS14907 standard; DNA; 7 BP.  
XX

AC AAS14907;  
DT 14-FEB-2002 (first entry)  
XX  
DE Melanogenesis associated oligonucleotide #3.  
XX  
KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;  
KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;  
KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;  
KW tumour necrosis factor inhibitor; photoging; hyperproliferative disease;  
KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;  
KW conjunctivitis; allergic rhinitis; vitiligo; ss.  
XX  
OS Synthetic.  
XX  
XX WO200174342-A2.  
XX  
XX 11-OCT-2001.  
XX  
XX 30-MAR-2001; 2001WO-US10162.  
XX  
XX 31-MAR-2000; 2000US-0540843.  
XX  
XX (UYBO-) UNIV BOSTON.  
XX  
XX Gilchrist BA, Yaar M, Eller M;  
XX  
XX WPI; 2001-626338/72.  
XX  
XX Inhibiting proliferation of epithelial cells, useful e.g. for treating  
XX carcinoma, using specific oligonucleotides that mimic the effects of  
XX ultra-violet light -  
XX  
XX Claim 1; Page 36; 74pp; English.  
XX  
XX The invention describes inhibition of mammalian epithelial cell  
XX proliferation by treating cells with at least one oligonucleotide, or  
XX its fragment. The compounds, which have cytostatic, anti-allergic,  
XX anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and  
XX immunosuppressive activities, function as 'ultra-violet mimics' to induce  
XX DNA repair processes (or a protective response to later exposure to  
XX radiation or chemicals), as a proliferation inhibitor, apoptosis inducer  
XX or a tumour necrosis factor inhibitor. Probably they mimic products of  
XX DNA damage, or processed DNA-damage intermediates, by inducing the p53  
XX pathway, resulting in transient arrest of cell growth, allowing more time  
XX for DNA repair to occur before cell division takes place. The method is  
XX especially used to treat carcinoma but may also be used to: treat other  
XX hyperproliferative states (e.g. psoriasis or precancerous conditions);  
XX reduce photoging, oxidative stress or damage; prevent skin cancer; treat  
XX allergically mediated inflammation (atopic or contact dermatitis,  
XX allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in  
XX cells caused by radiation or chemicals; increase melanin production  
XX (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to  
XX promote apoptosis in epithelial cells that contain damaged DNA. Also  
XX oligonucleotides that contain non-hydrolyzable backbones are used to  
XX inhibit apoptosis, in response to DNA damage, in epithelial cell. This  
XX sequence is melanogenesis associated oligonucleotide #3, a truncated  
XX version of the oligonucleotide shown in AAS14906, one of the  
XX oligonucleotides used to inhibit mammalian epithelial cell  
XX proliferation, described in the method of the invention.  
XX  
XX Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 5; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.7e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CATAC 5  
Db |||||  
6 CATAC 2

RESULT 7

AAS14911/c  
ID AAS14911 standard; DNA; 7 BP.  
XX  
AC AAS14911;  
XX  
DT 14-FEB-2002 (first entry)  
XX  
DE Melanogenesis associated oligonucleotide #7.  
XX  
KW Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;  
KW anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;  
KW immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;  
KW tumour necrosis factor inhibitor; photoging; hyperproliferative disease;  
KW carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;  
KW conjunctivitis; allergic rhinitis; vitiligo; ss.  
XX  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
XX modified\_base 1 /\*tag= a  
XX FT /mod\_base= a  
XX FT /note= "Phosphorylated"  
XX  
XX WO200174342-A2.  
XX  
XX 11-OCT-2001.  
XX  
XX 30-MAR-2001; 2001WO-US10162.  
XX  
XX 31-MAR-2000; 2000US-0540843.  
XX  
XX (UYBO-) UNIV BOSTON.  
XX  
XX Gilchrist BA, Yaar M, Eller M;  
XX  
XX WPI; 2001-626338/72.  
XX  
XX Inhibiting proliferation of epithelial cells, useful e.g. for treating  
XX carcinoma, using specific oligonucleotides that mimic the effects of  
XX ultra-violet light -  
XX  
XX Claim 1; Page 38; 74pp; English.  
XX  
XX The invention describes inhibition of mammalian epithelial cell  
XX proliferation by treating cells with at least one oligonucleotide, or  
XX its fragment. The compounds, which have cytostatic, anti-allergic,  
XX anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and  
XX immunosuppressive activities, function as 'ultra-violet mimics' to induce  
XX DNA repair processes (or a protective response to later exposure to  
XX radiation or chemicals), as a proliferation inhibitor, apoptosis inducer  
XX or a tumour necrosis factor inhibitor. Probably they mimic products of  
XX DNA damage, or processed DNA-damage intermediates, by inducing the p53  
XX pathway, resulting in transient arrest of cell growth, allowing more time  
XX for DNA repair to occur before cell division takes place. The method is  
XX especially used to treat carcinoma but may also be used to: treat other  
XX hyperproliferative states (e.g. psoriasis or precancerous conditions);  
XX reduce photoging, oxidative stress or damage; prevent skin cancer; treat  
XX allergically mediated inflammation (atopic or contact dermatitis,  
XX allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in  
XX cells caused by radiation or chemicals; increase melanin production  
XX (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to  
XX promote apoptosis in epithelial cells that contain damaged DNA. Also  
XX oligonucleotides that contain non-hydrolyzable backbones are used to  
XX inhibit apoptosis, in response to DNA damage, in epithelial cell. This  
XX sequence is melanogenesis associated oligonucleotide #7, one of the  
XX oligonucleotides used to inhibit mammalian epithelial cell  
XX proliferation, described in the method of the invention.  
XX  
XX Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 5; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.7e+08;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
| | | | |  
Db 6 CATAC 2

RESULT 8  
AAD02250  
ID AAD02250 standard; DNA; 8 BP.

XX AC AAD02250;  
XX DT 28-MAR-2001 (first entry)  
XX DE Direct repeat sequence that binds to SB protein.

XX DE Sleeping Beauty; SB; AdSB10; adenovirus; transposase;  
XX KW non-integrating viral vector; cytosolic; anti-diabetic; cardiant;  
XX KW neuroprotective; genetic disease; gene therapy; therapy; cancer;  
XX KW cystic fibrosis; diabetes; cardiovascular disease; brain malfunction;  
XX KW genome analysis; chemotherapy; transgenic host cell; direct repeat; ds.  
XX PS Unidentified.  
XX OS WO200068399-A2.  
XX PN 16-NOV-2000.  
XX PD 11-MAY-2000; 2000WO-US12827.  
XX PF 11-MAY-1999; 99US-0133569.  
XX PR (MINU ) UNIV MINNESOTA.  
XX PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
XX PA (MCIV/) MCIVOR R S.  
XX PA (HACK/) HACKETT P B.  
XX PA (AGUI/) AGUILAR-CORDOVA E.  
XX PI Mcivor RS, Hackett PB, Aguilar-Cordova E;  
XX DR WPI; 2001-024870/03.

XX PT Non-integrating (adenovirus-based) viral vectors useful in gene  
XX PT therapy, especially for treating patients suffering from a genetic  
XX PT disease, e.g. cystic fibrosis, diabetes, cardiovascular disease, cancer  
XX PT or brain malfunction -  
XX PS Disclosure; Page 14; 62pp; English.

XX CC The patent discloses non-integrating viral vectors comprising a  
XX CC polynucleotide flanked by inverted repeats that bind a transposase, a  
XX CC transposase-encoding polynucleotide operably linked to a regulatory  
XX CC sequence comprising an operator, that alters expression of the  
XX CC transposase-encoding polynucleotide. Transposon sequences can integrate  
XX CC into genomic DNA whether or not the cell is dividing. AdSB10 is a SB  
XX CC (Sleeping Beauty) transposase-transducing adenoviral non-integrating  
XX CC vector. The non-integrating viral vectors are useful for treating  
XX CC genetic disease characterised by subnormal production of a polypeptide or  
XX CC RNA, e.g. for replacement of a defective gene, delivery of a polypeptide  
XX CC drug or supplementation of a metabolic activity. These genetic diseases  
XX CC include cystic fibrosis, diabetes, cardiovascular disease, cancer or  
XX CC brain malfunction. The non-integrating viral vectors are useful as  
XX CC nucleic acid delivery systems, e.g. for genome analysis or gene therapy  
XX CC and can also be used for applications that involve long-term production  
XX CC of a polypeptide. The non-integrating viral vectors are also useful for  
XX CC creating transgenic host cells that provide normal cells with protection  
XX CC against toxic side effects of chemotherapy.  
XX CC The sequence of the present invention is a direct repeat sequence that  
XX CC binds to SB protein.

XX PS Sequence 8 BP; 4 A; 3 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 5; DB 22; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3.2e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
| | | | |  
Db 2 CATAC 6

RESULT 9  
AAV22350/c  
ID AAV22350 standard; RNA; 9 BP.

XX AC AAV22350;  
XX DT 29-JUN-1998 (first entry)  
XX DE A promoter regulatory motif found in the utrons of the invention.

XX DE 3' untranslated region; UTR; inhibition; gene expression; ICAM-7;  
XX KW interferon-gamma; IFN-gamma; major histocompatibility complex; MHC;  
XX KW antigen expression; gene promoter; utron; B7-1; B7-2; Fc gamma R;  
XX KW HIV gene expression; transplant rejection; treatment;  
XX KW autoimmune disease; inflammatory disease; ss.  
XX OS Unidentified.  
XX OS WO9744450-A1.  
XX PN 27-NOV-1997.  
XX PD 21-MAY-1997; 97WO-US09459.  
XX PF 21-MAY-1996; 96US-0646789.  
XX PR (UYUA ) UNIV YALE.  
XX PA Peyman JA;  
XX PI WPI; 1998-018505/02.

XX DR Utrons, RNA molecules containing promoter regulatory motifs -  
XX PT useful to suppress expression from promoter of interest,  
XX PT specifically T9U nucleic acid suppression of MHC Class I and II gene  
XX PT expression  
XX PS Claim 20; Page 20; 200pp; English.

XX CC The present sequence represents a promoter regulatory element,  
XX CC found in the utrons of the invention. Utrons are from, or are  
XX CC homologous to, the 3' untranslated region (UTR), of an mRNA that  
XX CC stimulates or inhibits a cellular response by sequence specific  
XX CC interactions. The utron is able to suppress constitutive and  
XX CC interferon-gamma (IFN-gamma) induced major histocompatibility complex  
XX CC (MHC) class I and class II antigen expression and expression of other  
XX CC antigens, the gene promoters of which contain related sequence motifs  
XX CC that are stimulated by the same factors which stimulate MHC class I and  
XX CC class II antigen expression. Such utrons can be used to regulate  
XX CC gene expression in a subject, e.g. a human or a cell in vitro.  
XX CC specifically inhibiting MHC Class I or II, ICAM-7, B7-1, B7-2,  
XX CC Fc gamma R, IL-2 or HIV gene expression. They can be used to inhibit  
XX CC transplant rejection, or treat an autoimmune or inflammatory disease or  
XX CC disorder.

XX PS Sequence 9 BP; 3 A; 0 C; 3 G; 3 U; 0 other;

Query Match 100.0%; Score 5; DB 19; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.9e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
| | | | |  
Db 5 CATAC 1

## RESULT 10

AAV22283/c  
ID AAV22283 standard; DNA; 9 BP.

XX  
AC AAV22283;  
XX

XX 29-JUN-1998 (first entry)  
XX

XX GAS complement gene promoter motif found in a trophoblast STAT utron.  
XX

XX Trophoblast STAT utron; TSU; 3' untranslated region; UTR; inhibition;  
KW interferon-gamma; IFN-gamma; major histocompatibility complex; MHC;  
KW antigen expression; gene promoter; Class I; Class II; IFN signalling;  
KW GAS; ISRE; interleukin-4 response element; gene expression; ICAM-7;  
KW B7-1; B7-2; FC gamma R; HIV gene expression; transplant rejection;  
KW treatment; autoimmune disease; inflammatory disease; ss.

XX Unidentified.

XX WO9744450-A1.

XX 27-NOV-1997.

XX 21-MAY-1997; 97WO-US09459.

XX 21-MAY-1996; 96US-0646789.

XX (UYUA ) UNIV YALE.

XX Peyman JA;

XX WPI; 1998-018505/02.

XX Utrons, RNA molecules containing promoter regulatory motifs -  
XX useful to suppress expression from promoter of interest,  
XX specifically TSU nucleic acid suppression of MHC Class I and II gene  
XX expression

XX Claim 22; Page 90; 200pp; English.

XX The present sequence represents a GAS complement gene promoter motif  
XX found in a trophoblast STAT utron (TSU). TSUs be isolated from a CDNA  
XX library prepared from mRNA isolated from trophoblast cells. Utrons are  
XX from, or are homologous to, the 3' untranslated region (UTR), of an mRNA  
XX that stimulates or inhibits a cellular response by sequence specific  
XX interactions. The TSU is able to suppress constitutive and  
XX interferon-gamma (IFN-gamma) induced major histocompatibility complex  
XX (MHC) class I and class II antigen expression and expression of other  
XX antigens, the gene promoters of which contain related sequence motifs  
XX that are stimulated by the same factors which stimulate MHC class I and  
XX class II antigen expression. The TSU sequence contains motifs related to  
XX IFN signalling (GAS, ISRE and interleukin-4 response elements). The  
XX nucleic acid can be used to regulate gene expression in a subject, e.g. a  
XX human or a cell in vitro, specifically inhibiting MHC Class I or II,  
XX ICAM-7, B7-1, B7-2, FC gamma R, IL-2 or HIV gene expression. It can be  
XX used to inhibit transplant rejection, or treat an autoimmune or  
XX inflammatory disease or disorder. It can also be used to inhibit the  
XX action of STAT1-6, or a cytokine.

XX Sequence 9 BP; 3 A; 0 C; 3 G; 3 T; 0 other;

Query Match 100.0%; Score 5; DB 19; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.9e+08;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5

DB 5 CATAC 1

## RESULT 11

## AAV15899/c

ID AAV15899 standard; DNA; 9 BP.

XX  
AC AAV15899;

XX 26-MAY-1998 (first entry)  
XX

XX Cyclin D transcription factor DMPI nonamer consensus sequence.  
XX

XX cyclin D transcription factor; binding affinity; D-type cyclin; probe;  
KW cell cycle inhibitor; tumour; detection; cancer; DMPI; competitor;  
KW nonamer consensus sequence; ss.

XX Mus musculus.

XX Homo sapiens.

XX WO9743415-A1.

XX 20-NOV-1997.

XX 16-MAY-1997; 97WO-US08480.

XX 15-MAY-1997; 97US-0017815.

XX 16-MAY-1996; 96US-0017815.

XX 16-MAY-1996; 96US-0648837.

XX (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.

XX Hirai H, Inoue K, Sherr CJ;

XX WPI; 1998-008884/01.

XX Cyclin D transcription factor and related DNA - can be used to

XX develop products for treatment of, e.g. cancer

XX Claim 3; Page 99; 120pp; English.

XX This is a nonamer consensus sequence of a cyclin D transcription factor  
XX DMPI. DMPI is an amino acid polymer which has binding affinity for a  
XX D-type cyclin, in vitro, and for a specific DNA nucleotide sequence and  
XX is a transcription factor involved in the activation of genes that  
XX prevent cell proliferation. The DMPI nucleic acid is operatively linked  
XX to an expression control sequence in an expression vector. The expression  
XX vector has a transcription control sequence comprising this nonamer  
XX sequence operably associated with a recombinant gene or a cassette  
XX insertion site for a recombinant gene. The vector is homologously  
XX recombined in a chromosome of a transgenic animal. A probe or a  
XX competitor in DMPI transactivation assays is designed based on this  
XX nonamer sequence. The presence of activity of DMPI can be determined by  
XX detecting binding of DMPI and a probe by contacting a biological sample  
XX from a mammal with the probe under conditions that allow binding of the  
XX probe to DMPI, where the probe contains the core sequence GTA, and where  
XX the presence or activity of DMPI is suspected in the sample. DMPI can  
XX function as a cell cycle inhibitor when expressed in a tumour cell.  
XX Modulating the expression of DMPI can be used to treat tumours and other  
XX cancers. DMPI can also be used for controlling expression of heterologous  
XX proteins. Antisense sequences and ribozymes can be used to inhibit  
XX expression of the transcription factor. Detecting the level and activity  
XX of DMPI in cells is useful for detection of cancer cells or  
XX dysproliferative cells.

XX Sequence 9 BP; 1 A; 3 C; 2 G; 3 T; 0 other;

Query Match 100.0%; Score 5; DB 19; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.9e+08;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5

DB 8 CATAC 4

## RESULT 12



```

AAZ10692/C
ID AAZ10692 standard; DNA; 9 BP.
XX
AC AAZ10692;
XX
XX
DT 23-NOV-1999 (first entry)
XX
DE Oligonucleotide sequence that increases p53 activity in a cell.
XX
XX p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
XX UV-induced hyperproliferative disease; psoriasis; vitiligo;
XX atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
XX skin cancer; ss.
XX
OS Synthetic.
XX
XX GB2336157-A.
XX
XX 13-OCT-1999.
XX
XX 24-MAR-1999; 99GB-0006758.
XX
XX 26-MAR-1998; 98US-0048927.
XX
XX (UYBO-) UNIV BOSTON.
XX
XX Gilchrist BA, Yaar M, Eller M;
XX
XX WPI; 1999-543520/46.
XX
XX DNA fragments useful for increasing p53 activity in a cell and reducing
XX susceptibility to UV-induced hyperproliferative diseases -
XX
XX Claim 11; Page 29; 44pp; English.
XX
XX AAZ10692-97 represent DNA fragments that are used for increasing p53
XX activity in a cell. The oligonucleotides are UV mimetics and
XX protect cells against subsequent exposure to UV-irradiation or
XX chemicals. The oligonucleotides are useful for increasing p53 activity
XX in a cell, reducing the susceptibility to UV-induced hyperproliferative
XX diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
XX rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
XX and reducing susceptibility to skin cancer.
XX
XX Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;
XX
XX Query Match 100.0%; Score 5; DB 20; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 2.9e+08;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CATAC 5
XX |||||
XX 7 CATAC 3
XX
XX
XX RESULT 13
XX AAS14905/C
XX ID AAS14905 standard; DNA; 9 BP.
XX
XX AC AAS14905;
XX
XX
XX 14-FEB-2002 (first entry)
XX
XX Melanogenesis associated oligonucleotide #1.
XX
XX Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
XX anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
XX immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
XX tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
XX carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
XX conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
XX OS Synthetic.
XX
AAZ10692/C
ID AAZ10692 standard; DNA; 9 BP.
XX
AC AAZ10692;
XX
XX
DT 23-NOV-1999 (first entry)
XX
DE Oligonucleotide sequence that increases p53 activity in a cell.
XX
XX p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
XX UV-induced hyperproliferative disease; psoriasis; vitiligo;
XX atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
XX skin cancer; ss.
XX
OS Synthetic.
XX
XX GB2336157-A.
XX
XX 13-OCT-1999.
XX
XX 24-MAR-1999; 99GB-0006758.
XX
XX 26-MAR-1998; 98US-0048927.
XX
XX (UYBO-) UNIV BOSTON.
XX
XX Gilchrist BA, Yaar M, Eller M;
XX
XX WPI; 1999-543520/46.
XX
XX DNA fragments useful for increasing p53 activity in a cell and reducing
XX susceptibility to UV-induced hyperproliferative diseases -
XX
XX Claim 11; Page 29; 44pp; English.
XX
XX AAZ10692-97 represent DNA fragments that are used for increasing p53
XX activity in a cell. The oligonucleotides are UV mimetics and
XX protect cells against subsequent exposure to UV-irradiation or
XX chemicals. The oligonucleotides are useful for increasing p53 activity
XX in a cell, reducing the susceptibility to UV-induced hyperproliferative
XX diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
XX rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
XX and reducing susceptibility to skin cancer.
XX
XX Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;
XX
XX Query Match 100.0%; Score 5; DB 20; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 2.9e+08;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CATAC 5
XX |||||
XX 7 CATAC 3
XX
XX
XX RESULT 13
XX AAS14905/C
XX ID AAS14905 standard; DNA; 9 BP.
XX
XX AC AAS14905;
XX
XX
XX 14-FEB-2002 (first entry)
XX
XX Melanogenesis associated oligonucleotide #1.
XX
XX Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;
XX anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;
XX immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;
XX tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;
XX carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
XX conjunctivitis; allergic rhinitis; vitiligo; ss.
XX
XX OS Synthetic.
XX

```

Differential display method; leucine-rich motif; transmembrane protein; secreted protein; primer; PCR; ss; human.

Homo sapiens.  
Synthetic.

WO200259259-A2.

01-AUG-2002.

23-JAN-2002; 2002WO-IL00071.

23-JAN-2001; 2001US-263158P.

(UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.

Wreschner DH;

WPI; 2002-599769/64.

Differential display method for identifying secreted or transmembrane protein, comprises contacting a DNA with a first primer that hybridizes to a sequence coding for a leucine-rich motif and with a second oligonucleotide primer -

Claim 52; Page 17; 37pp; English.

The invention relates to a differential display comprising contacting cDNA with a first primer that hybridizes to an oligonucleotide sequence coding for a leucine-rich motif, and with a second oligonucleotide primer to form a cDNA-hybrid molecule. The method comprises obtaining mRNA from at least 2 samples, synthesizing cDNA from the RNA of each sample, contacting the cDNA with a first primer that hybridizes to an oligonucleotide sequence coding for a leucine-rich motif, and with a second oligonucleotide primer to form cDNA-hybrid molecules, amplifying the cDNA-hybrid molecules, detecting amplified products and comparing the amplified products from each sample to identify distinctive amplified products coding for at least one secreted or transmembrane protein. The method is useful for discovering novel secreted and/or transmembrane proteins which are important for cell processes and play an important role in determining its phenotype, and which act as mediators for the transfer of signals from external environment into the cell itself, thus modulating gene expression. Sequences ABX03772-ABX03790 represent PCR primers used in the differential display method of the invention.

Sequence 9 BP; 1 A; 0 C; 2 G; 2 T; 4 other;

Query Match 100.0%; Score 5; DB 24; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.9e+08;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATAC 5

|||||

9 CATAC 5

RESULT 15

ABQ71504

ID ABQ71504 standard; DNA; 9 BP.

AC ABQ71504;

DT 28-AUG-2002 (first entry)

DE Zinc finger protein related oligonucleotide target SEQ ID NO:623.

XX Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.

OS Homo sapiens.

OS Synthetic.

PN WO200242459-A2.

XX

PD 30-MAY-2002.

XX

PF 20-NOV-2001; 2001WO-US43438.

XX

PR 20-NOV-2000; 2000US-0716637.

XX

PA (SANG-) SANGAMO BIOSCIENCES INC.

XX

PI Liu Q;

XX

DR WPI; 2002-500284/53.

XX

PT New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus -

PT

XX Example 1; Page 45; 81pp; English.

XX

The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (i) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (3) designing (W) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determine the phenotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ71213 to ABQ72214 and ABQ48191 to ABQ51230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention.

Sequence 9 BP; 2 A; 2 C; 3 G; 2 T; 0 other;

Query Match 100.0%; Score 5; DB 24; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.9e+08;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CATAC 5

|||||

Db 2 CATAC 6

Search completed: December 31, 2003, 15:08:15

Job time : 145.494 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model  
Run on: December 31, 2003, 13:58:09 ; Search time 574.494 Seconds  
(without alignments)  
211.530 Million cell updates/sec

Title: US-09-540-843-6  
Perfect score: 5  
Sequence: 1 catcac 5

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues  
Total number of hits satisfying chosen parameters: 33330

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 1: em\_estba.\*
- 2: em\_esthum.\*
- 3: em\_estin.\*
- 4: em\_estmu.\*
- 5: em\_estov.\*
- 6: em\_estpl.\*
- 7: em\_estro.\*
- 8: em\_esti.\*
- 9: gb\_esti.\*
- 10: gb\_est2.\*
- 11: gb\_estc.\*
- 12: gb\_est3.\*
- 13: gb\_est4.\*
- 14: gb\_est5.\*
- 15: em\_estfun.\*
- 16: em\_estom.\*
- 17: em\_gss\_hum.\*
- 18: em\_gss\_inv.\*
- 19: em\_gss\_pln.\*
- 20: em\_gss\_vrt.\*
- 21: em\_gss\_fun.\*
- 22: em\_gss\_mam.\*
- 23: em\_gss\_mus.\*
- 24: em\_gss\_pro.\*
- 25: em\_gss\_rtd.\*
- 26: em\_gss\_phg.\*
- 27: em\_gss\_vrl.\*
- 28: gb\_gss1.\*
- 29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	100.0	14	12	BM398220 5009-0-42
2	5	100.0	16	9	AI424037 t51n06.x
3	5	100.0	16	9	AI685758 tuj7g09.x
4	5	100.0	16	9	AI721735 fc31g08.x

5	5	100.0	16	12	BM3982185
6	7	100.0	17	12	BM3982060
7	6	100.0	17	13	BQ595683
8	5	100.0	17	14	C21103
9	5	100.0	18	12	BM397954
10	5	100.0	19	9	AA977115
11	5	100.0	19	9	AI120725
12	5	100.0	19	9	AI747751
13	5	100.0	19	14	C00646
14	5	100.0	19	28	AZ341880
15	5	100.0	19	28	AZ345849
16	5	100.0	19	28	AZ355195
17	5	100.0	19	28	AZ406137
18	5	100.0	19	28	AZ422163
19	5	100.0	19	28	AZ434551
20	5	100.0	19	28	AZ464990
21	5	100.0	19	28	AZ486152
22	5	100.0	19	28	AZ579566
23	5	100.0	19	28	AZ614702
24	5	100.0	19	28	AZ626685
25	5	100.0	19	28	AZ645469
26	5	100.0	19	28	AZ647364
27	5	100.0	19	28	AZ759906
28	5	100.0	19	28	AZ766086
29	5	100.0	19	28	AZ799396
30	5	100.0	19	28	AZ815067
31	5	100.0	19	28	AZ817238
32	5	100.0	19	28	AZ839614
33	5	100.0	19	28	AZ864822
34	5	100.0	19	28	AZ943806
35	5	100.0	19	28	AZ948421
36	5	100.0	19	28	AZ949895
37	5	100.0	19	28	AZ953217
38	5	100.0	19	28	AZ987324
39	5	100.0	19	28	AZ990856
40	5	100.0	20	9	AB088508
41	5	100.0	20	13	BQ593049
42	5	100.0	20	28	AZ336039
43	5	100.0	20	28	AZ359199
44	5	100.0	20	28	AZ369273
45	5	100.0	20	28	AZ387347

ALIGNMENTS

RESULT 1  
BM398220  
LOCUS  
DEFINITION  
Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION  
BM398220  
VERSION  
EST.  
KEYWORDS  
Tetrahymena thermophila  
SOURCE  
Tetrahymena thermophila  
ORGANISM  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymena.  
REFERENCE  
1 (bases 1 to 14)  
Turkewitz A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J., and Klobutcher, L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
TITLE  
JOURNAL  
COMMENT  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.  
Location/Qualifiers  
1. .14

/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript 2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."  
4 a 5 c 0 g 5 t

BASE COUNT  
ORIGIN

Query Match 100.0%; Score 5; DB 12; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 CATAC 5  
|||||  
1 CATAC 5

RESULT 2  
LOCUS AI424037 16 bp mRNA linear EST 09-MAR-1999  
DEFINITION t51h06.x1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:2102843 3', similar to TR:Q69566 Q69566 ;, mRNA sequence.  
ACCESSION AI424037  
VERSION AI424037.1 GI:4269968  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 16)  
REFERENCE NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
AUTHORS National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index  
TITLE Unpublished  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers

FEATURES  
source

1..16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2102843"  
/tissue\_type="glioblastoma (pooled)"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Brn23"  
/note="Organ: brain; Vector: p7T73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAGTCGGAGCGCCGATATCTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T73 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaldo."  
8 a 6 c 1 g 1 t

BASE COUNT  
ORIGIN

Query Match 100.0%; Score 5; DB 9; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CATAC 5  
|||||  
Db 2 CATAC 6

RESULT 3  
LOCUS AI685758 16 bp mRNA linear EST 27-MAY-1999  
DEFINITION t337909.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:2253280 3', similar to TR:Q02393 Q02393 HUMAN PAPILLOMAVIRUS 18 E5 CENTRAL SEQUENCE MOTIF PROTEIN 1 ; contains element LTR4 repetitive element ;, mRNA sequence.  
ACCESSION AI685758  
VERSION AI685758.1 GI:4897052  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 16)  
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
TITLE Unpublished  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Sequencing by: Greg Lennon, Ph.D.  
Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers

FEATURES  
source

1..16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2253280"  
/sex="male"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Pr28"  
/note="Organ: prostate; Vector: p7T73D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 985608-986759, 1101192-1101959, and 1217928-1220615).  
Subtraction by Bento Soares and M. Fatima Bonaldo."  
7 a 7 c 1 g 1 t

BASE COUNT  
ORIGIN

Query Match 100.0%; Score 5; DB 9; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CATAC 5  
|||||  
Db 5 CATAC 9

BASE COUNT  
ORIGIN

```

RESULT 4
AI721735      16 bp      mRNA      linear      EST 07-JUN-2001
LOCUS      fc31g08.x1 Zebrafish WashU MPIMG EST Danio xario cDNA clone
DEFINITION      IMAGE:3723038 3' similar to SW:Y14_PASTE P15615 HYPOTHETICAL 47.2
KD PROTEIN ; mRNA sequence.
AI721735
AI721735.1 GI:5040064
EST.
Danio rerio (zebrafish)
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
1 (bases 1 to 16)
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy
, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood
, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,
Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,
Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
and Wilson, R.
WashU Zebrafish EST Project 1998
Unpublished
Other_ESTs: fc31g08.y1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrfish@wustl.edu
cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
Ressourcenzentrum Primat Datenbank, Berlin, Germany (web address:
www.rzpd.de)
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: T7 ET from AmerSham
High quality sequence stop: 1.
Location/Qualifiers
1. .16
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:3723038"
/sex="mixed"
/tissue types="26 somite embryos, adult livers, shield
stage embryos"
/lab_host="XLI-blue MRF"
/clone_lib="Zebrafish WashU MPIMG EST"
/notes="vector: pSPORT1; Site_1: NotI; Site_2: SalI; 1st
strand cDNA was primed with a Not I - oligo(dT)15 primer
[5'PGACTAGTCTTAGATCGGAGCGCCCTTTTCTTTTCTTTT3'];
double-stranded cDNA was ligated to Sal I adaptors (BRL),
digested with Not I and cloned into the Not I and Sal I
sites of the pSPORT1 vector (BRL). Library was constructed
by Matthew Clark (Lehrach lab; ICRF, London and Max Planck
Institut fuer Molekulare Genetik, Berlin). cDNAs for EST
analysis were selected following oligonucleotide
hybridization fingerprinting of arrayed clones from
zebrafish late somitogenesis (26 ss), adult liver or
embryonic shield stage (5.6 h) libraries. Fingerprint
data were used to computationally cluster cDNAs, and a
single cDNA from each cluster was chosen for sequencing.
In some cases multiple members of the same cluster were
sequenced to assess clustering parameters or single clones
were sequenced additional times to assess quality
control."
BASE COUNT      6 a      8 c      1 g      1 t

FEATURES
source
1. .16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/notes="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"
BASE COUNT      4 a      6 c      2 g      3 t      1 others

Query Match      100.0%; Score 5; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATAC 5
Db      9 CATAC 13

RESULT 5
BG928185      16 bp      mRNA      linear      EST 06-NOV-2001
LOCUS      HNC65-1-D12.R.R HNC (Human Normal Cartilage) Homo sapiens cDNA,
DEFINITION      mRNA sequence.
ACCESSION      BG928185
VERSION      BG928185.1 GI:14322708
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16)
Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J.,
Sathe, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and
Lark, M.W.
Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteochondritic cartilage cDNA libraries
Osteochondr. Cartil. 9 (7), 641-653 (2001)
21482651
11597177
Contact: Sanjay Kumar
UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@gsk.com
Seq primer: T7.
Location/Qualifiers
1. .16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/notes="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"
BASE COUNT      4 a      6 c      2 g      3 t      1 others

Query Match      100.0%; Score 5; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATAC 5
Db      8 CATAC 12

RESULT 6
BG929060      17 bp      mRNA      linear      EST 06-NOV-2001
LOCUS      HNC11-1-G8.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
DEFINITION      sequence.
ACCESSION      BG929060
VERSION      BG929060.1 GI:14323583
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16)
Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J.,
Sathe, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and
Lark, M.W.
Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteochondritic cartilage cDNA libraries
Osteochondr. Cartil. 9 (7), 641-653 (2001)
21482651
11597177
Contact: Sanjay Kumar
UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@gsk.com
Seq primer: T7.
Location/Qualifiers
1. .16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/notes="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"
BASE COUNT      4 a      6 c      2 g      3 t      1 others

Query Match      100.0%; Score 5; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATAC 5
Db      8 CATAC 12

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 17)  
AUTHORS Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J.,  
Sathre, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and  
Lark, M.W.

TITLE Identification and initial characterization of 5000 expressed  
sequenced tags (ESTs) each from adult human normal and  
osteoarthritic cartilage cDNA libraries  
Osteoarthr. Cartil. 9 (7), 641-653 (2001)

JOURNAL  
MEDLINE  
PUBMED

COMMENT 21482651  
11597177  
Contact: Sanjay Kumar  
UW2109

GlaxoSmithKline  
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
Tel: 610-270-7245  
Fax: 610-270-5598  
Email: sanjay.kumar-1@gsk.com  
Seq primer: 17

FEATURES  
source  
1..17 Location/Qualifiers

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="cartilage"  
/lab\_host="E.coli DH10 B"  
/clone\_lib="HNC (Human Normal Cartilage)"  
/note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI;  
Directional"

BASE COUNT 5 a 8 c 2 g 2 t

ORIGIN

Query Match 100.0%; Score 5; DB 12; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATAC 5  
|||||  
6 CATAC 10

RESULT 7

LOCUS BQ595683  
DEFINITION E012692-024-022-H17-SP6 MP1Z-ADIS-024-developing root Beta vulgaris  
cDNA clone 024-022-H17 5-PRIME, mRNA sequence.  
ACCESSION BQ595683  
VERSION BQ595683.1 GI:26125266  
KEYWORDS EST.

SOURCE Beta vulgaris  
ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 17)

REFERENCE  
AUTHORS Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,  
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.  
and Radelof, U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)

COMMENT Contact: Weishaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851  
Email: weissaha@mpiz-koeln.mpg.de

Insert Length: 17 Std Error: 0.00  
Plate: 22 row: H column: 17

Seq primer: SP6; CATACGTTTGGTGACACTATAG.  
Location/Qualifiers

FEATURES  
source  
1..17

/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line  
)"  
/db\_xref="GABI:191174"  
/db\_xref="taxon:161934"  
/clones="024-022-H17"  
/tissue\_type="developing root"  
/lab\_host="EMDH108"  
/clone\_lib="MP1Z-ADIS-024-developing root"  
/note="Vector: pCMVSORT6; Site\_1: SalI; Site\_2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
orientation:  
SP6-SalI-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet project  
, local PI: Dr. Katharina Schneider, coordinator: Prof.  
Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

BASE COUNT 4 a 8 c 2 g 3 t

ORIGIN

Query Match 100.0%; Score 5; DB 13; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5

Db |||||  
3 CATAC 7

RESULT 8

LOCUS C21103  
DEFINITION HUNG0002626 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA  
sequence.  
ACCESSION C21103  
VERSION C21103.1 GI:1622213  
KEYWORDS EST.

SOURCE Homo sapiens (human)

REFERENCE  
AUTHORS Okubo, K.  
TITLE BodyMap; human gene expression database  
JOURNAL Unpublished  
COMMENT Contact: Okubo, K.  
Institute for Molecular and Cellular Biol  
Osaka University  
1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan  
Tel: 06-877-5111 (ex.3315)  
Email: kousaku@imcb.osaka-u.ac.jp

We are not submitting the same cDNA sequence redundantly to DBU  
since 1993. For the abundance information of clones with this  
sequence in this library and as well as in other 3'-directed  
libraries, see: http://www.imcb.osaka-u.ac.jp/bodymap. The  
sequences of the clones represented by this GS sequences is also  
found there.

FEATURES  
source  
1..17 Location/Qualifiers

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev stage="adult"  
/clone\_lib="Human adult (K.Okubo)"  
/note="One or more human adult tissue"

BASE COUNT 5 a 5 c 2 g 5 t

ORIGIN

Query Match 100.0%; Score 5; DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
|  
|  
|  
|  
Db 9 CATAC 13

## RESULT 9

BM397954

LOCUS

DEFINITION

5009-0-39-G08.t.1 Chilcoat/Turkewitz cDNA (large fraction)

Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION

BM397954

VERSION

BM397954.1

KEYWORDS

EST.

SOURCE

ORGANISM

Tetrahymena thermophila

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

UNPUBLISHED

Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;

Hymenostomatida; Tetrahymenina; Tetrahymena.

Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel

J. and Klobutcher, L.

EST from Tetrahymena thermophila, strain CU428.1, growing cells

Unpublished

Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3.

FEATURES

source

1. .18

/organism="Tetrahymena thermophila"

/mol\_type="mRNA"

/db\_xref="taxon:5911"

/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"

/notes="Vector: Bluescript2 SK+; Details on library

preparation can be found in Chilcoat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

3 a 7 c 5 g 3 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5

|  
|  
|  
|  
Db 1 CATAC 5

RESULT 10

AA977115/c

LOCUS

DEFINITION

Oq24c08.s1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1587278 3'

similar to TR:Q69566 Q69566 ; mRNA sequence.

ACCESSION

AA977115

VERSION

AA977115.1

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 19)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgaps-x@mail.nih.gov

Trace considered overall poor quality

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1. .19

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1587278"

/tissue\_type="pooled germ cell tumors"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP GC4"

/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

2 a 0 c 7 g 10 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5

|  
|  
|  
|  
Db 13 CATAC 9

RESULT 11

AA120725

LOCUS

DEFINITION

ub72b11.r1 Soares mammary gland NMLMG Mus musculus cDNA clone IMAGE:1383261 5' similar to TR:Q15009 Q15009 ORF, COMPLETE CDS. ; mRNA sequence.

ACCESSION

AA120725

VERSION

AA120725.1

KEYWORDS

EST.

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theisinger, B., Wylie, I., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HMI Mouse EST Project

Unpublished

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:905729

Trace considered overall poor quality

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1. .19

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1587278"

/tissue\_type="pooled germ cell tumors"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP GC4"

/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

2 a 0 c 7 g 10 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5

|  
|  
|  
|  
Db 13 CATAC 9

RESULT 11

AA120725

LOCUS

DEFINITION

ub72b11.r1 Soares mammary gland NMLMG Mus musculus cDNA clone IMAGE:1383261 5' similar to TR:Q15009 Q15009 ORF, COMPLETE CDS. ; mRNA sequence.

ACCESSION

AA120725

VERSION

AA120725.1

KEYWORDS

EST.

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theisinger, B., Wylie, I., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HMI Mouse EST Project

Unpublished

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:905729

Trace considered overall poor quality

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1. .19

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1587278"

/tissue\_type="pooled germ cell tumors"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP GC4"

/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

2 a 0 c 7 g 10 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5

|  
|  
|  
|  
Db 13 CATAC 9

RESULT 11

AA120725

LOCUS

DEFINITION

ub72b11.r1 Soares mammary gland NMLMG Mus musculus cDNA clone IMAGE:1383261 5' similar to TR:Q15009 Q15009 ORF, COMPLETE CDS. ; mRNA sequence.

ACCESSION

AA120725

VERSION

AA120725.1

KEYWORDS

EST.

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theisinger, B., Wylie, I., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HMI Mouse EST Project

Unpublished

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:905729

Trace considered overall poor quality

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1. .19

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1587278"

/tissue\_type="pooled germ cell tumors"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP GC4"

/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

2 a 0 c 7 g 10 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5

Possible reversed clone: similarity on wrong strand  
Seq primer: -28ml3 rev2 ET from Amersham  
High quality sequence stop: 1.

## FEATURES

source  
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/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1383261"  
/sex="female (lactating)"  
/tissue\_type="mammary gland"  
/lab\_host="DH10B"

/clone\_lib="Soares mammary gland NLMG"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

## BASE COUNT

9 a 3 c 4 g 3 t

## ORIGIN

Query Match 100.0%; Score 5; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATAC 5

|||||

7 CATAC 11

## RESULT 12

## LOCUS

## DEFINITION

AI747751 19 bp mRNA linear EST 22-JUN-1999  
ul2ih05.xl Sugano mouse embryo mewa Mus musculus cDNA clone  
IMAGE:2088249 3' similar to TR:P79101 P79101 CLEAVAGE AND  
POLYADENYLATION SPECIFICITY FACTOR PROTEIN. ; mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## JOURNAL

## COMMENT

Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 19)  
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,  
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person  
B., Swaller,T., Gibbons,M., Pape,D., Harvey,M., Schurk,R., Ritter  
E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,  
Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999

## TITLE

## JOURNAL

## COMMENT

Unpublished  
Contact: Marra M/WashU-NCI Mouse EST Project 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LNL ; contact the

Image Consortium (info@image.llnl.gov) for further information.

MGI:995933

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: custom primer used

High quality sequence stop: 1.

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="CS7BL"

/db\_xref="taxon:10090"

## FEATURES

source

100.0%; Score 5; DB 14; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY

1 CATAC 5

/clone="IMAGE:2088249"  
/dev stage="embryo, 14 dpc"  
/lab host="DH10B"

/clone\_lib="Sugano mouse embryo mewa"

/note="Vector: pME18S-FL3; Site\_1: DraIII (CACTGTGTG);

Site\_2: DraIII (CACTGTGTG); 1st strand cDNA was primed

with an oligo(dT) primer [ATGTGGCTTTTITTTTTTTT];

double-stranded cDNA was ligated to a DraIII adaptor

[TGTGGCTACTGG], digested and cloned into distinct DraIII

sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site

CACTGTGTG). XhoI should be used to isolate the cDNA

insert. Size selection was performed to exclude fragments

<1.5kb. Library constructed by Dr. Sumio Sugano

(University of Tokyo Institute of Medical Science).

Custom primers for sequencing: 5' end primer

CTTCTGCTCTAAAGCTGG and 3' end primer

CGACTGAGCTCGAGACA."

6 a 2 c 8 g 3 t

## BASE COUNT

## ORIGIN

Query Match 100.0%; Score 5; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATAC 5

|||||

17 CATAC 13

## RESULT 13

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## JOURNAL

## COMMENT

## TITLE

## COMMENT

## COMMENT

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## COMMENT



```

Db          18 CATAC 14          |||||
RESULT 14
AZ341880/c 19 bp DNA linear GSS 29-SEP-2000
LOCUS
DEFINITION
1M0074004R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0074004 R, genomic survey sequence.
ACCESSION
AZ341880
VERSION
AZ341880.1 GI:10418570
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished
COMMENT
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0074 row: 0 column: 04
Seq primer: CACACGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0074004"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT 4 a 4 c 6 g 5 t
ORIGIN
Query Match
Best Local Similarity 100.0%; Score 5; DB 28; Length 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AZ341880 19 bp DNA linear GSS 29-SEP-2000
LOCUS
DEFINITION
1M0080D16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0080D16 R, genomic survey sequence.
ACCESSION
AZ341880
VERSION
AZ341880.1 GI:10425086
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished
COMMENT
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: D column: 16
Seq primer: CACACGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080D16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
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polynucleotide kinase. Adaptor oligonucleotides were
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adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT 9 a 4 c 0 g 6 t
ORIGIN
Query Match
Best Local Similarity 100.0%; Score 5; DB 28; Length 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Ov 1 CATAC 5  
|||  
Db 1 CATAC 5

Search completed: December 31, 2003, 19:41:24  
Job time : 574.494 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 14:40:05 ; Search time 19.4304 Seconds  
(without alignments)  
113.581 Million cell updates/sec

Title: US-09-540-843-6  
Perfect score: 5  
Sequence: 1 catac 5

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 547746

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: +  
1: /cgn2\_6/ptodata/1/ina/5A COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PTUS COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	5	100.0	5	3	US-08-855-372B-20
C 2	5	100.0	5	3	US-09-048-927-4
C 3	5	100.0	5	4	US-09-498-851-20
C 4	5	100.0	7	1	US-08-615-170-10
C 5	5	100.0	7	1	US-08-615-170-12
C 6	5	100.0	7	3	US-09-048-927-3
C 7	5	100.0	8	4	US-09-142-593-11
C 8	5	100.0	9	2	US-08-583-276-1
C 9	5	100.0	9	3	US-08-646-789A-8
C 10	5	100.0	9	3	US-08-646-789A-80
C 11	5	100.0	9	3	US-09-048-927-1
C 12	5	100.0	9	4	US-09-319-648-68
C 13	5	100.0	10	1	US-08-335-565A-27
C 14	5	100.0	10	1	US-08-250-951-1
C 15	5	100.0	10	1	US-08-232-233-1
C 16	5	100.0	10	1	US-08-222-177A-422
C 17	5	100.0	10	1	US-08-351-748-23
C 18	5	100.0	10	1	US-08-351-748-25
C 19	5	100.0	10	1	US-08-202-927-25
C 20	5	100.0	10	1	US-08-430-536A-23
C 21	5	100.0	10	1	US-08-430-536A-25
C 22	5	100.0	10	1	US-08-171-718-45
C 23	5	100.0	10	2	US-08-703-601-1
C 24	5	100.0	10	2	US-08-684-547-23
C 25	5	100.0	10	2	US-08-684-547-25
C 26	5	100.0	10	3	US-08-469-318-174
C 27	5	100.0	10	3	US-08-468-609A-174

C	28	5	100.0	10	3	US-08-478-087-45	Sequence 45, Appl
C	29	5	100.0	10	3	US-09-063-450-24	Sequence 24, Appl
C	30	5	100.0	10	3	US-09-063-450-33	Sequence 33, Appl
C	31	5	100.0	10	3	US-09-123-638-1	Sequence 1, Appl
C	32	5	100.0	10	3	US-08-646-695-30	Sequence 30, Appl
C	33	5	100.0	10	3	US-08-875-533-31	Sequence 31, Appl
C	34	5	100.0	10	4	US-08-446-872A-174	Sequence 174, App
C	35	5	100.0	10	4	US-09-724-753-1	Sequence 1, Appl
C	36	5	100.0	10	4	US-08-762-227A-174	Sequence 174, App
C	37	5	100.0	10	4	US-09-475-947A-23	Sequence 23, Appl
C	38	5	100.0	10	4	US-09-427-834A-34	Sequence 34, Appl
C	39	5	100.0	10	4	US-09-445-388A-7	Sequence 7, Appl
C	40	5	100.0	10	4	US-09-508-753B-252	Sequence 252, App
C	41	5	100.0	10	4	US-09-508-753B-265	Sequence 265, App
C	42	5	100.0	10	4	US-09-508-753B-273	Sequence 273, App
C	43	5	100.0	10	4	US-09-508-753B-278	Sequence 278, App
C	44	5	100.0	10	4	US-09-508-753B-294	Sequence 294, App
C	45	5	100.0	10	4	US-09-508-753B-303	Sequence 303, App

ALIGNMENTS

RESULT 1

US-08-855-372B-20/c  
; Sequence 20, Application US/08855372B  
; Patent No. 6090549  
; GENERAL INFORMATION:

APPLICANT: Mirzabekov, Andrei D  
APPLICANT: Parinov, Sergei V  
APPLICANT: Barsky, Victor S  
APPLICANT: Kirillov, Eugene V  
APPLICANT: Dubiley, Svetlana A  
TITLE OF INVENTION: Use of Continuous/Contiguous Stacking Hybridization as a Diagnostic  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHERSKOV & FLAYNIK  
STREET: 20 N. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.50 inch, 1.4 MB storage  
COMPUTER: PC  
OPERATING SYSTEM: Microsoft Windows 98  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/855,372B  
FILING DATE: 13-MAY-97  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/587,332  
FILING DATE: 16-JAN-96  
ATTORNEY/AGENT INFORMATION:  
NAME: Cherskov, Michael J.  
REGISTRATION NUMBER: 33,664  
REFERENCE/DOCKET NUMBER: ANL-IN-95-027  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 621-1330  
TELEFAX: (312) 621-0088  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 bases  
TYPE: nucleic acid  
STRANDEDNESS: No. 6090549 Applicable  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOTHETICAL: yes  
US-08-855-372B-20

Query Match 100.0%; Score 5; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. NO. 8.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 CATAC 5
Db 5 CATAC 1

US-09-048-927-4/c
; Sequence 4, Application US/09048927
; Patent No. 6147056
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Yaar, Mina
; APPLICANT: Eller, Mark
; TITLE OF INVENTION: Use of Locally Applied DNA Fragments
; FILE REFERENCE: BU94-68A2
CURRENT APPLICATION NUMBER: US/09/048,927
CURRENT FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 08/952,697
EARLIER FILING DATE: 1996-06-03
EARLIER APPLICATION NUMBER: 08/467,012
EARLIER FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 5
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DNA Fragment
US-09-048-927-4

Query Match 100.0%; Score 5; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 8.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATAC 5
5 CATAC 1

US-09-498-851-20/c
; Sequence 20, Application US/09498851
; Patent No. 6440671
; GENERAL INFORMATION:
; APPLICANT: Mirzabekov, Andrei D
; APPLICANT: Parinov, Sergei V
; APPLICANT: Barsky, Victor E
; APPLICANT: Kirillov, Eugene V
; APPLICANT: Dubiley, Svetlana A
TITLE OF INVENTION: Use of Continuous/Contiguous
TITLE OF INVENTION: Stacking Hybridization as a Diagnostic Tool.
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSER: CHERSKOV & FLAYNIK
STREET: 20 N. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 inch, 1.4 MB storage
COMPUTER: PC
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,851
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/855,372
FILING DATE: 13-MAY-97
APPLICATION NUMBER: U.S. 08/587,332
```

```
; FILING DATE: 16-JAN-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Cherskov, Michael J.
; REGISTRATION NUMBER: 33,664
; REFERENCE/DOCKET NUMBER: ANL-IN-95-027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 621-1330
; TELEFAX: (312) 621-0088
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 bases
; TYPE: nucleic acid
; STRANDEDNESS: No. 6440671 Applicable
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHEICAL: yes
; US-09-498-851-20

Query Match 100.0%; Score 5; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 8.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5
Db 5 CATAC 1

US-08-615-170-10
; Sequence 10, Application US/08615170
; Patent No. 5776776
; GENERAL INFORMATION:
; APPLICANT: ORDAHL, Charles P.
; APPLICANT: AZAKIE, Anthony
; APPLICANT: MAR, Janet H.
; APPLICANT: FARRANCE, Iain K.G.
; APPLICANT: HALL, Deborah E.
; APPLICANT: STEWART, Alexandre F.R.
; APPLICANT: LARKIN, Sarah B.
TITLE OF INVENTION: DTEF-1 ISOFORMS AND USES THEREOF
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend Kourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,170
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01526
FILING DATE: 06-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/191,493
FILING DATE: 04-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 2307U-053120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 10:
```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..7
; OTHER INFORMATION: /standard name= "Sph-II binding
; OTHER INFORMATION: site in SV40"
US-08-615-170-10

```

```

Query Match      100.0%; Score 5; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.8e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 CATAC 5

Db 1 CATAC 5

## RESULT 5

```

US-08-615-170-12
Sequence 12, Application US/08615170
Patent No. 5776776

```

```

GENERAL INFORMATION:
APPLICANT: ORDAHL, Charles P.

```

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APPLICANT: AZAKIE, Anthony
APPLICANT: MAR, Janet H.

```

```

APPLICANT: FARRANCE, Iain K.G.
APPLICANT: HALL, Deborah E.

```

```

APPLICANT: STEWART, Alexandre F.R.
APPLICANT: LARKIN, Sarah B.

```

```

TITLE OF INVENTION: DTEP-1 ISOFORMS AND USES THEREOF
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:

```

```

ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco

```

```

STATE: California
COUNTRY: US

```

```

ZIP: 94105-1493

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

```

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

```

```

APPLICATION NUMBER: US/08/615,170
FILING DATE:

```

```

CLASSIFICATION: 435

```

```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01526

```

```

FILING DATE: 06-FEB-1995
CLASSIFICATION: 435

```

```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/191,493

```

```

FILING DATE: 04-FEB-1994
CLASSIFICATION: 435

```

```

ATTORNEY/AGENT INFORMATION:
NAME: Healin, James M.

```

```

REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 2307U-053120

```

```

TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422

```

```

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:

```

```

LENGTH: 7 base pairs
TYPE: nucleic acid

```

```

STRANDEDNESS: single
TOPOLOGY: linear

```

```


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```


```

```


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```


```

```

; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..7
; OTHER INFORMATION: /standard name= "Rat beta-Myoisin
; OTHER INFORMATION: Heavy Chain M-CAT binding element"
US-08-615-170-12

```

```

Query Match      100.0%; Score 5; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.8e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 CATAC 5

Db 1 CATAC 5

## RESULT 6

```

US-09-048-927-3/c
Sequence 3, Application US/09048927
Patent No. 6147056

```

```

GENERAL INFORMATION:
APPLICANT: Gilcrest, Barbara A.

```

```

APPLICANT: Yeager, Mina
APPLICANT: Eller, Mark

```

```

TITLE OF INVENTION: Use of Locally Applied DNA Fragments
FILE REFERENCE: BU94-68A2

```

```

CURRENT APPLICATION NUMBER: US/09/048,927
CURRENT FILING DATE: 1998-03-26

```

```

EARLIER APPLICATION NUMBER: 08/952,697
EARLIER FILING DATE: 1996-06-03

```

```

EARLIER APPLICATION NUMBER: 08/467,012
EARLIER FILING DATE: 1995-06-06

```

```

NUMBER OF SEQ ID NOS: 4
SOFTWARE: PastSeq for Windows Version 3.0

```

```

SEQ ID NO 3
LENGTH: 7

```

```

TYPE: DNA
ORGANISM: Artificial Sequence

```

```

FEATURE:
OTHER INFORMATION: DNA Fragment

```

```

US-09-048-927-3

```

```

Query Match      100.0%; Score 5; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.8e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 CATAC 5

Db 6 CATAC 2

## RESULT 7

```

US-09-142-593-11
Sequence 11, Application US/09142593
Patent No. 6489458

```

```

GENERAL INFORMATION:
APPLICANT: HACKETT ET AL.

```

```

TITLE OF INVENTION: DNA-BASED TRANSPOSON SYSTEM FOR THE
INTRODUCTION OF NUCLEIC ACID INTO DNA OF A CELL

```

```

NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:

```

```

ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203

```

```

CITY: MINNEAPOLIS
STATE: MINNESOTA

```

```

COUNTRY: USA
ZIP: 55402

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

```

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.30

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```

Copied from 09980559 on 05/19/2004

;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/142,593  
;; FILING DATE: 10-SEP-1998  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 60/040,664  
;; FILING DATE: 11-MAR-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 60/053,868  
;; FILING DATE: 28-JUL-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 60/065,303  
;; FILING DATE: 13-NOV-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US98/04687  
;; FILING DATE: 11-MAR-1998  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: SANDBERG, VICTORIA A.  
;; REGISTRATION NUMBER: 41,287  
;; REFERENCE/DOCKET NUMBER: 110.00450101  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 612-305-1226  
;; TELEFAX: 612-305-1228  
;; INFORMATION FOR SEQ ID NO: 11:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 8 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; -09-142-593-11  
Query Match 100.0%; Score 5; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 CATAC 5  
|||||  
2 CATAC 6  
;;  
;; RESULT 8  
;; -08-583-276-1/c  
;; Sequence 1, Application US/08583276  
;; Patent No. 5837536  
;; GENERAL INFORMATION:  
;; APPLICANT: McDonagh, Kevin T.  
;; APPLICANT: Nienhuis, Arthur  
;; APPLICANT: Tolstoshev, Paul  
;; TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN  
;; TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED  
;; TITLE OF INVENTION: SELECTION OF CELLS TRANSFECTED WITH SUCH GENES  
;; NUMBER OF SEQUENCES: 19  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSER: Carella, Byrne, Bain, Gilfillan,  
;; ADDRESSER: Cecchi & Stewart  
;; STREET: 6 Becker Farm Road  
;; CITY: Roseland  
;; STATE: New Jersey  
;; COUNTRY: USA  
;; ZIP: 07068  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5 inch diskette  
;; COMPUTER: IBM PS/2  
;; OPERATING SYSTEM: PC-DOS  
;; SOFTWARE: DW4.V2  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/583,276  
;; FILING DATE: 05-JAN-1996  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/332,444  
;; FILING DATE: 31-OCT-1994

;; APPLICATION NUMBER: 07/887,712  
;; FILING DATE: 22-MAY-1992  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 9 bases  
;; TYPE: nucleic acid  
;; STRANDEDNESS: singular  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: Genomic DNA  
;; DESCRIPTION: Genomic DNA  
;; US-08-583-276-1  
Query Match 100.0%; Score 5; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.5e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CATAC 5  
Db 8 CATAC 4  
;;  
;; RESULT 9  
;; US-08-646-789A-8/c  
;; Sequence 8, Application US/08646789A  
;; Patent No. 6022863  
;; GENERAL INFORMATION:  
;; APPLICANT: Peyman, John A.  
;; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION  
;; NUMBER OF SEQUENCES: 101  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: PENNIE & EDMONDS  
;; STREET: 1155 Avenue of the Americas  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: U.S.A.  
;; ZIP: 10036-2711  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/646,789A  
;; FILING DATE: May 21, 1996  
;; CLASSIFICATION: 800  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mistrock, S. Leslie  
;; REGISTRATION NUMBER: 18,872  
;; REFERENCE/DOCKET NUMBER: 6523-006  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 790-9090  
;; TELEFAX: (212) 869-9741/8864  
;; TELEX: 66141 PENNIE  
;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 9 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
;; US-08-646-789A-8  
Query Match 100.0%; Score 5; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.5e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CATAC 5  
Db 5 CATAC 1  
;;  
;; RESULT 10  
;; US-08-646-789A-80/c

; Sequence 80, Application US/08646789A  
; Patent No. 6022863

; GENERAL INFORMATION:  
; APPLICANT: Peyman, John A.  
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION  
; NUMBER OF SEQUENCES: 101  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/646,789A

; APPLICATION NUMBER: US/08/646,789A  
; FILING DATE: May 21, 1996  
; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 6523-006  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 80:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA  
; US-08-646-789A-80

Query Match 100.0%; Score 5; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.5e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
Db 5 CATAC 1

# RESULT 11

US-09-048-927-1/c  
; Sequence 1, Application US/09048927  
; Patent No. 6147056

; GENERAL INFORMATION:  
; APPLICANT: Gilchrest, Barbara A.  
; APPLICANT: Yaar, Mina  
; APPLICANT: Eller, Mark  
; TITLE OF INVENTION: Use of Locally Applied DNA Fragments  
; FILE REFERENCE: BU94-68A2  
; CURRENT APPLICATION NUMBER: US/09/048,927  
; CURRENT FILING DATE: 1998-03-26  
; EARLIER APPLICATION NUMBER: 08/952,697  
; EARLIER FILING DATE: 1996-06-03  
; EARLIER APPLICATION NUMBER: 08/467,012  
; EARLIER FILING DATE: 1995-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1  
; LENGTH: 9

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: DNA Fragment  
; US-09-048-927-1

Query Match 100.0%; Score 5; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.5e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
Db 7 CATAC 3

# RESULT 12

US-09-319-648-68  
; Sequence 68, Application US/09319648  
; Patent No. 6451530

; GENERAL INFORMATION:

; APPLICANT: Hawkins, Mary  
; TITLE OF INVENTION: Fluorescent Nucleotide Analog Hairpin  
; FORMATION FOR DETECTION OF NUCLEIC ACID HYBRIDIZATION  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/319,648  
; FILING DATE: 30-Jul-1999  
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/032,844  
; FILING DATE: 13-DEC-1996

; APPLICATION NUMBER: WO PCT/US97/22448  
; FILING DATE: 10-DEC-1997

; ATTORNEY/AGENT INFORMATION:  
; NAME: Fang, Carol  
; REGISTRATION NUMBER: 48,631  
; REFERENCE/DOCKET NUMBER: 015280-288100US

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 68:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

; MOLECULE TYPE: DNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 68:  
US-09-319-648-68

Query Match 100.0%; Score 5; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.5e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
Db 3 CATAC 7

# RESULT 13

US-08-335-565A-27/c  
; Sequence 27, Application US/08335565A  
; Patent No. 5527671

; GENERAL INFORMATION:

; APPLICANT: Li, Kening  
; APPLICANT: Rouse, Douglas I.

APPLICANT: German, Thomas L.  
TITLE OF INVENTION: ASSAY FOR VERTICILLIUM DAHLIAE  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Quarles and Brady  
STREET: 1 South Pinckney St., PO BOX 2113  
CITY: Madison  
STATE: WI  
COUNTRY: USA  
ZIP: 53701-2113  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/335,565A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J  
REGISTRATION NUMBER: 27,386  
REFERENCE/DOCKET NUMBER: 960296.93065  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 608-251-5000  
TELEFAX: 608-251-9166  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-335-565A-27  
Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.6e+04;  
Matches 5; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
1 CACATC 5  
|||||  
10 CACATC 6

RESULT 14  
US-08-250-951-1  
Sequence 1, Application US/08250951  
Patent No. 5532129  
GENERAL INFORMATION:  
APPLICANT: Heller, Michael J  
TITLE OF INVENTION: SELF-ORGANIZING MOLECULAR PHOTONIC  
STRUCTURES BASED ON CHROMOPHORE- AND FLUOROPHORE-CONTAINING  
POLYNUCLEOTIDES AND METHODS OF THEIR USE  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bingham & Fitting  
STREET: 12526 High Bluff Drive, Suite 300  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92130  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/250,951  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/790,262  
FILING DATE: 07-NOV-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: HEL0002P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-792-3680  
TELEFAX: 619-792-8477  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 10  
OTHER INFORMATION: /note= "Donor chromophore at the 3'  
OTHER INFORMATION: T nucleotide"  
US-08-250-951-1  
Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.6e+04;  
Matches 5; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
1 CACATC 5  
|||||  
4 CACATC 8

RESULT 15  
US-08-232-233-1  
Sequence 1, Application US/08232233  
Patent No. 5565322  
GENERAL INFORMATION:  
APPLICANT: Michael J. Heller  
TITLE OF INVENTION: SELF-ORGANIZING MOLECULAR PHOTONIC  
STRUCTURES BASED ON CHROMOPHORE- AND FLUOROPHORE-CONTAINING  
POLYNUCLEOTIDES AND METHODS OF THEIR USE  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,233  
FILING DATE: May 4, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/790,262  
FILING DATE: No. 5565322ember 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Murphy, David B.  
REGISTRATION NUMBER: 31,125  
REFERENCE/DOCKET NUMBER: 207/170  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid



```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 10
; OTHER INFORMATION: /note="Donor chromophore at the 3' T nucleotide"
US-08-232-233-1

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.6e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATAC 5
       |||||
Cb      4 CATAC 8

Search completed: January 1, 2004, 00:32:18
Job time : 19.5415 secs
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 17:10:00 ; Search time 58.2911 Seconds  
(without alignments)  
296.896 Million cell updates/sec

Title: US-09-540-843-6

Perfect score: 5

Sequence: 1 catac 5

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2263443 seqs, 1730637950 residues

Total number of hits satisfying chosen parameters: 998502

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:  
15: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:  
16: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:  
17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:  
18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	5	100.0	5	15	US-10-122-630-4
C 2	5	100.0	5	15	US-10-122-630-6
C 3	5	100.0	5	15	US-10-122-633-4
C 4	5	100.0	5	15	US-10-122-633-6
C 5	5	100.0	7	13	US-10-027-632-178029
C 6	5	100.0	7	13	US-10-027-632-178043
C 7	5	100.0	7	14	US-10-027-632-178029
C 8	5	100.0	7	14	US-10-027-632-178043
C 9	5	100.0	7	15	US-10-122-630-3
C 10	5	100.0	7	15	US-10-122-630-7
C 11	5	100.0	7	15	US-10-122-633-3
C 12	5	100.0	7	15	US-10-122-633-7
C 13	5	100.0	8	9	US-09-142-593-11
C 14	5	100.0	8	10	US-09-927-886-17
C 15	5	100.0	8	10	US-09-861-014-6

Sequence 224, Appl  
Sequence 11, Appl  
Sequence 11, Appl  
Sequence 623, Appl  
Sequence 2220, Appl  
Sequence 2256, Appl  
Sequence 623, Appl  
Sequence 2220, Appl  
Sequence 623, Appl  
Sequence 2256, Appl  
Sequence 1, Appl  
Sequence 32, Appl  
Sequence 16, Appl  
Sequence 16, Appl  
Sequence 31, Appl  
Sequence 622, Appl  
Sequence 636, Appl  
Sequence 1338, Appl  
Sequence 1341, Appl  
Sequence 1342, Appl  
Sequence 1343, Appl  
Sequence 31, Appl  
Sequence 7, Appl  
Sequence 8, Appl  
Sequence 622, Appl  
Sequence 636, Appl  
Sequence 1338, Appl

#### ALIGNMENTS

#### RESULT 1

US-10-122-630-4/c  
; Sequence 4, Application US/10122630  
; Publication No. US20030032610A1  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrist, Barbara A.  
; APPLICANT: Eller, Mark S.  
; APPLICANT: Yaar, Mina  
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
; FILE OF INVENTION: Oligonucleotides  
; FILE REFERENCE: 0054.1088-018  
; CURRENT APPLICATION NUMBER: US/10/122,630  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US 08/467,012  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: PCT/US96/08386  
; PRIOR FILING DATE: 1996-06-03  
; PRIOR APPLICATION NUMBER: US 09/048,927  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: US 09/540,843  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: PCT/US01/10162  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 5  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA Fragment  
US-10-122-630-4

Query Match 100.0%; Score 5; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6.7e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 CATAC 5

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Db          5 CATAC 1
|||||
Query Match 100.0%; Score 5; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
US-10-122-630-6
; Sequence 6, Application US/10122630
; Publication No. US20030032610A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-018
; CURRENT APPLICATION NUMBER: US/10/122,630
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 08/467,012
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US96/08386
; PRIOR FILING DATE: 1996-06-03
; PRIOR APPLICATION NUMBER: US 09/048,927
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-6

Query Match 100.0%; Score 5; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

          1 CATAC 5
          |||||
          1 CATAC 5

RESULT 3
US-10-122-633-4/c
; Sequence 4, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-4

Query Match 100.0%; Score 5; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

          1 CATAC 5
          |||||
          1 CATAC 5

RESULT 4
US-10-122-633-6
; Sequence 6, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Eller, Mark S.
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE OF INVENTION: Oligonucleotides
; FILE REFERENCE: 0054.1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 5
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-6

Query Match 100.0%; Score 5; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

          1 CATAC 5
          |||||
          1 CATAC 5

RESULT 5
US-10-027-632-178029
; Sequence 178029, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178029
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; LENGTH: 7  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-178029

Query Match 100.0%; Score 5; DB 13; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.8e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
Db 1 CATAC 5

## RESULT 6

US-10-027-632-178043  
Sequence 178043, Application US/10027632  
Publication No. US20030204075A9  
GENERAL INFORMATION:

APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 178043

LENGTH: 7

TYPE: DNA

ORGANISM: Human

US-10-027-632-178043

Query Match 100.0%; Score 5; DB 13; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.8e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
Db 1 CATAC 5

## RESULT 7

US-10-027-632-178029  
Sequence 178029, Application US/10027632  
Publication No. US20030032610A1  
GENERAL INFORMATION:

APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 178029  
; LENGTH: 7  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-178029

Query Match 100.0%; Score 5; DB 14; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.8e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
Db 1 CATAC 5

## RESULT 8

US-10-027-632-178043  
Sequence 178043, Application US/10027632  
Publication No. US20030032610A1  
GENERAL INFORMATION:

APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 178043

LENGTH: 7

TYPE: DNA

ORGANISM: Human

US-10-027-632-178043

Query Match 100.0%; Score 5; DB 14; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.8e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
Db 1 CATAC 5

## RESULT 9

US-10-122-630-3/c  
Sequence 3, Application US/10122630  
Publication No. US20030032610A1  
GENERAL INFORMATION:

APPLICANT: Gilchrist, Barbara A.

APPLICANT: Eller, Mark S.

APPLICANT: Yaar, Mina

; TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
; FILE REFERENCE: 0054.1088-018  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US 08/122,630  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: PCT/US96/08386  
; PRIOR FILING DATE: 1996-06-03  
; PRIOR APPLICATION NUMBER: US 09/048,927  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: US 09/540,843  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: PCT/US01/10162  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 7  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
; OTHER INFORMATION: Synthetic DNA Fragment  
US-10-122-630-3  
Query Match 100.0%; Score 5; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.8e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATAC 5  
|||||  
6 CATAC 2

RESULT 10  
US-10-122-630-7/c  
; Sequence 7, Application US/10122630  
; Publication No. US20030032610A1  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrest, Barbara A.  
; APPLICANT: Eller, Mark S.  
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
; FILE REFERENCE: 0054.1088-018  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US 08/122,630  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: PCT/US96/08386  
; PRIOR FILING DATE: 1996-06-03  
; PRIOR APPLICATION NUMBER: US 09/048,927  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: US 09/540,843  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: PCT/US01/10162  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 7  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
; OTHER INFORMATION: Synthetic DNA Fragment  
US-10-122-630-7  
Query Match 100.0%; Score 5; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.8e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
|||||

Db 6 CATAC 2  
RESULT 11  
US-10-122-633-3/c  
; Sequence 3, Application US/10122633  
; Publication No. US20030032611A1  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrest, Barbara A.  
; APPLICANT: Eller, Mark S.  
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
; FILE REFERENCE: 0054.1088-019  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US 09/540,843  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: PCT/US01/10162  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 7  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
; OTHER INFORMATION: Synthetic DNA Fragment  
US-10-122-633-3  
Query Match 100.0%; Score 5; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.8e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
|||||  
6 CATAC 2

RESULT 12  
US-10-122-633-7/c  
; Sequence 7, Application US/10122633  
; Publication No. US20030032611A1  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrest, Barbara A.  
; APPLICANT: Eller, Mark S.  
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
; FILE REFERENCE: 0054.1088-019  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US 09/540,843  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: PCT/US01/10162  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 7  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
; OTHER INFORMATION: Synthetic DNA Fragment  
US-10-122-633-7  
Query Match 100.0%; Score 5; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.8e+08;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAC 5  
|||||  
6 CATAC 2

RESULT 13  
US-09-142-593-11  
; Sequence 11, Application US/09142593  
; Patent No. US20020016975A1  
; GENERAL INFORMATION:  
; APPLICANT: HACKETT ET AL.  
; TITLE OF INVENTION: DNA-BASED TRANSPONSON SYSTEM FOR THE  
; INTRODUCTION OF NUCLEIC ACID INTO DNA OF A CELL  
; NUMBER OF SEQUENCES: 63  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.  
; STREET: 119 NORTH FOURTH STREET, SUITE 203  
; CITY: MINNEAPOLIS  
; STATE: MINNESOTA  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/142,593  
; FILING DATE: 10-SEP-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/040,664  
; FILING DATE: 11-MAR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/053,868  
; FILING DATE: 28-JUL-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/065,303  
; FILING DATE: 13-NOV-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US98/04687  
; FILING DATE: 11-MAR-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SANDBERG, VICTORIA A.  
; REGISTRATION NUMBER: 41,287  
; REFERENCE/DOCKET NUMBER: 110.00450101  
; TELEPHONE: 612-305-1226  
; TELEFAX: 612-305-1228  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-09-142-593-11

Query Match 100.0%; Score 5; DB 9; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.2e+08;  
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QY 1 CATAC 5  
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US-09-927-886-17  
; Sequence 17, Application US/09927886  
; Patent No. US20020103152A1  
; GENERAL INFORMATION:  
; APPLICANT: Kay, Mark A.  
; APPLICANT: Yant, Stephen  
; TITLE OF INVENTION: Methods of In Vivo Gene Transfer Using a  
; Sleeping Beauty Transposon System

; FILE REFERENCE: STAN-160CIP  
; CURRENT APPLICATION NUMBER: US/09/927,886  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/162,279  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: 09/440,301  
; PRIOR FILING DATE: 1999-11-17  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 8  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: transposon repeat sequence  
US-09-927-886-17

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US-09-861-014-6  
; Sequence 6, Application US/09861014  
; Patent No. US20020115216A1  
; GENERAL INFORMATION:  
; APPLICANT: Steer, Clifford  
; APPLICANT: Kren, Betsy  
; APPLICANT: Linehan-Stieers, Cheryle  
; APPLICANT: McIvor, R.  
; APPLICANT: Hackett, Perry  
; TITLE OF INVENTION: Composition for Delivery of Compounds to Cells  
; FILE REFERENCE: 110.01330101  
; CURRENT APPLICATION NUMBER: US/09/861,014  
; CURRENT FILING DATE: 2001-05-19  
; PRIOR APPLICATION NUMBER: US 60/206,002  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: US 60/285,121  
; PRIOR FILING DATE: 2001-04-20  
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DB 2 CATAC 6

Search completed: January 1, 2004, 01:10:37  
Job time : 58.2911 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 11:36:21 ; Search time 644.443 Seconds  
(without alignments)  
444.364 Million cell updates/sec

Title: US-09-540-843-7  
Perfect score: 7  
Sequence: 1 agtatga 7

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 1010434

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
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Listing first 45 summaries

Database :

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- 2: gb\_htg:\*\*
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- 13: gb\_un:\*\*
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- 15: em\_ba:\*\*
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- 17: em\_hum:\*\*
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- 35: em\_htg\_rod:\*\*
- 36: em\_htg\_man:\*\*
- 37: em\_htg\_vrt:\*\*
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- 41: em\_htgo\_other:\*\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	7	100.0	7	6	AX268759 Sequence
3	7	100.0	9	6	AX268753 Sequence
C 4	7	100.0	10	6	AX377258 Sequence
C 5	7	100.0	10	6	AX573597 Sequence
C 6	7	100.0	10	6	AX573610 Sequence
8	7	100.0	10	6	BD007857 LPS activ
9	7	100.0	10	6	BD083254 Human mat
10	7	100.0	11	6	AX470905 Sequence
11	7	100.0	11	6	AX624159 Sequence
12	7	100.0	11	6	AX624334 Sequence
C 13	7	100.0	11	6	AX625574 Sequence
14	7	100.0	11	6	AX626182 Sequence
15	7	100.0	11	6	AX626780 Sequence
C 16	7	100.0	11	6	AX629189 Sequence
17	7	100.0	11	6	AX631580 Sequence
18	7	100.0	12	6	AX631755 Sequence
C 19	7	100.0	12	6	A91497 Sequence 24
C 20	7	100.0	12	6	AX573600 Sequence
C 21	7	100.0	12	6	AX573602 Sequence
C 22	7	100.0	13	6	BD023279 Method fo
23	7	100.0	13	6	AR285089 Sequence
C 24	7	100.0	13	6	AX018746 Sequence
C 25	7	100.0	13	6	AX523264 Sequence
26	7	100.0	14	6	A33152 Synthetic H
27	7	100.0	14	6	AR082813 Sequence
C 28	7	100.0	14	6	AR088823 Sequence
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C 30	7	100.0	14	6	AX343036 Sequence
31	7	100.0	15	6	A33153 Synthetic H
C 32	7	100.0	15	6	AR041154 Sequence
C 33	7	100.0	15	6	AR082814 Sequence
C 34	7	100.0	15	6	AR130719 Sequence
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C 39	7	100.0	15	6	AX377250 Sequence
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42	7	100.0	15	6	AX638053 Sequence
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ALIGNMENTS

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DEFINITION	AX268755	Sequence 3 from Patent WO0174342.				
ACCESSION	AX268755.1	GI:16541827				
VERSION	AX268755.1	GI:16541827				
KEYWORDS		synthetic construct				
SOURCE		synthetic construct				
ORGANISM		artificial sequences.				
REFERENCE	1					
AUTHORS	Gilchrest,B.A., Yaar,M. and Eller,M.					
TITLE	Use of locally applied dna fragments					
JOURNAL	Patent: WO 0174342-A 3 11-OCT-2001;					
	TRUSTEES OF BOSTON UNIVERSITY (US)					

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DEFINITION Sequence 7 from Patent WO0174342.
ACCESSION AX268759
VERSION AX268759.1 GI:16541831
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Gilchrist,B.A., Yaar,M. and Eller,M.
TITLE Use of locally applied dna fragments
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DEFINITION Sequence 1 from Patent WO0174342.
ACCESSION AX268753
VERSION AX268753.1 GI:16541825
KEYWORDS
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ORGANISM
REFERENCE
AUTHORS Gilchrist,B.A., Yaar,M. and Eller,M.
TITLE Use of locally applied dna fragments
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DEFINITION Sequence 20 from Patent WO0212562.
ACCESSION AX377258
VERSION AX377258.1 GI:19573546
KEYWORDS
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ORGANISM
REFERENCE
AUTHORS Kazemi,A., Klien,S.E. and Koshy,B.
TITLE Haplotypes of the pla2glb gene
JOURNAL Patent: WO 0212562-A 20 14-FEB-2002;
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DEFINITION Sequence 7 from Patent WO02079467.
ACCESSION AX573597
VERSION AX573597.1 GI:27551267
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Nielsen,P.E. and Good,L.
TITLE Antibiotic-free bacterial strain selection with antisense molecules
JOURNAL Patent: WO 02079467-A 7 10-OCT-2002;
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VERSION     AX573610.1  GI:27551280
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            artificial sequences.
SOURCE      1
ORGANISM    1
            Nielsen, P.E. and Good, L.
REFERENCE   1
AUTHORS     Nielsen, P.E. and Good, L.
TITLE       Antibiotic-free bacterial strain selection with antisense molecules
JOURNAL     Patent: WO 02079467-A 20 10-OCT-2002;
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LOCUS      10 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION  BD007857
VERSION     BD007857.1  GI:18636230
KEYWORDS    JP 2001069993-A/133.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens (human)
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Matsushima, K., Hashimoto, S. and Suzuki, T.
TITLE       LPS activated human monocyte expressing genes
JOURNAL     Patent: JP 2001069993-A 133 21-MAR-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS Homo sapiens (human)
            PN JP 2001069993-A/133
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            PR KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI PC
            C12N15/09, C07K14/47, C07K16/18, G01N33/50, G01N33/53/A61K45/00, PC
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LOCUS      10 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Human matured/activated dendritic cell expression genes.
ACCESSION  BD083254
VERSION     BD083254.1  GI:22628864
KEYWORDS    JP 2001327293-A/175.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Matsushima, K., Hashimoto, S., Suzuki, T. and Nagai, S.
TITLE       Human matured/activated dendritic cell expression genes
JOURNAL     Patent: JP 2001327293-A 175 27-NOV-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS Homo sapiens (human)
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ACCESSION  AX470905
VERSION     AX470905.1  GI:22206030
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SOURCE      Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Hofmann, K., Conrad, M. and Petersohn, D.
TITLE       Method for determining skin stress or skin ageing in vitro
JOURNAL     Patent: WO 02053773-A 482 11-JUL-2002;
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DEFINITION Sequence 1200 from Patent WO02053774.
ACCESSION AX624159
VERSION AX624159.1 GI:28452100
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1200 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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ACCESSION AX624334
VERSION AX624334.1 GI:28452275
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1375 11-JUL-2002;
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KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2615 11-JUL-2002;
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ACCESSION AX626182
VERSION AX626182.1 GI:28454220
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3223 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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KEYWORDS
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ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 3821 11-JUL-2002;
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DEFINITION Sequence 6230 from Patent WO02053774.
ACCESSION AX629189
VERSION AX629189.1 GI:28457227
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 6230 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
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Query Match 100.0%; Score 7; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. NO. 9.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGTATGA 7
b 10 AGTATGA 4

```

Search completed: December 31, 2003, 17:09:47  
 Job time : 644.443 secs



```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 10
; OTHER INFORMATION: /note="Donor chromophore at the 3' T nucleotide"
; US-08-232-233-1

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.6e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTATG 5
pb      |||||
        8 GTATG 4

Search completed: January 1, 2004, 00:32:18
Job time : 19.5415 secs

```





```

RESULT 2
; US-09-048-927-1
; Sequence 1, Application US/09048927
; Patent No. 6147056
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Yaar, Mina
; APPLICANT: Eller, Mark
; TITLE OF INVENTION: Use of Locally Applied DNA Fragments
; FILE REFERENCE: BU94-68A2
; CURRENT APPLICATION NUMBER: US/09/048,927
; CURRENT FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/952,697
; EARLIER FILING DATE: 1996-06-03
; EARLIER APPLICATION NUMBER: 08/467,012

```

EARLIER FILING DATE: 1995-06-06  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 9  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: DNA Fragment  
US-09-048-927-1

Query Match 100.0%; Score 7; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+07;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7  
|||||  
2 AGTATGA 8

RESULT 3  
US-09-922-445-12/c  
Sequence 12, Application US/09922445  
Patent No. 6528268  
GENERAL INFORMATION:  
APPLICANT: Andersson, Maria K.  
APPLICANT: Berglund, Lars G. T.  
APPLICANT: Reneland, Rikard H.  
APPLICANT: Adam, Gail I. R.  
TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTION OF HEART FAILURE  
FILE REFERENCE: GG126US  
CURRENT APPLICATION NUMBER: US/09/922,445  
CURRENT FILING DATE: 2001-08-03  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 12  
LENGTH: 13  
TYPE: DNA  
ORGANISM: synthetic  
US-09-922-445-12

Query Match 100.0%; Score 7; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7  
|||||  
9 AGTATGA 3

RESULT 4  
US-09-922-445-22  
Sequence 22, Application US/09922445  
Patent No. 6528268  
GENERAL INFORMATION:  
APPLICANT: Andersson, Maria K.  
APPLICANT: Berglund, Lars G. T.  
APPLICANT: Reneland, Rikard H.  
APPLICANT: Adam, Gail I. R.  
TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTION OF HEART FAILURE  
FILE REFERENCE: GG126US  
CURRENT APPLICATION NUMBER: US/09/922,445  
CURRENT FILING DATE: 2001-08-03  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 22  
LENGTH: 13  
TYPE: DNA  
ORGANISM: synthetic  
US-09-922-445-22

Query Match 100.0%; Score 7; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 8.6e+03;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AGTATGA 7  
|||||  
Db 5 AGTATGA 11

RESULT 5  
US-08-485-133-27  
Sequence 27, Application US/08485133  
Patent No. 5976789  
GENERAL INFORMATION:  
APPLICANT: Allibert, Patrice A.  
APPLICANT: Cros, Philippe  
APPLICANT: Mach, Bernard F.  
APPLICANT: Mandrand, Bernard F.  
APPLICANT: Tiercy, Jean-Marie  
TITLE OF INVENTION: SYSTEM OF PROBES ENABLING HLA-DR TYPING  
TITLE OF INVENTION: TO BE PERFORMED, AND TYPING METHOD USING SAID PROBES  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OLIFF & BERRIDGE  
STREET: P.O. Box 19928  
CITY: Alexandria  
STATE: Virginia  
ZIP: 22320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,133  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER:  
APPLICATION NUMBER: US 08/030,143  
FILING DATE: 11-MAR-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Berridge, William P.  
REGISTRATION NUMBER: 30,024  
REFERENCE/DOCKET NUMBER: WPB 28596A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6400  
TELEFAX: 703-836-2787  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-485-133-27

Query Match 100.0%; Score 7; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7  
|||||  
Db 8 AGTATGA 14

RESULT 6  
US-08-744-905A-4/c  
Sequence 4, Application US/08744905A  
Patent No. 5990294  
GENERAL INFORMATION:  
APPLICANT: Murphy, Gerald  
APPLICANT: Boynton, Alton  
APPLICANT: Sehgal, Anil  
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID  
TITLE OF INVENTION: SEQUENCES OF C4-2, A TUMOR SUPPRESSOR GENE,

```

; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/744,905A
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Baldwin, Geraldine P
; REGISTRATION NUMBER: 31,232
; REFERENCE/DOCKET NUMBER: 8511-009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)7909090
; TELEFAX: 66141 PENNIE
; TELEX: (212)8698864
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified Base
; LOCATION: 1
; OTHER INFORMATION: Where N is any nucleotide
;
;
; Query Match 100.0%; Score 7; DB 2; Length 14;
; Best Local Similarity 100.0%; Pred. No. 8.6e+03;
; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
;
; 1 AGTATGA 7
; |||||
; 14 AGTATGA 8
;
;
; RESULT 7
; NS-08-334-847-24
; Sequence 24, Application US/08334847
; Patent No. 5693532
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Draper, Kenneth
; APPLICANT: Pavco, Pan
; APPLICANT: Woolf, Tod
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; OPERATING SYSTEM: INHIBITING RESPIRATORY
; TITLE OF INVENTION: SYNCYTIAL VIRUS
; NUMBER OF SEQUENCES: 909
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;
;
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; OPERATING SYSTEM: INHIBITING RESPIRATORY
; TITLE OF INVENTION: SYNCYTIAL VIRUS
; NUMBER OF SEQUENCES: 909
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;

```

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; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/334,847
; FILING DATE: NO. 5693532ember 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-334-847-24
;
; Query Match 100.0%; Score 7; DB 1; Length 15;
; Best Local Similarity 71.4%; Pred. No. 8.6e+03;
; Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
;
;
; QY 1 AGTATGA 7
; |||||
; DB 5 AGAUGA 11
;
;
; RESULT 8
; US-08-334-847-327
; Sequence 327, Application US/08334847
; Patent No. 5693532
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Draper, Kenneth
; APPLICANT: Pavco, Pan
; APPLICANT: Woolf, Tod
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; OPERATING SYSTEM: INHIBITING RESPIRATORY
; TITLE OF INVENTION: SYNCYTIAL VIRUS
; NUMBER OF SEQUENCES: 909
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;
;
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; OPERATING SYSTEM: INHIBITING RESPIRATORY
; TITLE OF INVENTION: SYNCYTIAL VIRUS
; NUMBER OF SEQUENCES: 909
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;
;
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; OPERATING SYSTEM: INHIBITING RESPIRATORY
; TITLE OF INVENTION: SYNCYTIAL VIRUS
; NUMBER OF SEQUENCES: 909
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;

```

TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 327:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-334-847-327

Query Match 100.0%; Score 7; DB 1; Length 15;  
Best Local Similarity 71.4%; Pred. No. 8.6e+03;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7  
||:|:  
5 AGAUGA 11

RESULT 9  
US-08-671-071B-2/c  
Sequence 2, Application US/08671071B  
Patent No. 5811270  
GENERAL INFORMATION:

APPLICANT: Grandgenett, Duane  
TITLE OF INVENTION: An in vitro method for concerted integration of  
TITLE OF INVENTION: donor DNA molecules using retroviral integrase proteins.  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Grandgenett, Duane  
STREET: 8610 Henrietta Ave  
CITY: Brentwood  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63144

COMPUTER READABLE FORM:  
MEDIUM TYPE: Distette, 3.5 inch;  
COMPUTER: Gateway 2000, 4DX2-66E(Intel)  
OPERATING SYSTEM: IBM clone

SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/671,071B  
FILING DATE: 06/27/96  
CLASSIFICATION: 435

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 962-0064  
TELEFAX: (314) 577-8406

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 bases

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

HYPOTHETICAL: no

ANTI-SENSE: no

ORIGINAL SOURCE: Combination of avian or HIV-1 retrovirus

ORIGINAL SOURCE: DNA, p1an7 plasmid and pGEM plasmid.

IMMEDIATE SOURCE: Same as in 2,vi.

FEATURE:

OTHER INFORMATION: The sequence is the bottom strand of

OTHER INFORMATION: M-2 U5 and the pGEM target of the top clone shown in

OTHER INFORMATION: Figure 14 of original application.

US-08-671-071B-2

Query Match 100.0%; Score 7; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7  
|||||  
9 AGTATGA 3

## RESULT 10

US-08-747-121-4/c

Sequence 4, Application US/08747121

Patent No. 5874290

GENERAL INFORMATION:

APPLICANT: Murphy, Gerald

APPLICANT: Boynton, Alton

APPLICANT: Sehgal, Anil

TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID

TITLE OF INVENTION: SEQUENCES OF A D2-2 GENE ASSOCIATED WITH

TITLE OF INVENTION: BRAIN TUMORS AND METHODS BASED THEREON

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/747,121

FILING DATE: 08-NOV-1996

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Baldwin, Geraldine F

REGISTRATION NUMBER: 31,232

REFERENCE/DOCKET NUMBER: 8511-008

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)7909090

TELEFAX: (212)8698864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: Modified Base

LOCATION: 1

OTHER INFORMATION: Where N is any nucleotide

US-08-747-121-4

Query Match 100.0%; Score 7; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 8.6e+03;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7

Db 15 AGTATGA 9

## RESULT 11

US-08-585-684B-130

Sequence 130, Application US/08585684B

Patent No. 5877021

GENERAL INFORMATION:

APPLICANT: Stinchcomb, Daniel T.

APPLICANT: Jarvis, Thale

APPLICANT: McSwiggen, James

TITLE OF INVENTION: METHOD AND REAGENT FOR THE

TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE

TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES

```

; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/585,684B
; FILING DATE: January 16, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/000,951
; FILING DATE: July 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 130:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-585-684B-130

Query Match 100.0%; Score 7; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 8.6e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7
||:|:|
5 AGUAUGA 11

; US-08-585-684B-1315
; Sequence 1315, Application US/08585684B
; Patent No. 5877021
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/08/585,684B
; FILING DATE: January 16, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/000,951
; FILING DATE: July 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1315:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-585-684B-1315

Query Match 100.0%; Score 7; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 8.6e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATGA 7
Db 5 AGUAUGA 11

; US-08-485-133-28
; Sequence 28, Application US/08485133
; Patent No. 5976789
; GENERAL INFORMATION:
; APPLICANT: Allibert, Patrice A.
; APPLICANT: Cros, Philippe
; APPLICANT: Mach, Bernard F.
; APPLICANT: Mandrand, Bernard F.
; APPLICANT: Tiercy, Jean-Marie
; TITLE OF INVENTION: SYSTEM OF PROBES ENABLING HLA-DR TYPING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE
; STREET: P.O. Box 19928
; CITY: Alexandria
; STATE: Virginia
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,133
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/030,143
; FILING DATE: 11-MAR-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 28596A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid

```

STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-485-133-28

Query Match 100.0%; Score 7; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7  
Db 9 AGTATGA 15

RESULT 14  
US-09-094-714A-33/C  
Sequence 33, Application US/09094714A  
Patent No. 6117847

GENERAL INFORMATION:  
APPLICANT: C. Frank Bennett, Nicholas M. Dean  
TITLE OF INVENTION: OLIGONUCLEOTIDES FOR ENHANCED MODULATION OF  
TITLE OF INVENTION: PROTEIN KINASE C EXPRESSION  
NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6117847ris, LLP  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103

COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 8.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/094,714A  
FILING DATE: June 15, 1998  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/601,269  
FILING DATE: 14-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/478,178  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/089,996  
FILING DATE: 09-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/852,852  
FILING DATE: 16-MAR-1992

ATTORNEY/AGENT INFORMATION:  
NAME: Paul K. Legard  
REGISTRATION NUMBER: 38,534  
REFERENCE/DOCKET NUMBER: ISIS-2943  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-09-094-714A-33

Query Match 100.0%; Score 7; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7  
Db 12 AGTATGA 6

RESULT 15

US-09-094-714A-34/C  
Sequence 34, Application US/09094714A  
Patent No. 6117847

GENERAL INFORMATION:  
APPLICANT: C. Frank Bennett, Nicholas M. Dean  
TITLE OF INVENTION: OLIGONUCLEOTIDES FOR ENHANCED MODULATION OF  
TITLE OF INVENTION: PROTEIN KINASE C EXPRESSION  
NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6117847ris, LLP  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103

COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 8.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/094,714A  
FILING DATE: June 15, 1998  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/601,269  
FILING DATE: 14-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/478,178  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/089,996  
FILING DATE: 09-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/852,852  
FILING DATE: 16-MAR-1992

ATTORNEY/AGENT INFORMATION:  
NAME: Paul K. Legard  
REGISTRATION NUMBER: 38,534  
REFERENCE/DOCKET NUMBER: ISIS-2943  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-09-094-714A-34

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Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7  
Db 14 AGTATGA 8

Search completed: January 1, 2004, 00:32:18  
Job time : 27.3136 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 11:36:21 ; Search time 828.57 Seconds  
(without alignments)  
444.364 Million cell updates/sec

Title: US-09-540-843-1  
Perfect score: 9  
Sequence: 1 gagtatgag 9

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 1010434

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	9	100.0	10	6	AX573597	AX573597 Sequence
3	9	100.0	10	6	AX573610	AX573610 Sequence
4	9	100.0	12	6	AX573600	AX573600 Sequence
5	9	100.0	15	6	ARI30719	ARI30719 Sequence
6	9	100.0	15	6	ARI30720	ARI30720 Sequence
7	9	100.0	17	6	AR039517	AR039517 Sequence
8	9	100.0	17	6	AR039519	AR039519 Sequence
9	9	100.0	17	6	AR039521	AR039521 Sequence
10	9	100.0	17	6	AR039523	AR039523 Sequence
11	9	100.0	17	6	AX693123	AX693123 Sequence
12	9	100.0	17	6	AX693124	AX693124 Sequence
13	9	100.0	17	6	AX693125	AX693125 Sequence
14	9	100.0	17	6	AX693126	AX693126 Sequence
15	9	100.0	17	6	AX693127	AX693127 Sequence
16	9	100.0	17	6	AX693128	AX693128 Sequence
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18	9	100.0	17	6	AX693130	AX693130 Sequence
19	9	100.0	17	6	AX693131	AX693131 Sequence
20	9	100.0	18	6	AX306555	AX306555 Sequence
21	9	100.0	19	6	AX709273	AX709273 Sequence
22	9	100.0	20	6	ARI16520	ARI16520 Sequence
23	9	100.0	20	6	ARI16521	ARI16521 Sequence
24	9	100.0	20	6	AR213251	AR213251 Sequence
25	9	100.0	20	6	AR229019	AR229019 Sequence
26	9	100.0	20	6	AR230824	AR230824 Sequence
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38	9	100.0	23	6	AX404121	AX404121 Sequence
39	9	100.0	24	6	AX493338	AX493338 Sequence
40	9	100.0	25	6	AX454970	AX454970 Sequence
41	9	100.0	25	6	AX693696	AX693696 Sequence
42	9	100.0	25	6	AX693697	AX693697 Sequence
43	9	100.0	25	6	AX693698	AX693698 Sequence
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ACCESSION	AX268753	Sequence 1 from Patent WO0174342.				
VERSION	AX268753.1	GI:16541825				
KEYWORDS		synthetic construct				
SOURCE		synthetic construct				
ORGANISM		artificial sequences.				
REFERENCE	1					
AUTHORS		Gilchrest,B.A., Yaar,M. and Eller,M.				
TITLE		Use of locally applied dna fragments				
JOURNAL		Patent: WO 0174342-A 1 11-OCT-2001;				
		TRUSTEES OF BOSTON UNIVERSITY (US)				

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    artificial sequences.
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  AUTHORS
    Nielsen, P.E. and Good, L.
  TITLE
    Antibiotic-free bacterial strain selection with antisense molecules
  JOURNAL
    Patent: WO 02079467-A 7 10-OCT-2002;
    Koebenhavns Universitet (DK)
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  REFERENCE
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  AUTHORS
    Nielsen, P.E. and Good, L.
  TITLE
    Antibiotic-free bacterial strain selection with antisense molecules
  JOURNAL
    Patent: WO 02079467-A 20 10-OCT-2002;
    Koebenhavns Universitet (DK)
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  REFERENCE
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  AUTHORS
    Nielsen, P.E. and Good, L.
  TITLE
    Antibiotic-free bacterial strain selection with antisense molecules
  JOURNAL
    Patent: WO 02079467-A 10 10-OCT-2002;
    Koebenhavns Universitet (DK)
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  VERSION
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  KEYWORDS
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  SOURCE
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  ORGANISM
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  REFERENCE
    1 (bases 1 to 15)
  AUTHORS
    Nielsen, P.E. and Good, L.
  TITLE
    Methods of bacterial gene function determination using peptide
  JOURNAL
    Patent: US 6190866-A 6 20-FEB-2001;
    Koebenhavns Universitet (DK)
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QY 1 GAGTATGAG 9  
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DEFINITION Sequence 7 from patent US 6190866.  
ACCESSION AR130720  
VERSION AR130720.1 GI:14119045  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 15)  
AUTHORS Nielsen, P.E. and Good, L.  
TITLE Methods of bacterial gene function determination using peptide nucleic acids  
JOURNAL Patent: US 6190866-A 7 20-FEB-2001;  
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DEFINITION Sequence 365 from patent US 5807743.  
ACCESSION AR039517  
VERSION AR039517.1 GI:5958880  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)  
AUTHORS Stinchcomb, D.T. and McSwiggen, J.A.  
TITLE Interleukin-2 receptor gamma-chain ribozymes  
JOURNAL Patent: US 5807743-A 365 15-SEP-1998;  
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DEFINITION Sequence 367 from patent US 5807743.  
ACCESSION AR039519  
VERSION AR039519.1 GI:5958882  
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SOURCE Unknown.  
ORGANISM Unknown.

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DEFINITION Sequence 369 from patent US 5807743.  
ACCESSION AR039521  
VERSION AR039521.1 GI:5958884  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)  
AUTHORS Stinchcomb, D.T. and McSwiggen, J.A.  
TITLE Interleukin-2 receptor gamma-chain ribozymes  
JOURNAL Patent: US 5807743-A 369 15-SEP-1998;  
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ACCESSION AR039523  
VERSION AR039523.1 GI:5958886  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)  
AUTHORS Stinchcomb, D.T. and McSwiggen, J.A.  
TITLE Interleukin-2 receptor gamma-chain ribozymes  
JOURNAL Patent: US 5807743-A 371 15-SEP-1998;  
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AUTHORS Stinchcomb, D.T. and McSwiggen, J.A.  
TITLE Interleukin-2 receptor gamma-chain ribozymes  
JOURNAL Patent: US 5807743-A 367 15-SEP-1998;  
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ACCESSION AR039521  
VERSION AR039521.1 GI:5958884  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)  
AUTHORS Stinchcomb, D.T. and McSwiggen, J.A.  
TITLE Interleukin-2 receptor gamma-chain ribozymes  
JOURNAL Patent: US 5807743-A 369 15-SEP-1998;  
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ACCESSION AR039523  
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SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)  
AUTHORS Stinchcomb, D.T. and McSwiggen, J.A.  
TITLE Interleukin-2 receptor gamma-chain ribozymes  
JOURNAL Patent: US 5807743-A 371 15-SEP-1998;  
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ACCESSION AX693123
VERSION AX693123.1 GI:29416087
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL mdz12
Patent: EP 1281758-A 5855 05-FEB-2003;
Aeomica, Inc. (US)
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ACCESSION AX693124
VERSION AX693124.1 GI:29416088
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL mdz12
Patent: EP 1281758-A 5856 05-FEB-2003;
Aeomica, Inc. (US)
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DEFINITION Sequence 5857 from Patent EP1281758.
ACCESSION AX693125
VERSION AX693125.1 GI:29416089
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL mdz12
Patent: EP 1281758-A 5857 05-FEB-2003;
Aeomica, Inc. (US)
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DEFINITION Sequence 5858 from Patent EP1281758.
ACCESSION AX693126
VERSION AX693126.1 GI:29416090
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL mdz12
Patent: EP 1281758-A 5858 05-FEB-2003;
Aeomica, Inc. (US)
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BASE COUNT 3 a 5 c 0 g 9 t
ORIGIN
Query Match 100.0%; Score 9; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GAGTATGAG 9
14 GAGTATGAG 6

RESULT 15
AX693127/c
LOCUS 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5859 from Patent EP1281758.
ACCESSION AX693127

```

```

VERSION      AX693127.1  GI:29416091
KEYWORDS
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1 Shannon,M., Gu,Y. and Nguyen,C.T.
AUTHORS      Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
TITLE        mdz12
JOURNAL      Patent: EP 1281758-A 5859 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES     source
              1..17
              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT   3 a 5 c 1 g 8 t
ORIGIN
Query Match 100.0%; Score 9; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GAGTATGAG 9
|||||
13 GAGTATGAG 5
Search completed: December 31, 2003, 17:09:38
Job time : 830.57 secs

```





PT DNA fragments useful for increasing p53 activity in a cell and reducing  
 PT susceptibility to UV-induced hyperproliferative diseases -  
 PS Claim 11; Page 29; 44pp; English.

CC AA210692-97 represent DNA fragments that are used for increasing p53  
 CC activity in a cell. The oligonucleotides are are UV mimetics and  
 CC protect cells against subsequent exposure to UV-irradiation or  
 CC chemicals. The oligonucleotides are useful for increasing p53 activity  
 CC in a cell, reducing the susceptibility to UV-induced hyperproliferative  
 CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic  
 CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging  
 CC and reducing susceptibility to skin cancer.

XX Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;

SQ Query Match 100.0%; Score 9; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+08;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GAGTATGAG 9  
 |||||  
 1 GAGTATGAG 9

RESULT 2  
 AAS14905  
 AAS14905 standard; DNA; 9 BP.

AAS14905;

14-FEB-2002 (first entry)

Melanogenesis associated oligonucleotide #1.

Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;  
 anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;  
 immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;  
 tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;  
 carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;  
 conjunctivitis; allergic rhinitis; vitiligo; ss.

Synthetic.

Key Location/Qualifiers  
 modified\_base 1  
 /\*tag= a  
 /mod\_base= g  
 /note= "Optionally phosphorylated"

WO200174342-A2.

11-OCT-2001.

30-MAR-2001; 2001WO-US10162.

31-MAR-2000; 2000US-0540843.

(UYBO-) UNIV BOSTON.

Gilchreest BA, Yaar M, Eller M;

WPI; 2001-626338/72.

Inhibiting proliferation of epithelial cells, useful e.g. for treating  
 carcinoma, using specific oligonucleotides that mimic the effects of  
 ultra-violet light -

Claim 1; Page 36; 74pp; English.

The invention describes inhibition of mammalian epithelial cell  
 proliferation by treating cells with at least one oligonucleotide, or  
 its fragment. The compounds, which have cytostatic, anti-allergic,

CC anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and  
 CC immunosuppressive activities, function as 'ultra-violet mimics' to induce  
 CC DNA repair processes (or a protective response to later exposure to  
 CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer  
 CC or a tumour necrosis factor inhibitor. Probably they mimic products of  
 CC DNA damage, or processed DNA-damage intermediates, by inducing the p53  
 CC pathway, resulting in transient arrest of cell growth, allowing more time  
 CC for DNA repair to occur before cell division takes place. The method is  
 CC especially used to treat carcinoma but may also be used to treat other  
 CC hyperproliferative states (e.g. psoriasis or precancerous conditions);  
 CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat  
 CC allergically mediated inflammation (atopic or contact dermatitis,  
 CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in  
 CC cells caused by radiation or chemicals; increase melanin production  
 CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to  
 CC promote apoptosis in epithelial cells that contain damaged DNA. Also  
 CC oligonucleotides that contain non-hydrolyzable backbones are used to  
 CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This  
 CC sequence is melanogenesis associated oligonucleotide #1, one of the  
 CC oligonucleotides used to inhibit mammalian epithelial cell  
 CC proliferation, described in the method of the invention.

XX Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;

SQ Query Match 100.0%; Score 9; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+08;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9  
 |||||  
 Db 1 GAGTATGAG 9

RESULT 3  
 AAL44343/c  
 ID AAL44343 standard; DNA; 10 BP.

XX AAL44343;

XX 24-OCT-2002 (first entry)

XX Peptide nucleic acid (PNA) oligomer #3.

XX PNA oligomer; PNA; peptide nucleic acid; polyamide backbone; ss;  
 KW aminoethylglycine; aeg; aminoethylprolyl; aep; aminoethylpyrrolidine;  
 KW pyr; gene downregulation; bacterial infection; viral infection; cancer;  
 KW metabolic disease; immunological disorder; PNA-clamping.

XX Synthetic.

Key Location/Qualifiers  
 modified\_base 1..10  
 /\*tag= a  
 /mod\_base= OTHER  
 /note= "This sequence is a peptide nucleic acid, (i.e. it  
 contains a polyamide backbone instead of a deoxyribose  
 backbone"

modified\_base 10  
 /\*tag= b  
 /mod\_base= OTHER  
 /note= "The base is modified with Lys-NH2"

XX WO200242316-A2.

XX 30-MAY-2002.

XX 23-NOV-2001; 2001WO-DK00779.

XX 24-NOV-2000; 2000DK-0001776.

XX 06-MAR-2001; 2001DK-0000371.

XX 16-JUL-2001; 2001DK-0001117.

XX (PANT-) PANTHECO AS.

XX PI Nielsen PE, Pueschl A;  
 XX DR WPI; 2002-490198/52.  
 XX XX  
 XX PT New peptide nucleic acid oligomer, useful as antisense molecules to  
 XX PT treat bacterial and viral infections, has single units comprising  
 XX PT different amino acid backbones such as aminoethyglycine -  
 XX XX  
 XX PS Example 7; Page 34; 40pp; English.  
 XX XX  
 XX CC The invention comprises peptide nucleic acid (PNA) oligomers, where the  
 XX CC single units of the oligomers comprise different amino acid backbones  
 XX CC selected from any amino acid, such as: including aminoethyglycine (aeg);  
 XX CC aminoethylprolyl (aep); and aminoethylpyrrolidine (pyr). The PNA  
 XX CC oligomers of the invention are useful for the downregulation of specific  
 XX CC genes by targeting the genes at the mRNA or DNA level. The PNA oligomers  
 XX CC are useful for treating bacterial and viral infections, cancer, metabolic  
 XX CC diseases and immunological disorders. The PNA oligomers are also useful  
 XX CC in PCR monitoring/modulation by PNA-clamping. The present DNA sequence  
 XX CC represents a PNA oligomer of the invention.  
 XX XX  
 XX SE Sequence 10 BP; 2 A; 4 C; 0 G; 4 T; 0 other;  
 XX  
 XX Query Match 100.0%; Score 9; DB 24; Length 10;  
 XX Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 GAGTATGAG 9  
 XX | || || || || || || || ||  
 XX Db 9 GAGTATGAG 1  
 XX  
 XX RESULT 4  
 XX ID ABX15951/C  
 XX AC ABX15951 standard; DNA; 10 BP.  
 XX AC ABX15951;  
 XX  
 XX DT 31-MAR-2003 (first entry)  
 XX XX  
 XX DE Antisense oligonucleotide for the E. coli Acpp gene #1.  
 XX XX  
 XX KW Acpp; antisense; ss; protein nucleic acid; PNA; bacterial infection;  
 XX KW genetically modified micro-organism.  
 XX OS Escherichia coli.  
 XX XX  
 XX PH Key Location/Qualifiers  
 XX modified\_base 1  
 XX /\*tag= a  
 XX /mod\_base= OTHER  
 XX /note= "C is covalently linked to a Lysine residue"  
 XX  
 XX FT misc\_binding 1.1.5  
 XX /tag= b  
 XX /bound moiety= "Bases 15..6 of the acpp sequence  
 XX appearing as ABX15967"  
 XX  
 XX FT misc\_binding 1.1.10  
 XX /tag= c  
 XX /bound moiety= "Bases 15..6 of the acpp sequence  
 XX appearing as ABX15966"  
 XX  
 XX FT modified\_base 10  
 XX /\*tag= d  
 XX /mod\_base= OTHER  
 XX /note= "T is amidated"  
 XX  
 XX PN WO200279467-A2.  
 XX XX  
 XX PD 10-OCT-2002.  
 XX XX  
 XX PF 26-MAR-2002; 2002WO-DK00208.  
 XX XX  
 XX PR 29-MAR-2001; 2001DK-0000523.  
 XX XX  
 XX PA (UYKO-) UNIV KOBENHAVNS.  
 XX XX  
 XX PI Nielsen PE, Good L;  
 XX XX  
 XX DR WPI; 2003-103273/09.  
 XX XX  
 XX PT Selecting genetically modified cells useful for isolation and  
 XX PT industrial growth of transformed organisms comprises treating the  
 XX PT modified cells with an antisense or antigene construct directed against  
 XX PT the essential gene X of the cells -  
 XX XX

PS Claim 24; Page 52; 92pp; English.  
 XX  
 XX CC The invention relates to selecting genetically modified cells comprising:  
 XX CC (a) modifying cells containing a growth essential gene X, with a vector  
 XX CC containing gene Y; and (b) treating the modified cells with an antisense  
 XX CC or antigene construct directed against the essential gene X of the cells  
 XX CC to obtain preferential growth of the modified cells over other non-  
 XX CC modified cells. Also included is a product manufactured fully or  
 XX CC partially by use of the new method. The method is useful for selecting  
 XX CC genetically modified cells and manufacturing a product. It is useful for  
 XX CC research the isolation and industrial growth maintenance of transformed  
 XX CC organisms. The new method has the advantage of selecting and maintaining  
 XX CC a plasmid containing bacterial culture without the use of antibiotics.  
 XX CC This has a wide variety of applications in research, development, and  
 XX CC industrial production involving genetically modified micro-organisms. The  
 XX CC method inhibits bacterial infections in eukaryotic cell cultures.  
 XX CC The present sequence is an antisense oligonucleotide (incorporated into a  
 XX CC peptide nucleic acid (PNA) molecule) which targets the E. coli acpp  
 XX CC gene (Gene X in this example).  
 XX  
 XX SE Sequence 10 BP; 2 A; 4 C; 0 G; 4 T; 0 other;  
 XX  
 XX Query Match 100.0%; Score 9; DB 25; Length 10;  
 XX Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 GAGTATGAG 9  
 XX | || || || || || || || ||  
 XX Db 9 GAGTATGAG 1  
 XX  
 XX RESULT 5  
 XX ID ABX15964/C  
 XX AC ABX15964 standard; DNA; 10 BP.  
 XX AC ABX15964;  
 XX  
 XX DT 31-MAR-2003 (first entry)  
 XX XX  
 XX DE Antisense oligonucleotide for the E. coli Acpp gene, SP4.  
 XX XX  
 XX KW Acpp; antisense; ss; protein nucleic acid; PNA; bacterial infection;  
 XX KW genetically modified micro-organism.  
 XX OS Escherichia coli.  
 XX XX  
 XX PH Key Location/Qualifiers  
 XX modified\_base 1  
 XX /\*tag= a  
 XX /mod\_base= OTHER  
 XX /note= "C is covalently linked to the peptide  
 XX appearing as ABG73942 via a polyethylene glycol moiety"  
 XX  
 XX FT misc\_binding 1.1.5  
 XX /tag= b  
 XX /bound moiety= "Bases 15..6 of the acpp sequence  
 XX appearing as ABX15967"  
 XX  
 XX FT misc\_binding 1.1.10  
 XX /tag= c  
 XX /bound moiety= "Bases 15..6 of the acpp sequence  
 XX appearing as ABX15966"  
 XX  
 XX FT modified\_base 10  
 XX /\*tag= d  
 XX /mod\_base= OTHER  
 XX /note= "T is amidated"  
 XX  
 XX PN WO200279467-A2.  
 XX XX  
 XX PD 10-OCT-2002.  
 XX XX  
 XX PF 26-MAR-2002; 2002WO-DK00208.  
 XX XX  
 XX PR 29-MAR-2001; 2001DK-0000523.  
 XX XX

PA (UYKO-) UNIV KOBENHAVNS.  
XX  
PI Nielsen PE, Good L;  
XX  
DR WPI; 2003-103273/09.  
XX  
PT Selecting genetically modified cells useful for isolation and  
PT industrial growth of transformed organisms comprises treating the  
PT modified cells with an antisense or antigen construct directed against  
PT the essential gene X of the cells -  
XX  
PS Claim 29; Fig 1; 92pp; English.  
XX  
CC The invention relates to selecting genetically modified cells comprising:  
CC (a) modifying cells containing a growth essential gene X, with a vector  
CC containing gene Y; and (b) treating the modified cells with an antisense  
CC or antigen construct directed against the essential gene X of the cells  
CC to obtain preferential growth of the modified cells over other non-  
CC modified cells. Also included is a product manufactured fully or  
CC partially by use of the new method. The method is useful for selecting  
CC genetically modified cells and manufacturing a product. It is useful for  
CC research the isolation and industrial growth maintenance of transformed  
CC organisms. The new method has the advantage of selecting and maintaining  
CC a plasmid containing bacterial culture without the use of antibiotics.  
CC This has a wide variety of applications in research, development, and  
CC industrial production involving genetically modified micro-organisms. The  
CC method inhibits bacterial infections in eukaryotic cell cultures.  
CC The present sequence is an antisense oligonucleotide (incorporated into a  
CC peptide nucleic acid (PNA) molecule) which targets the E. coli acpP  
CC gene (gene X in this example).  
XX  
SQ Sequence 10 BP; 2 A; 4 C; 0 G; 4 T; 0 other;  
XX  
Query Match 100.0%; Score 9; DB 25; Length 10;  
XX Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
1 GAGTATGAG 9  
XXXXXXXXXX  
9 GAGTATGAG 1  
XXXXXXXXXX  
XX  
RESULT 6  
XX ABI05192  
XX ABI05192 standard; DNA; 12 BP.  
XX ABI05192;  
XX  
22-FEB-2002 (first entry)  
XX  
Oligonucleotide primer SEQ ID NO 305165 for detecting SNP TSC0021329.  
XX  
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
Homo sapiens.  
XX  
WO200177384-A2.  
XX  
18-OCT-2001.  
XX  
06-APR-2001; 2001WO-IB00713.  
XX  
07-APR-2000; 2000DE-1019173.  
XX  
(EPITG-) EPIGENOMICS AG.  
XX  
Olek A, Piepenbrock C, Berlin K;  
XX  
WPI; 2001-657177/75.  
XX  
Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single nucleotide polymorphisms and cytosine  
PT methylation status -  
XX  
PS Claim 1; SEQ ID 305165; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation.  
CC AB000010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and  
CC ABT00010-ABT99989 represent the oligomers described in the invention.  
CC NOTE: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 other;  
XX  
Query Match 100.0%; Score 9; DB 23; Length 12;  
XX Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
1 GAGTATGAG 9  
XXXXXXXXXX  
1 GAGTATGAG 9  
XXXXXXXXXX  
XX  
RESULT 7  
XX ABI06838  
XX ABI06838 standard; DNA; 12 BP.  
XX  
AC ABI06838;  
XX  
22-FEB-2002 (first entry)  
XX  
Oligonucleotide primer SEQ ID NO 306811 for detecting SNP TSC0022179.  
XX  
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
Homo sapiens.  
XX  
WO200177384-A2.  
XX  
18-OCT-2001.  
XX  
06-APR-2001; 2001WO-IB00713.  
XX  
07-APR-2000; 2000DE-1019173.  
XX  
(EPITG-) EPIGENOMICS AG.  
XX  
Olek A, Piepenbrock C, Berlin K;  
XX  
WPI; 2001-657177/75.  
XX  
Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single nucleotide polymorphisms and cytosine  
PT methylation status -  
XX  
PS Claim 1; SEQ ID 306811; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation.  
XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and





KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX WO200177384-A2.  
XX 18-OCT-2001.  
XX 06-APR-2001; 2001WO-IB00713.  
XX 07-APR-2000; 2000DE-1019173.  
XX (EPIG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single nucleotide polymorphisms and cytosine  
XX methylation status -  
XX Claim 1; SEQ ID 326072; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX range of diseases including immune system, gastrointestinal, respiratory,  
XX central nervous system, cardiovascular and metabolic disorders. The  
XX oligomers are also used for detecting cell type differentiation.  
XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and  
XX ABT00010-ABT99989 represent the oligomers described in the invention.  
XX NOTE: The sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences.  
XX Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 other;  
XX Query Match 100.0%; Score 9; DB 23; Length 12;  
XX Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX 1 GAGTATGAG 9  
XX |||||  
XX 4 GAGTATGAG 12  
XX  
XX RESULT 11  
XX ABI48017/C  
XX ABI48017 standard; DNA; 12 BP.  
XX AC ABI48017;  
XX DT 22-FEB-2002 (first entry)  
XX DE Oligonucleotide primer SEQ ID NO 347990 for detecting SNP TSC0045390.  
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX WO200177384-A2.  
XX 18-OCT-2001.  
XX 06-APR-2001; 2001WO-IB00713.  
XX 07-APR-2000; 2000DE-1019173.  
XX

XX (EPIG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX designed to detect single nucleotide polymorphisms and cytosine  
XX methylation status -  
XX Claim 1; SEQ ID 347990; 29pp + Sequence Listing; German.  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
XX and cytosine methylation status in chemically pretreated genomic DNA. The  
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
XX range of diseases including immune system, gastrointestinal, respiratory,  
XX central nervous system, cardiovascular and metabolic disorders. The  
XX oligomers are also used for detecting cell type differentiation.  
XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and  
XX ABT00010-ABT99989 represent the oligomers described in the invention.  
XX NOTE: The sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic format from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences.  
XX Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 other;  
XX Query Match 100.0%; Score 9; DB 23; Length 12;  
XX Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX 1 GAGTATGAG 9  
XX |||||  
XX 10 GAGTATGAG 2  
XX  
XX RESULT 12  
XX ABK91038/C  
XX ID ABK91038 standard; DNA; 12 BP.  
XX AC ABK91038;  
XX DT 15-NOV-2002 (first entry)  
XX DE Modified peptide nucleic acid (PNA) molecule #8.  
XX KW Peptide nucleic acid; PNA; bacterial infection; 23S ribosomal RNA; rRNA;  
KW translation; viral infection; cardiac disease; vascular disease;  
KW metabolic disease; diabetes; metabolism; immunological disorder;  
KW Gram-positive; Gram-negative; anti-infective; ss.  
XX Unidentified.  
XX OS Synthetic.  
XX Key Location/Qualifiers  
XX modified\_base 1 /\*tag= a  
XX /mod\_base= OTHER  
XX /note= "OTHER = 5' H and T monomer comprising  
XX N-(2-Boc-aminoethyl)-N-(thymine-1-yl-acetyl)  
XX derived from an unknown amino acid"  
XX modified\_base 4 /\*tag= b  
XX /mod\_base= OTHER  
XX /note= "OTHER = T monomer comprising  
XX N-(2-Boc-aminoethyl)-N-(thymine-1-yl-acetyl)  
XX derived from an unknown amino acid"  
XX modified\_base 7 /\*tag= c  
XX /mod\_base= OTHER  
XX /note= "OTHER = T monomer comprising  
XX N-(2-Boc-aminoethyl)-N-(thymine-1-yl-acetyl)"  
XX

FT modified\_base 12 derived from an unknown amino acid"  
 FT /\*tag= e  
 FT /mod\_base= OTHER  
 FT /note= "OTHER = T monomer comprising  
 FT N-(2-Boc-aminoethyl)-N-(thymine-1-yl-acetyl)lysine  
 FT and is a C-terminal amide"  
 XX WO200253574-A2.  
 XX 11-JUL-2002.  
 XX 03-JAN-2002; 2002WO-DK000005.  
 XX 05-JAN-2001; 2001DK-0000021.  
 XX (PANT-) PANTHECO AS.  
 XX Nielsen PE, Manoharan M, Puschl A;  
 XX WPI; 2002-575409/61.  
 XX New peptide nucleic acid monomer useful e.g. in the treatment of  
 XX immunological disorders -  
 XX Example 1; Page 23; 58pp; English.  
 XX The invention discloses peptide nucleic acid (PNA) monomers which can be  
 XX used to combat diseases, especially bacterial infections, by targeting  
 XX molecules such as 23S ribosomal RNA and inhibiting translation. They are  
 XX useful in the manufacture of a medicament for the treatment of a diseases  
 XX e.g. bacterial and viral infections, cardiac or vascular diseases,  
 XX metabolic diseases (e.g. diabetes or inborn errors of metabolism) and  
 XX immunological disorders. The microorganisms that can be inhibited include  
 XX Gram-positive organisms (e.g. Streptococcus, Staphylococcus, Peptococcus,  
 XX Bacillus, Listeria, Clostridium, Propionibacterium), Gram-negative  
 XX bacteria (e.g. Bacteroides, Fusobacterium, Escherichia, Klebsiella,  
 XX Salmonella, Shigella, Proteus, Pseudomonas, Vibrio, Legionella,  
 XX Haemophilus, Bordetella, Brucella, Campylobacter, Neisseria, Branhamella)  
 XX and organisms which stain poorly with Gram's stain (e.g. Mycobacteria,  
 XX Treponema, Leptospira, Borrelia, Mycoplasma, Chlamydia, Rickettsia,  
 XX Coxiella). The PNA molecule enables specific and efficient inhibition of  
 XX bacterial genes with nanomolar concentrations and enhances anti-infective  
 XX effect with different orientation of the peptide in relation to the  
 XX PNA-sequence. The sequence presented is the modified PNA molecule, #8.  
 XX Sequence 12 BP; 3 A; 4 C; 0 G; 5 T; 0 other;  
 XX Query Match 100.0%; Score 9; DB 24; Length 12;  
 XX Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX 1 GAGTATGAG 9  
 XX |||||  
 XX 11 GAGTATGAG 3  
 XX Db  
 XX RESULT 13  
 XX ABK91039  
 XX ID ABK91039 standard; DNA; 12 BP.  
 XX AC ABK91039;  
 XX 15-NOV-2002 (first entry)  
 XX DE Modified peptide nucleic acid (PNA) molecule #8 complementary DNA.  
 XX Peptide nucleic acid; PNA; bacterial infection; 23S ribosomal RNA; rRNA;  
 XX translation; viral infection; cardiac disease; vascular disease;  
 XX metabolic disease; diabetes; metabolism; immunological disorder;  
 XX Gram-positive; Gram-negative; anti-infective; ss.  
 XX Unidentified.

XX WO200253574-A2.  
 XX 11-JUL-2002.  
 XX 03-JAN-2002; 2002WO-DK000005.  
 XX 05-JAN-2001; 2001DK-0000021.  
 XX (PANT-) PANTHECO AS.  
 XX Nielsen PE, Manoharan M, Puschl A;  
 XX WPI; 2002-575409/61.  
 XX New peptide nucleic acid monomer useful e.g. in the treatment of  
 XX immunological disorders -  
 XX Example 1; Page 23; 58pp; English.  
 XX The invention discloses peptide nucleic acid (PNA) monomers which can be  
 XX used to combat diseases, especially bacterial infections, by targeting  
 XX molecules such as 23S ribosomal RNA and inhibiting translation. They are  
 XX useful in the manufacture of a medicament for the treatment of a diseases  
 XX e.g. bacterial and viral infections, cardiac or vascular diseases,  
 XX metabolic diseases (e.g. diabetes or inborn errors of metabolism) and  
 XX immunological disorders. The microorganisms that can be inhibited include  
 XX Gram-positive organisms (e.g. Streptococcus, Staphylococcus, Peptococcus,  
 XX Bacillus, Listeria, Clostridium, Propionibacterium), Gram-negative  
 XX bacteria (e.g. Bacteroides, Fusobacterium, Escherichia, Klebsiella,  
 XX Salmonella, Shigella, Proteus, Pseudomonas, Vibrio, Legionella,  
 XX Haemophilus, Bordetella, Brucella, Campylobacter, Neisseria, Branhamella)  
 XX and organisms which stain poorly with Gram's stain (e.g. Mycobacteria,  
 XX Treponema, Leptospira, Borrelia, Mycoplasma, Chlamydia, Rickettsia,  
 XX Coxiella). The PNA molecule enables specific and efficient inhibition of  
 XX bacterial genes with nanomolar concentrations and enhances anti-infective  
 XX effect with different orientation of the peptide in relation to the  
 XX PNA-sequence. The sequence presented is the modified PNA molecule, #8  
 XX (ABK91038) complementary DNA sequence.  
 XX Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 other;  
 XX Query Match 100.0%; Score 9; DB 24; Length 12;  
 XX Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX 1 GAGTATGAG 9  
 XX |||||  
 XX 2 GAGTATGAG 10  
 XX Db  
 XX RESULT 14  
 XX ABK91040  
 XX ID ABK91040 standard; RNA; 12 BP.  
 XX AC ABK91040;  
 XX 15-NOV-2002 (first entry)  
 XX DE Modified peptide nucleic acid (PNA) molecule #8 complementary RNA.  
 XX Peptide nucleic acid; PNA; bacterial infection; 23S ribosomal RNA; rRNA;  
 XX translation; viral infection; cardiac disease; vascular disease;  
 XX metabolic disease; diabetes; metabolism; immunological disorder;  
 XX Gram-positive; Gram-negative; anti-infective; ss.  
 XX Unidentified.  
 XX WO200253574-A2.  
 XX 11-JUL-2002.  
 XX 03-JAN-2002; 2002WO-DK000005.

```
XX PR 05-JAN-2001; 2001DK-0000021.
XX PA (PANT-) PANTHECO AS.
XX PI Nielsen PE, Manoharan M, Puschl A;
XX DR WPI; 2002-575409/61.
XX PT New peptide nucleic acid monomer useful e.g. in the treatment of
XX PT immunological disorders
XX PS Example 1; Page 23; 58pp; English.
XX CC The invention discloses peptide nucleic acid (PNA) monomers which can be
XX CC used to combat diseases, especially bacterial infections, by targeting
XX CC molecules such as 23S ribosomal RNA and inhibiting translation. They are
XX CC useful in the manufacture of a medicament for the treatment of a diseases
XX CC e.g. bacterial and viral infections, cardiac or vascular diseases,
XX CC metabolic diseases (e.g. diabetes or inborn errors of metabolism) and
XX CC immunological disorders. The microorganisms that can be inhibited include
XX CC Gram-positive organisms (e.g. Streptococcus, Staphylococcus, Peptococcus,
XX CC Bacillus, Listeria, Clostridium, Propionibacteria), Gram-negative
XX CC bacteria (e.g. Bacteroides, Fusobacterium, Escherichia, Klebsiella,
XX CC Salmonella, Shigella, Proteus, Pseudomonas, Vibrio, Legionella,
XX CC Haemophilus, Bordetella, Brucella, Campylobacter, Neisseria, Branhamella)
XX CC and organisms which stain poorly with Gram's stain (e.g. Mycobacteria,
XX CC Treponema, Leptospira, Borrelia, Mycoplasma, Chlamydia, Rickettsia,
XX CC Coxiella). The PNA molecule enables specific and efficient inhibition of
XX CC bacterial genes with nanomolar concentrations and enhances anti-infective
XX CC effect with different orientation of the peptide in relation to the
XX CC PNA-sequence. The sequence presented is the modified PNA molecule, #8
XX CC (ABK91038) complementary RNA sequence.
XX CC Sequence 12 BP; 5 A; 0 C; 4 G; 3 U; 0 other;
XX CC Query Match 100.0%; Score 9; DB 24; Length 12;
XX CC Best Local Similarity 77.8%; Pred. No. 1.1e+04;
XX CC Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX CC 1 GAGTATGAG 9
XX CC |||:|:|
XX CC 2 GAGUAUGAG 10
XX CC
XX CC RESULT 15
XX CC AAL44340/c
XX CC AAL44340 standard; DNA; 12 BP.
XX CC AAL44340;
XX CC 24-OCT-2002 (first entry)
XX CC Peptide nucleic acid (PNA) oligomer #1.
XX CC PNA oligomer; PNA; peptide nucleic acid; polyamide backbone; ss;
XX CC aminocetyllysine; acg; aminoethylprolyl; aep; aminoethylpyrrolidine;
XX CC pyr; Gene downregulation; bacterial infection; viral infection; cancer;
XX CC metabolic disease; immunological disorder; PNA-clamping.
XX CC Synthetic.
XX CC
XX CC Key Location/Qualifiers
XX CC modified_base 1..12
XX CC /*tag= a
XX CC /mod_base= OTHER
XX CC /note= "This sequence is a peptide nucleic acid, (i.e. it
XX CC contains a polyamide backbone instead of a deoxyribose
XX CC backbone"
XX CC modified_base 6
XX CC /*tag= b
XX CC /mod_base= OTHER
XX CC /note= "Optional (3S, 5R) pyrrolidone PNA monomer or (2R,
XX CC 4S) pyrrolidone PNA monomer (A12)"
XX CC modified_base 12
XX CC /*tag= c
XX CC /mod_base= OTHER
XX CC /note= "The base is modified with Lys-NH2"
XX CC
XX CC WO200242316-A2.
XX CC 30-MAY-2002.
XX CC 23-NOV-2001; 2001WO-DK00779.
XX CC 24-NOV-2000; 2000DK-0001776.
XX CC 06-MAR-2001; 2001DK-0000371.
XX CC 16-JUL-2001; 2001DK-0001117.
XX CC (PANT-) PANTHECO AS.
XX CC Nielsen PE, Puschl A;
XX CC WPI; 2002-490198/52.
XX CC New peptide nucleic acid oligomer, useful as antisense molecules to
XX CC treat bacterial and viral infections, has single units comprising
XX CC different amino acid backbones such as aminoethylglycine -
XX CC Example 2; Page 19; 40pp; English.
XX CC The invention comprises peptide nucleic acid (PNA) oligomers, where the
XX CC single units of the oligomers comprise different amino acid backbones
XX CC selected from any amino acid, such as: including aminoethylglycine (aeg);
XX CC aminoethylprolyl (aep); and aminoethylpyrrolidine (pyr). The PNA
XX CC oligomers of the invention are useful for the downregulation of specific
XX CC genes by targeting the genes at the mRNA or DNA level. The PNA oligomers
XX CC are useful for treating bacterial and viral infections, cancer, metabolic
XX CC diseases and immunological disorders. The PNA oligomers are also useful
XX CC in PCR monitoring/modulation by PNA-clamping. The present DNA sequence
XX CC represents a PNA oligomer of the invention.
XX CC Sequence 12 BP; 3 A; 4 C; 0 G; 5 T; 0 other;
XX CC Query Match 100.0%; Score 9; DB 24; Length 12;
XX CC Best Local Similarity 100.0%; Pred. No. 1.1e+04;
XX CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC QY 1 GAGTATGAG 9
XX CC |||:|:|
XX CC DB 11 GAGTATGAG 3
XX CC
XX CC Search completed: December 31, 2003, 15:08:12
XX CC Job time : 261.089 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 13:58:09 ; Search time 1034.09 Seconds  
(without alignments)  
211.530 Million cell updates/sec

Title: US-09-540-843-1

Perfect score: 9

Sequence: 1 gagtatgag 9

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 33330

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST.\*

1: em\_estba.\*

2: em\_esthum.\*

3: em\_estin.\*

4: em\_estmu.\*

5: em\_estov.\*

6: em\_estpl.\*

7: em\_estro.\*

8: em\_htc.\*

9: gb\_est1.\*

10: gb\_est2.\*

11: gb\_htc.\*

12: gb\_est3.\*

13: gb\_est4.\*

14: gb\_est5.\*

15: em\_estfun.\*

16: em\_estom.\*

17: em\_gss\_hum.\*

18: em\_gss\_inv.\*

19: em\_gss\_pln.\*

20: em\_gss\_vrt.\*

21: em\_gss\_fun.\*

22: em\_gss\_mam.\*

23: em\_gss\_mus.\*

24: em\_gss\_pro.\*

25: em\_gss\_rod.\*

26: em\_gss\_phg.\*

27: em\_gss\_vxl.\*

28: gb\_gss1.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	9	100.0	22	28	AZ658158
2	9	100.0	28	28	BH904074
3	9	100.0	29	28	BH856420
4	8	88.9	24	9	AW059679

C	5	8	88.9	24	28	AZ478673
C	6	8	88.9	25	28	AZ605844
C	7	8	88.9	27	14	D45824
C	8	8	88.9	30	29	AL766985
C	9	7.4	82.2	17	12	BC926068
C	10	7.4	82.2	19	9	AI747751
C	11	7.4	82.2	19	28	AZ358656
C	12	7.4	82.2	19	28	AZ457990
C	13	7.4	82.2	19	28	AZ991531
C	14	7.4	82.2	20	28	AZ646291
C	15	7.4	82.2	21	28	AZ806440
C	16	7.4	82.2	22	9	AI052322
C	17	7.4	82.2	22	9	AI630912
C	18	7.4	82.2	22	28	AZ591103
C	19	7.4	82.2	22	28	BH811671
C	20	7.4	82.2	22	29	TA119E04Q
C	21	7.4	82.2	23	28	AZ484572
C	22	7.4	82.2	23	28	AZ660131
C	23	7.4	82.2	23	28	AZ830077
C	24	7.4	82.2	24	28	AZ370614
C	25	7.4	82.2	24	28	AZ772496
C	26	7.4	82.2	24	28	AZ847502
C	27	7.4	82.2	24	28	BH865517
C	28	7.4	82.2	25	9	AA871952
C	29	7.4	82.2	25	13	BQ594927
C	30	7.4	82.2	25	28	AZ810630
C	31	7.4	82.2	25	28	AZ831709
C	32	7.4	82.2	25	28	BH856297
C	33	7.4	82.2	25	28	BH857761
C	34	7.4	82.2	26	28	AZ345602
C	35	7.4	82.2	26	28	AZ625488
C	36	7.4	82.2	27	28	BH909563
C	37	7.4	82.2	28	9	AI497442
C	38	7.4	82.2	28	28	AZ591954
C	39	7.4	82.2	28	29	BZ594385
C	40	7.4	82.2	29	14	T80769
C	41	7.4	82.2	29	28	AZ389780
C	42	7.4	82.2	29	28	AZ772808
C	43	7.4	82.2	29	28	BH847329
C	44	7.4	82.2	29	28	BH847334
C	45	7.4	82.2	29	28	BH856155

ALIGNMENTS

RESULT 1  
AZ658158  
LOCUS  
DEFINITION  
1M0534H17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0534H17 R, genomic survey sequence.  
ACCESSION  
AZ658158  
VERSION  
GSS.  
KEYWORDS  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0534 Row: H Column: 17  
 Seq primer: CACACAGGAAAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 22.

## FEATURES

source

1. 22  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUC1M0534H17"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT  
 6 a 0 c 9 g 7 t

Query Match 100.0%; Score 9; DB 28; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GAGTATGAG 9  
 |||||  
 12 GAGTATGAG 20

RESULT 2  
 BH904074/c

LOCUS BH904074.1 GI:22715629 linear GSS 04-SEP-2002  
 DEFINITION SALK\_103904.28.95.x Arabidopsis thaliana TDNA insertion lines  
 Arabidopsis thaliana genomic clone SALK\_103904.28.95.x, genomic survey sequence.

ACCESSION BH904074

VERSION BH904074.1

KEYWORDS GSS

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
 ; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 28)

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At4g23060.  
 Class: TDNA tagged.

## FEATURES

source

1. 28  
 Location/Qualifiers  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_103904.28.95.x"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
 /notes="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

BASE COUNT 5 a 10 c 3 g 9 t

ORIGIN

Query Match 100.0%; Score 9; DB 28; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+04;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9

Db 13 GAGTATGAG 5

RESULT 3

BH856420/c

LOCUS BH856420.1

DEFINITION SALK\_079762.18.10.x Arabidopsis thaliana TDNA insertion lines

Arabidopsis thaliana genomic clone SALK\_079762.18.10.x, genomic survey sequence.

ACCESSION BH856420

VERSION BH856420.1

KEYWORDS GSS

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 29)

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished

Contact: Joseph R. Ecker

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10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within an annotated exon of At5g63570.

Class: TDNA tagged.

## FEATURES

source

1. 29  
 Location/Qualifiers  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_079762.18.10.x"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
 /notes="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)

# BASE COUNT

6 a 10 c 4 g 9 t

Query Match 100.0%; Score 9; DB 28; Length 29;  
Best Local Similarity 100.0%; Pred. No. 4.4e+04;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9  
Db 22 GAGTATGAG 14

# RESULT 4

LOCUS AW059679/c 24 bp mRNA linear EST 23-AUG-2000  
DEFINITION AHUTH.bsst.dnc15.aa.A050g08 DNC15 Homo sapiens cDNA, mRNA sequence.  
ACCESSION AW059679  
VERSION AW059679.1 GI:6652001  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 24)  
AUTHORS Brenner,S., Williams,S.R., Vermaas,E.H., Storck,T., Moon,K.,  
McCollum,C., Mao,J.I., Kirchner,J.J., Eletr,S., DuBridge,R.B.,  
Burcham,T. and Albrecht,G.

TITLE In vitro cloning of complex mixtures of DNA on microbeads: Physical  
separation of differentially expressed cDNAs

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)

MEDLINE 20144098

PUBMED 10677516

# COMMENT

Contact: Burcham TS  
LNX Therapeutics, Inc.  
25861 Industrial Blvd., Hayward, CA 94545, USA  
Tel: 510 670 9338  
Fax: 510 670 9302

Email: tim@lynxgen.com  
Sequence obtained from LNX Therapeutics Megasort technology.  
Collected from the down-regulated gate.  
High quality sequence stop: 24.

# FEATURES

source

1..24  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cell\_type="monocytic leukemia"  
/cell\_line="THP-1 (TIB-202)"  
/clone\_lib="DNC15"  
/note="vector: PCR2.1; Cloning of PCR products from  
micro-beads carrying 3' end of down-regulated cDNA. THP-1  
cells non-induced (treated with DMSO only)."

# BASE COUNT

9 a 6 c 1 g 8 t

Query Match 88.9%; Score 8; DB 9; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGA 8  
Db 24 GAGTATGA 17

# RESULT 5

LOCUS AZ478673/c 24 bp DNA linear GSS 04-OCT-2000  
DEFINITION IM0298J20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0298J20 R, genomic survey sequence.  
ACCESSION AZ478673

AZ478673.1 GI:10637794

# KEYWORDS

Mus musculus (house mouse)

# ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

# REFERENCE

# AUTHORS

1 (bases 1 to 24)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D.,Weiss,R.

# TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

# JOURNAL

# COMMENT

Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: rdunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0298 row: J column: 20

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 24.

# FEATURES

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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0298J20"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F."  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWB42 (GI4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

# BASE COUNT

6 a 8 c 3 g 7 t

# ORIGIN

Query Match 88.9%; Score 8; DB 28; Length 24;

Best Local Similarity 100.0%; Pred. No. 1.8e+05;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGTATGAG 9

Db 8 AGTATGAG 1

# RESULT 6

AZ605844/c 25 bp DNA linear GSS 13-DEC-2000  
LOCUS 1M0427J22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0427J22 F, genomic survey sequence.

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ACCESSION AZ605844
VERSION AZ605844.1 GI:11728034
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0427 row: J column: 22
Seq primer: CGTTGTAACGACGCCGAGT
Class: plasmid ends
High quality sequence stop: 25.
FEATURES             Location/Qualifiers
     source
     1..25
     /organism="Mus musculus"
     /mol_type="genomic DNA"
     /strain="C57BL/6J"
     /db_xref="taxon:10090"
     /clone="UUC1M0427J22"
     /sex="Male"
     /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
     /clone_lib="Mouse 10kb plasmid library"
     /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      7 a      6 c      5 g      7 t
ORIGIN
Query Match      88.9%; Score 8; DB 28; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AGTATGAG 9
Db 17 AGTATGAG 10
|||||
RESULT 7
D45824/c
LOCUS
DEFINITION HUMG03044 Human adult lung 3' directed MboI cDNA Homo sapiens cDNA
EST 21-FEB-1995
3', mRNA sequence.
D45824
VERSION D45824.1 GI:662778
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 27)
Itoh,K., Okubo,K., Yosii,J., Yokouchi,H. and Matsubara,K.
TITLE An expression profile of active genes in human lung
JOURNAL DNA Res. 1, 279-287 (1994)
MEDLINE 95236275
PUBMED 7719923
COMMENT Contact: Kohichi Itoh
Institute for Molecular and Cellular Biology
Osaka University
3-1, Yamadaoka, Suita, Osaka, 565, Japan
Tel: 06-877-5111 x3910
Fax: 06-877-1922.
FEATURES             Location/Qualifiers
     source
     1..27
     /organism="Homo sapiens"
     /mol_type="mRNA"
     /db_xref="taxon:9606"
     /clone_lib="Human adult lung 3' directed MboI cDNA"
     /note="Adult human lung, 3' directed MboI"
BASE COUNT      12 a      6 c      1 g      8 t
ORIGIN
Query Match      88.9%; Score 8; DB 14; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAGTATGA 8
Db 24 GAGTATGA 17
|||||
RESULT 8
AL766985
LOCUS
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-215C11-014144,
genomic survey sequence.
ACCESSION AL766985
VERSION AL766985.1 GI:21520104
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
and Weisshaar,B.
TITLE A pipeline for automated high-throughput generation of PSTs
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformation lines
JOURNAL Unpublished
REFERENCE 2
Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
AUTHORS A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
TITLE for flanking sequence tag based reverse genetics
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 30)
Li,Y., Rosso,M., Strizhov,N. and Weisshaar,B.
AUTHORS Direct Submission
TITLE Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
JOURNAL Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
REFERENCE This sequence is recovered from the left border of the T-DNA. It
TITLE indicates an insertion within the locus defined by clone F911. The
JOURNAL sequences are generated at the MPI for Plant Breeding Research in
COMMENT the context of the GABI-Kat project. GABI-Kat is part of the German

```



Plant Genomics program designated 'GABI'. Information on line availability can be found at:  
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.  
 Location/Qualifiers  
 1..30  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="GK-215C11-014144"  
 /notes="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequences were processed for submission. T-DNA derived sequences were removed"

BASE COUNT 11 a 5 c 4 g 10 t

## ORIGIN

Query Match 88.9%; Score 8; DB 29; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 28+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GAGTATGA 8

11 |||||  
 19 GAGTATGA 26

## RESULT 9

LOCUS BG926068/c

DEFINITION HNC23-1-E10.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.

ACCESSION BG926068

VERSION BG926068.1 GI:14320591

KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 17)

REFERENCE Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W.

Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries

Osteoarthr. Cartil. 9 (7), 641-653 (2001)

21482651

11597177

Contact: Sanjay Kumar

UW2109

GlaxoSmithKline

709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

Tel: 610-270-7245

Fax: 610-270-5598

Email: sanjay.kumar-1@sk.com

Seq primer: T7.

## FEATURES

source

1..17

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/tissue\_type="cartilage"

/lab\_host="E.coli DH10 B"

/clone\_lib="HNC (Human Normal Cartilage)"

/note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI;

Directional"

## BASE COUNT

2 a 10 c 0 g 5 t

## ORIGIN

Query Match 82.2%; Score 7.4; DB 12; Length 17;  
 Best Local Similarity 88.9%; Pred. No. 3.8e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGTATGAG 9

13 GAGTGTGAG 5

## RESULT 10

LOCUS AI747751

DEFINITION

AI747751 19 bp mRNA linear EST 22-JUN-1999  
 ul21h05.x1 Sugano mouse embryo mewa Mus musculus cDNA clone  
 IMAGE:2088249.3 similar to TR:P79101 P79101 CLAVAGE AND  
 POLYADENYLATION SPECIFY FACTOR PROTEIN.; mRNA sequence.

ACCESSION AI747751

VERSION AI747751.1 GI:5126015

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)

REFERENCE Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999

Unpublished

TITLE

JOURNAL

COMMENT

Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LML; contact the

IMAGE Consortium (info@image.lml.gov) for further information.

MGI:995933

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: custom primer used

High quality sequence stop: 1.

## FEATURES

source

1..19

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL"

/db\_xref="taxon:10090"

/clone="IMAGE:2088249"

/dev\_stage="embryo, 14 dpc"

/lab\_host="DH10B"

/clone\_lib="Sugano mouse embryo mewa"

/note="Vector: pME18S-FL3; Site 1: DraIII (CACTGTGTG);

Site 2: DraIII (CACCAGTG); 1st strand cDNA was primed

with an oligo(dT) primer [ATGGGCGCTTTTCTTTTCTTTT];

double-stranded cDNA was ligated to a DraIII adaptor

[TGTGGCGCTACTGG], digested and cloned into distinct DraIII

sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site

CACCATGTG). XhoI should be used to isolate the cDNA

insert. Size selection was performed to exclude fragments

<1.5kb. Library constructed by Dr. Sumio Sugano

(University of Tokyo Institute of Medical Science).

Custom primers for sequencing: 5' end primer

CTTCTGCTTAAGCTCGG and 3' end primer

CGACCTGCAGCTCGACACA."

BASE COUNT 6 a 2 c 8 g 3 t

## ORIGIN

Query Match 82.2%; Score 7.4; DB 9; Length 19;  
 Best Local Similarity 88.9%; Pred. No. 4e+05;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9  
 |||||  
 Db 11 GAGTATGTG 19

RESULT 11  
 AZ358656/c  
 LOCUS  
 DEFINITION IM0101K12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0101K12 F, genomic survey sequence.

ACCESSION AZ358656  
 VERSION AZ358656.1 GI:10472356

KEYWORDS GSS  
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
 Plate: 0101 row: K column: 12  
 Seq primer: CGTTGTAACACGACGCCAGT

Class: plasmid ends  
 High quality sequence stop: 19.

Location/Qualifiers  
 1..19  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0101K12"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 5 a 8 c 0 g 6 t  
 ORIGIN

Query Match

82.2%; Score 7.4; DB 28; Length 19;

Best Local Similarity 88.9%; Pred. No. 4e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9  
 |||||  
 Db 13 GAGTGTGAG 5

RESULT 12  
 AZ457990/c

LOCUS  
 DEFINITION IM0261E11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0261E11 R, genomic survey sequence.

ACCESSION AZ457990  
 VERSION AZ457990.1 GI:10616115

KEYWORDS GSS  
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
 Plate: 0261 row: E column: 11  
 Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends  
 High quality sequence stop: 19.

Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0261E11"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 8 a 5 c 0 g 6 t  
 ORIGIN

Query Match 82.2%; Score 7.4; DB 28; Length 19;  
 Best Local Similarity 88.9%; Pred. No. 4e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGTATGAG 9  
 |||||  
 Db 17 GAGTATGAG 9

RESULT 13  
 AZ991531/c 19 bp DNA linear GSS 27-APR-2001  
 LOCUS 2M0275K15R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
 DEFINITION clone UUGC2M0275K15 R, genomic survey sequence.

ACCESSION AZ991531  
 VERSION AZ991531.1 GI:13862758

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.  
 and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL Unpublished  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0275 row: K column: 15  
 Seq primer: CACACAGGAACAGCTATGACG  
 Class: plasmid ends  
 High quality sequence stop: 19.

FEATURES  
 source

1. .19  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0275K15"  
 /sex="Female"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC2M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (female) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

4 a 9 c 2 g 4 t

BASE COUNT  
 ORIGIN

Query Match 82.2%; Score 7.4; DB 28; Length 19;  
 Best Local Similarity 88.9%; Pred. No. 4e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGTATGAG 9  
 |||||  
 Db 11 GAGTGTGAG 3

RESULT 14  
 AZ646291

LOCUS 20 bp DNA linear GSS 14-DEC-2000  
 DEFINITION 1M0512D07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0512D07 F, genomic survey sequence.

ACCESSION AZ646291

VERSION AZ646291.1 GI:11776438

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.  
 and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL Unpublished  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0512 row: D column: 07  
 Seq primer: CGTTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 20.

FEATURES  
 source

1. .20  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0512D07"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

4 a 3 c 9 g 4 t

BASE COUNT

## ORIGIN

Query Match 82.2%; Score 7.4; DB 28; Length 20;

Best Local Similarity 88.9%; Pred. No. 4.1e+05; Mismatches 0; Gaps 0; Indels 1; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9

Db 9 GAGTGTGAG 17

## RESULT 15

AZ806440

## LOCUS

DEFINITION 21 bp DNA linear GSS 20-FEB-2001

clone UUGC2M0068B05 R, genomic survey sequence.

ACCESSION AZ806440

VERSION AZ806440.1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,

M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.,

and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0068 row: B column: 05

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1..21

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0068B05"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

## BASE COUNT

ORIGIN 4 a 1 c 8 g 8 t

Query Match 82.2%; Score 7.4; DB 28; Length 21;

Best Local Similarity 88.9%; Pred. NO. 4.2e+05; Mismatches 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9

Db 13 GAGTTTGAG 21

Search completed: December 31, 2003, 19:41:09

Job time : 1039.09 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 14:40:05 ; Search time 34.9747 Seconds  
(without alignments)  
113.581 Million cell updates/sec

Title: US-09-540-843-1  
Perfect score: 9  
Sequence: 1 gagtatgag 9

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 547746

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/ptodata/1/ina/5A COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	100.0	9	3	US-09-048-927-1
2	9	100.0	15	3	US-09-049-190-6
3	9	100.0	15	3	US-09-049-190-7
4	9	100.0	15	4	US-08-932-140C-6
5	9	100.0	15	4	US-08-932-140C-7
6	9	100.0	17	1	US-08-758-306-365
7	9	100.0	17	1	US-08-758-306-367
8	9	100.0	17	1	US-08-758-306-369
9	9	100.0	17	1	US-08-758-306-371
10	9	100.0	20	3	US-09-287-796-101
11	9	100.0	20	3	US-09-287-796-102
12	9	100.0	20	3	US-09-130-616-101
13	9	100.0	20	3	US-09-130-616-102
14	9	100.0	20	4	US-09-105-058C-15
15	9	100.0	20	4	US-09-851-062-29
16	9	100.0	20	4	US-09-517-467B-84
17	9	100.0	20	4	US-09-422-978-6551
18	9	100.0	21	4	US-09-422-978-8965
19	9	100.0	21	6	5455029-26
20	9	100.0	23	4	US-09-088-274-8
21	9	100.0	24	4	US-09-245-248B-23
22	9	100.0	26	4	US-09-417-485D-32
23	9	100.0	27	4	US-08-932-140C-21
24	9	100.0	28	3	US-09-031-006-4
25	8	88.9	14	2	US-08-744-905A-4
26	8	88.9	15	1	US-08-334-847-24
27	8	88.9	15	2	US-08-747-121-4
28	8	88.9	15	2	US-08-585-684B-1315
29	8	88.9	15	3	US-09-038-073-1315
30	8	88.9	16	1	US-07-977-284A-59
31	8	88.9	16	2	US-08-256-426B-59
32	8	88.9	17	3	US-08-985-162-443
33	8	88.9	17	3	US-08-985-162-444
34	8	88.9	18	1	US-07-688-352C-8
35	8	88.9	18	1	US-08-363-585-55
36	8	88.9	18	1	US-08-358-995-10
37	8	88.9	18	2	US-08-474-379C-8
38	8	88.9	18	2	US-09-213-768-29
39	8	88.9	18	3	US-09-146-249A-8
40	8	88.9	18	3	US-08-206-188B-8
41	8	88.9	18	3	US-09-630-706-80
42	8	88.9	18	4	US-09-167-109-21
43	8	88.9	18	4	US-09-422-978-4648
44	8	88.9	18	4	US-09-422-978-4729
45	8	88.9	18	5	PCT-US91-02714-8

ALIGNMENTS

RESULT 1  
US-09-048-927-1  
; Sequence 1, Application US/09048927  
; Patent No. 6147056  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrist, Barbara A.  
; APPLICANT: Yaar, Mina  
; APPLICANT: Eller, Mark  
; TITLE OF INVENTION: Use of Locally Applied DNA Fragments  
; FILE REFERENCE: BU94-68A2  
; CURRENT APPLICATION NUMBER: US/09/048,927  
; CURRENT FILING DATE: 1998-03-26  
; EARLIER APPLICATION NUMBER: 08/952,697  
; EARLIER FILING DATE: 1996-06-03  
; EARLIER APPLICATION NUMBER: 08/467,012  
; EARLIER FILING DATE: 1995-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 9  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: DNA Fragment  
US-09-048-927-1

Query Match 100.0%; Score 9; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.7e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9  
Db 1 GAGTATGAG 9

RESULT 2  
US-09-049-190-6/c  
; Sequence 6, Application US/09049190  
; Patent No. 6190866  
; GENERAL INFORMATION:  
; APPLICANT: Nielsen et al.  
; TITLE OF INVENTION: Peptide Nucleic Acids Having  
; TITLE OF INVENTION: Antibacterial Activity  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: U.S.A.

ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/049,190  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: John W. Caldwell  
REGISTRATION NUMBER: 28,937  
REFERENCE/DOCKET NUMBER: ISIS-2560  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 2  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 3  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
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OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 6  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 7  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 8  
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OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 9  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site

LOCATION: 10  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 11  
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LOCATION: 13  
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OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 14  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 15  
OTHER INFORMATION: N-[acetyl(2-aminoethyl)]-C-lysine-glycine  
OTHER INFORMATION: backbone  
US-09-049-190-6  
Query Match 100.0%; Score 9; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9  
Db 11 GAGTATGAG 3

RESULT 3  
US-09-049-190-7/c  
Sequence 7, Application US/09049190  
Patent No. 6190866  
GENERAL INFORMATION:  
APPLICANT: Nielsen et al.  
TITLE OF INVENTION: Peptide Nucleic Acids Having  
TITLE OF INVENTION: Antibacterial Activity  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/049,190  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: John W. Caldwell  
REGISTRATION NUMBER: 28,937  
REFERENCE/DOCKET NUMBER: ISIS-2560  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100

```

TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
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FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
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FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
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FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
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FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
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FEATURE:
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LOCATION: 12
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FEATURE:
NAME/KEY: Modified-site
LOCATION: 13
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
FEATURE:

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NAME/KEY: Modified-site
LOCATION: 14
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
FEATURE:
NAME/KEY: Modified-site
LOCATION: 15
OTHER INFORMATION: N-[acetyl(2-aminoethyl)]-C-lysine-glycine
OTHER INFORMATION: backbone
US-09-049-190-7

Query Match 100.0%; Score 9; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTATGAG 9
DB 14 GAGTATGAG 6

RESULT 4
US-08-932-140C-6/c
Sequence 6, Application US/08932140C
Patent No. 6300318
GENERAL INFORMATION:
APPLICANT: Nielsen et al.
TITLE OF INVENTION: Peptide Nucleic Acids Having
TITLE OF INVENTION: Antibacterial Activity
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESS: Woodcock Washburn Kurtz Mackiewicz &
ADDRESS: No. 6300318ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932,140C
FILING DATE: September 16, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: John W. Caldwell
REGISTRATION NUMBER: 28,937
REFERENCE/DOCKET NUMBER: ISIS-2560
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3

```

OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 4  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 5  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 6  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 7  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 8  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 9  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 10  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 11  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 12  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 13  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 14  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 15  
OTHER INFORMATION: N-[acetyl(2-aminoethyl)]-C-  
OTHER INFORMATION: lysine-glycine backbone  
US-08-932-140C-6

Query Match 100.0%; Score 9; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTATGAG 9  
DB 11 GAGTATGAG 3

RESULT 5  
US-08-932-140C-7/c  
Sequence 7, Application US/08932140C  
Patent No. 6300318  
GENERAL INFORMATION:  
APPLICANT: Nielsen et al.  
TITLE OF INVENTION: Peptide Nucleic Acids Having  
TITLE OF INVENTION: Antibacterial Activity  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &

ADDRESSEE: No. 6300318ris LLP  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/932,140C  
FILING DATE: September 16, 1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: John W. Caldwell  
REGISTRATION NUMBER: 28,937  
REFERENCE/DOCKET NUMBER: ISIS-2560  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 2  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 3  
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NAME/KEY: Modified-site  
LOCATION: 4  
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NAME/KEY: Modified-site  
LOCATION: 7  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 8  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site



LOCATION: 9  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 10  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 11  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 12  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 13  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 14  
OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine  
OTHER INFORMATION: backbone  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 15  
OTHER INFORMATION: N-[acetyl(2-aminoethyl)]-C-  
OTHER INFORMATION: lysine-glycine backbone  
US-08-932-140C-7

Query Match 100.0%; Score 9; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9  
Db 14 GAGTATGAG 6

RESULT 6  
US-08-758-306-365/c  
Sequence 365, Application US/08758306  
Patent No. 5807743

GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Dan T.  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TREATMENT OF DISEASES  
TITLE OF INVENTION: ASSOCIATED WITH  
TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR  
TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION  
NUMBER OF SEQUENCES: 1379  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/758,306

FILING DATE: December 3, 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 212/132  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 365:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-758-306-365

Query Match 100.0%; Score 9; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9  
Db 17 GAGTATGAG 9

RESULT 7  
US-08-758-306-367/c  
Sequence 367, Application US/08758306  
Patent No. 5807743

GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Dan T.  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TREATMENT OF DISEASES  
TITLE OF INVENTION: ASSOCIATED WITH  
TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR  
TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION  
NUMBER OF SEQUENCES: 1379  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/758,306  
FILING DATE: December 3, 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 212/132  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 367:

SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-758-306-367

Query Match 100.0%; Score 9; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTATGAG 9  
DB 15 GAGTATGAG 7

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## RESULT 8

US-08-758-306-369/c  
Sequence 369, Application US/08758306  
Patent No. 5807743

## GENERAL INFORMATION:

APPLICANT: Stinchcomb, Dan T.  
APPLICANT: McSwiggen, James A.  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TREATMENT OF DISEASES  
TITLE OF INVENTION: ASSOCIATED WITH  
TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR  
TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION  
NUMBER OF SEQUENCES: 1379  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
STATE: Los Angeles  
COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/758,306

FILING DATE: December 3, 1996

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 212/132

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 369:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-758-306-369

Query Match 100.0%; Score 9; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTATGAG 9  
DB 12 GAGTATGAG 4

## RESULT 9

US-08-758-306-371/c  
Sequence 371, Application US/08758306  
Patent No. 5807743

## GENERAL INFORMATION:

APPLICANT: Stinchcomb, Dan T.  
APPLICANT: McSwiggen, James A.  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TREATMENT OF DISEASES  
TITLE OF INVENTION: ASSOCIATED WITH  
TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR  
TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION  
NUMBER OF SEQUENCES: 1379  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
STATE: Los Angeles  
COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/758,306

FILING DATE: December 3, 1996

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 212/132

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 371:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-758-306-371

Query Match 100.0%; Score 9; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTATGAG 9

DB 9 GAGTATGAG 1

## RESULT 10

US-09-287-796-101

Sequence 101, Application US/09287796A

Patent No. 6133246

GENERAL INFORMATION:

APPLICANT: McKay, Robert A.

APPLICANT: Dean, Nicholas M.

APPLICANT: Monia, Brett

APPLICANT: Nero, Pam

APPLICANT: Gaarde, William A.

TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS

TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS

; FILE REFERENCE: ISPH-0350  
; CURRENT APPLICATION NUMBER: US/09/287,796A  
; CURRENT FILING DATE: 1999-04-07  
; EARLIER APPLICATION NUMBER: 09/130,616  
; EARLIER FILING DATE: 1998-08-07  
; EARLIER APPLICATION NUMBER: 08/910,629  
; EARLIER FILING DATE: 1997-08-03  
; NUMBER OF SEQ ID NOS: 165  
; SEQ ID NO 101  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-287-796-101

Query Match 100.0%; Score 9; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGTATGAG 9  
| | | | |  
Db 9 GAGTATGAG 17

RESULT 11  
US-09-287-796-102  
Sequence 102, Application US/09287796A  
Patent No. 6133246

GENERAL INFORMATION:  
APPLICANT: McKay, Robert A.  
APPLICANT: Dean, Nicholas M.  
APPLICANT: Monia, Brett  
APPLICANT: Nero, Pam  
APPLICANT: Gaarde, William A.

TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS  
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS

FILE REFERENCE: ISPH-0350  
CURRENT APPLICATION NUMBER: US/09/287,796A  
CURRENT FILING DATE: 1999-04-07  
EARLIER APPLICATION NUMBER: 09/130,616  
EARLIER FILING DATE: 1998-08-07  
EARLIER APPLICATION NUMBER: 08/910,629  
EARLIER FILING DATE: 1997-08-03  
NUMBER OF SEQ ID NOS: 165  
SEQ ID NO 102  
LENGTH: 20

TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Sequence

US-09-287-796-102

Query Match 100.0%; Score 9; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGTATGAG 9  
| | | | |  
Db 9 GAGTATGAG 17

RESULT 12  
US-09-130-616-101  
Sequence 101, Application US/09130616C  
Patent No. 6221850

GENERAL INFORMATION:  
APPLICANT: McKay, Robert A.  
APPLICANT: Dean, Nicholas M.  
APPLICANT: Monia, Brett  
APPLICANT: Nero, Pam  
APPLICANT: Gaarde, William A.

TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS

; TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS  
; FILE REFERENCE: ISPH-0318  
; CURRENT APPLICATION NUMBER: US/09/130,616C  
; CURRENT FILING DATE: 1998-08-07  
; EARLIER APPLICATION NUMBER: 08/910,629  
; EARLIER FILING DATE: 1997-08-03  
; NUMBER OF SEQ ID NOS: 178  
; SEQ ID NO 101  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic sequence  
US-09-130-616-101

Query Match 100.0%; Score 9; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGTATGAG 9  
| | | | |  
Db 9 GAGTATGAG 17

RESULT 13

US-09-130-616-102  
Sequence 102, Application US/09130616C  
Patent No. 6221850

GENERAL INFORMATION:  
APPLICANT: McKay, Robert A.  
APPLICANT: Dean, Nicholas M.  
APPLICANT: Monia, Brett  
APPLICANT: Nero, Pam  
APPLICANT: Gaarde, William A.

TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS  
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS

FILE REFERENCE: ISPH-0318  
CURRENT APPLICATION NUMBER: US/09/130,616C  
CURRENT FILING DATE: 1998-08-07  
EARLIER APPLICATION NUMBER: 08/910,629  
EARLIER FILING DATE: 1997-08-03  
NUMBER OF SEQ ID NOS: 178  
SEQ ID NO 102  
LENGTH: 20

TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic sequence

US-09-130-616-102

Query Match 100.0%; Score 9; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGTATGAG 9  
| | | | |  
Db 9 GAGTATGAG 17

RESULT 14

US-09-105-058C-15  
Sequence 15, Application US/09105058C  
Patent No. 6403360

GENERAL INFORMATION:  
APPLICANT: Blonar, Michael A.  
APPLICANT: Dworetzky, Steven  
APPLICANT: Gribkoff, Valentin K.  
APPLICANT: Levesque, Paul C.  
APPLICANT: Little, Wayne A.  
APPLICANT: Neubauer, Michael G.  
APPLICANT: Yang, Wen-Pin

TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME  
FILE REFERENCE: 3053-4052

Fri Jan 2 09:33:09 2004

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; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Forward primer
; OTHER INFORMATION: from EST sequence similar to the KvLQT gene
US-09-105-058C-15

Query Match      100.0%; Score 9; DB 4; Length 20;
Best Local Similarity 100.0%; Pred.No.1.5e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      1 GAGTATGAG 9
      |||||
      1 GAGTATGAG 9

RESULT 15
US-09-851-062-29/c
Sequence 29, Application US/09851062
Patent No. 6448081
GENERAL INFORMATION:
APPLICANT: Brenda F. Baker
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P40 SUBUNIT EXPRESSION
FILE REFERENCE: RTS-0247
CURRENT APPLICATION NUMBER: US/09/851,062
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 87
      1 GAGTATGAG 9
      |||||
      1 GAGTATGAG 9

TYPE: DNA
LENGTH: 20
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-062-29

Query Match      100.0%; Score 9; DB 4; Length 20;
Best Local Similarity 100.0%; Pred.No.1.5e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      1 GAGTATGAG 9
      |||||
      19 GAGTATGAG 11

Search completed: January 1, 2004, 00:32:18
Job time : 35.0858 secs
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 17:10:00 ; Search time 104.924 Seconds  
(without alignments)  
296.896 Million cell updates/sec

Title: US-09-540-843-1

Perfect score: 9

Sequence: 1 gagatgag 9

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2263443 seqs, 1730637950 residues

Total number of hits satisfying chosen parameters: 998502

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:\*

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- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
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- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	100.0	9	15	US-10-122-630-1
2	9	100.0	9	15	US-10-122-633-1
3	9	100.0	12	15	US-10-150-779A-15
4	9	100.0	12	15	US-10-150-779A-16
5	9	100.0	17	9	US-09-866-108-2750
6	9	100.0	17	9	US-09-866-108-2751
7	9	100.0	17	9	US-09-866-108-2752
8	9	100.0	17	9	US-09-866-108-2753
9	9	100.0	17	9	US-09-866-108-2754
10	9	100.0	17	9	US-09-866-108-2755
11	9	100.0	17	9	US-09-866-108-2756
12	9	100.0	17	9	US-09-866-108-2757
13	9	100.0	17	9	US-09-866-108-2758
14	9	100.0	18	9	US-09-853-895-1
15	9	100.0	19	13	US-10-205-309-181

c	16	9	100.0	19	13	US-10-205-309-506	Sequence 506, App
	17	9	100.0	20	11	US-09-774-809-101	Sequence 101, App
	18	9	100.0	20	11	US-09-774-809-102	Sequence 102, App
	19	9	100.0	20	14	US-10-128-870-15	Sequence 15, Appl
	20	9	100.0	20	15	US-10-131-685-15	Sequence 15, Appl
c	21	9	100.0	20	15	US-10-067-514-32	Sequence 32, Appl
	22	9	100.0	24	9	US-09-815-656-23	Sequence 23, Appl
	23	9	100.0	25	9	US-09-866-108-5679	Sequence 5679, Ap
	24	9	100.0	25	9	US-09-866-108-5680	Sequence 5680, Ap
	25	9	100.0	25	9	US-09-866-108-5681	Sequence 5681, Ap
	26	9	100.0	25	9	US-09-866-108-5682	Sequence 5682, Ap
	27	9	100.0	25	9	US-09-866-108-5683	Sequence 5683, Ap
	28	9	100.0	25	9	US-09-866-108-5684	Sequence 5684, Ap
	29	9	100.0	25	9	US-09-866-108-5685	Sequence 5685, Ap
	30	9	100.0	25	9	US-09-866-108-5686	Sequence 5686, Ap
	31	9	100.0	25	9	US-09-866-108-5687	Sequence 5687, Ap
	32	9	100.0	25	9	US-09-866-108-5688	Sequence 5688, Ap
	33	9	100.0	25	9	US-09-866-108-5689	Sequence 5689, Ap
	34	9	100.0	25	9	US-09-866-108-5690	Sequence 5690, Ap
	35	9	100.0	25	9	US-09-866-108-5691	Sequence 5691, Ap
	36	9	100.0	25	9	US-09-866-108-5692	Sequence 5692, Ap
	37	9	100.0	25	9	US-09-866-108-5693	Sequence 5693, Ap
	38	9	100.0	25	9	US-09-866-108-5694	Sequence 5694, Ap
	39	9	100.0	25	9	US-09-866-108-5695	Sequence 5695, Ap
	40	9	100.0	25	11	US-09-911-904-37	Sequence 37, Appl
	41	9	100.0	25	15	US-10-215-112-4205	Sequence 4205, Ap
	42	9	100.0	25	15	US-10-215-112-4329	Sequence 4329, Ap
c	43	9	100.0	25	15	US-10-215-112-10765	Sequence 10765, A
c	44	9	100.0	25	15	US-10-215-112-10891	Sequence 10891, A
	45	9	100.0	25	15	US-10-098-2638-9340	Sequence 9340, Ap

#### ALIGNMENTS

#### RESULT 1

US-10-122-630-1  
; Sequence 1, Application US/10122630  
; Publication No. US20030032610A1  
; GENERAL INFORMATION:  
; APPLICANT: Glitchrest, Barbara A.  
; APPLICANT: Eller, Mark S.  
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
; TITLE OF INVENTION: Oligonucleotides  
; FILE REFERENCE: 0054.1088-018  
; CURRENT APPLICATION NUMBER: US/10/122,630  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US 08/467,012  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: PCT/US96/08386  
; PRIOR FILING DATE: 1996-06-03  
; PRIOR APPLICATION NUMBER: US 09/048,927  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: US 09/540,843  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: PCT/US01/10162  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 9  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA Fragment  
US-10-122-630-1

Query Match 100.0%; Score 9; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.8e+08;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTATGAG 9

Db 1 GAGTATGAG 9  
|||||||

## RESULT 2

US-10-122-633-1  
; Sequence 1, Application US/10122633  
; Publication No. US20030032611A1  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrest, Barbara A.  
; APPLICANT: Eller, Mark S.  
; APPLICANT: Yaaz, Mina  
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
; Oligonucleotides  
; FILE REFERENCE: 0054.1088-019  
; CURRENT APPLICATION NUMBER: US/10/122,633  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US 09/540,843  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: PCT/US01/10162  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 9  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic DNA Fragment  
US-10-122-633-1

Query Match 100.0%; Score 9; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.8e+08; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

1 GAGTATGAG 9  
|||||||

1 GAGTATGAG 9

## RESULT 3

US-10-150-779A-15/c  
; Sequence 15, Application US/10150779A  
; Publication No. US20030125241A1  
; GENERAL INFORMATION:  
; APPLICANT: WISSENBACH, MARGIT  
; APPLICANT: KOCH, TROELS  
; APPLICANT: ORUM, HENRICK  
; APPLICANT: HANSEN, BO  
; TITLE OF INVENTION: THERAPEUTIC USES OF LNA-MODIFIED OLIGONUCLEOTIDES IN  
; INFECTIOUS DISEASES  
; FILE REFERENCE: 55704 (45120)  
; CURRENT APPLICATION NUMBER: US/10/150,779A  
; CURRENT FILING DATE: 2003-02-07  
; PRIOR APPLICATION NUMBER: 60/291,830  
; PRIOR FILING DATE: 2001-05-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: oligonucleotide  
US-10-150-779A-15

Query Match 100.0%; Score 9; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

QY 1 GAGTATGAG 9  
|||||||

Db 12 GAGTATGAG 4

## RESULT 4

US-10-150-779A-16/c  
; Sequence 16, Application US/10150779A  
; Publication No. US20030125241A1  
; GENERAL INFORMATION:  
; APPLICANT: WISSENBACH, MARGIT  
; APPLICANT: KOCH, TROELS  
; APPLICANT: ORUM, HENRICK  
; APPLICANT: HANSEN, BO  
; TITLE OF INVENTION: THERAPEUTIC USES OF LNA-MODIFIED OLIGONUCLEOTIDES IN  
; INFECTIOUS DISEASES  
; FILE REFERENCE: 55704 (45120)  
; CURRENT APPLICATION NUMBER: US/10/150,779A  
; CURRENT FILING DATE: 2003-02-07  
; PRIOR APPLICATION NUMBER: 60/291,830  
; PRIOR FILING DATE: 2001-05-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 16  
LENGTH: 12  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: DNA oligonucleotide with phosphorothioate backbone  
US-10-150-779A-16

Query Match 100.0%; Score 9; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

QY 1 GAGTATGAG 9  
|||||||

Db 12 GAGTATGAG 4

## RESULT 5

US-09-866-108-2750  
; Sequence 2750, Application US/09866108  
; Patent No. US20020048000A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOmica-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 2750  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-2750

Query Match 100.0%; Score 9; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GAGTATGAG 9  
|||||  
9 GAGTATGAG 17

## RESULT 6

US-09-866-108-2751  
Sequence 2751, Application US/09866108  
Patent No. US20020048800A1  
GENERAL INFORMATION:  
APPLICANT: GU, Yizhong  
APPLICANT: JI, Yonggang  
APPLICANT: PENN, Sharron G.  
APPLICANT: HANZEL, David K.  
APPLICANT: RANK, David R.  
APPLICANT: CHEN, Wensheng  
APPLICANT: SHANNON, Mark  
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
FILE REFERENCE: AEOMICA-7  
CURRENT FILING DATE: 2001-05-25  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 2751  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-2751

Query Match 100.0%; Score 9; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTATGAG 9  
|||||  
Db 8 GAGTATGAG 16

## RESULT 7

US-09-866-108-2752  
Sequence 2752, Application US/09866108  
Patent No. US20020048800A1  
GENERAL INFORMATION:  
APPLICANT: GU, Yizhong  
APPLICANT: JI, Yonggang  
APPLICANT: PENN, Sharron G.  
APPLICANT: HANZEL, David K.  
APPLICANT: RANK, David R.  
APPLICANT: CHEN, Wensheng  
APPLICANT: SHANNON, Mark  
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
FILE REFERENCE: AEOMICA-7  
CURRENT FILING DATE: 2001-05-25  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 60/266,860  
PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 2752  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-2752

Query Match 100.0%; Score 9; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9  
Db 7 GAGTATGAG 15

## RESULT 8

US-09-866-108-2753  
; Sequence 2753, Application US/09866108  
; Patent No. US20020048800A1

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: AEOMICA-7

CURRENT APPLICATION NUMBER: US/09/866,108

CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 60/266,860

PRIOR FILING DATE: 2001-02-05

NUMBER OF SEQ ID NOS: 15752

SOFTWARE: Aeomica Sequence Listing Engine

SEQ ID NO 2753

LENGTH: 17

TYPE: DNA

ORGANISM: Homo sapiens

US-09-866-108-2753

Query Match 100.0%; Score 9; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9  
Db 6 GAGTATGAG 14

## RESULT 9

US-09-866-108-2754  
; Sequence 2754, Application US/09866108  
; Patent No. US20020048800A1

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: AEOMICA-7

CURRENT APPLICATION NUMBER: US/09/866,108

CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 60/266,860

PRIOR FILING DATE: 2001-02-05

NUMBER OF SEQ ID NOS: 15752

SOFTWARE: Aeomica Sequence Listing Engine

SEQ ID NO 2754

LENGTH: 17

TYPE: DNA

ORGANISM: Homo sapiens

US-09-866-108-2754

Query Match 100.0%; Score 9; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9  
Db 5 GAGTATGAG 13

## RESULT 10

US-09-866-108-2755  
; Sequence 2755, Application US/09866108  
; Patent No. US20020048800A1

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng



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; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOmica-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aecomica Sequence Listing Engine
SEQ ID NO 2755
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-2755

Query Match 100.0%; Score 9; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps

1 GAGTATGAG 9
|||||||
4 GAGTATGAG 12

RESULT 11
US-09-866-108-2756
; Sequence 2756, Application US/09866108
; Patent No. US2002004800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOmica-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359

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; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663  
 ; PRIOR FILING DATE: 2001-01-30  
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 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: US 60/234,687  
 ; PRIOR FILING DATE: 2000-09-21  
 ; PRIOR APPLICATION NUMBER: US 60/266,860  
 ; PRIOR FILING DATE: 2001-02-05  
 ; NUMBER OF SEQ ID NOS: 15752  
 ; SOFTWARE: Aecomica Sequence Listing Engine  
 ; SEQ ID NO 2756  
 ; LENGTH: 17  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-866-108-2756

Query Match 100.0%; Score 9; DB 9; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 1 GAGTATGAG 9  
 |||||  
 Db 3 GAGTATGAG 11

RESULT 12  
 US-09-866-108-2757  
 ; Sequence 2757, Application US/09866108  
 ; Patent No. US20020048800A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GU, Yizhong  
 ; APPLICANT: JI, Yonggang  
 ; APPLICANT: PENN, Sharon G.  
 ; APPLICANT: HANZEL, David K.  
 ; APPLICANT: RANK, David R.  
 ; APPLICANT: CHEN, Wensheng  
 ; APPLICANT: SHANNON, Mark  
 ; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
 ; FILE REFERENCE: AEOICA-7  
 ; CURRENT APPLICATION NUMBER: US 60/866,108  
 ; CURRENT FILING DATE: 2001-05-25  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: GB 24263.6  
 ; PRIOR FILING DATE: 2000-10-04  
 ; PRIOR APPLICATION NUMBER: US 60/236,359  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665

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;  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 2757  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-2757

Query Match 100.0%; Score 9; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GAGTATGAG 9  
|||||||  
2 GAGTATGAG 10

RESULT 13  
US-09-866-108-2758  
Sequence 2758, Application US/09866108  
Patent No. US20020048800A1  
GENERAL INFORMATION:  
APPLICANT: GU, Yizhong  
APPLICANT: JI, Yonggang  
APPLICANT: PENN, Sharon G.  
APPLICANT: HANZEL, David R.  
APPLICANT: RANK, David R.  
APPLICANT: CHEN, Wensheng  
APPLICANT: SHANNON, Mark

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
FILE REFERENCE: ACOMICA-7  
CURRENT APPLICATION NUMBER: US/09/866,108  
CURRENT FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670

;  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 2758  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-2758

Query Match 100.0%; Score 9; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9  
|||||||  
Db 1 GAGTATGAG 9

RESULT 14  
US-09-853-895-1/c  
Sequence 1, Application US/09853895  
Patent No. US20020045590A1  
GENERAL INFORMATION:  
APPLICANT: Johns, Roger  
APPLICANT: Tao, Yuan-Xiang  
TITLE OF INVENTION: Inhibition of interaction of PSD93 and  
FILE REFERENCE: 01107.00130  
CURRENT APPLICATION NUMBER: US/09/853,895  
CURRENT FILING DATE: 2001-05-14  
PRIOR APPLICATION NUMBER: 60/242590  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/203894  
PRIOR FILING DATE: 2000-05-12  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Rattus rattus  
US-09-853-895-1

Query Match 100.0%; Score 9; DB 9; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTATGAG 9  
|||||||  
Db 18 GAGTATGAG 10

RESULT 15  
US-10-205-309-181  
Sequence 181, Application US/10205309  
Publication No. US20030190635A1  
GENERAL INFORMATION:  
APPLICANT: McSwiggen, James  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Alzheimer's Disease Using  
TITLE OF INVENTION: Interfering RNA  
FILE REFERENCE: 900/033  
CURRENT APPLICATION NUMBER: US/10/205,309  
CURRENT FILING DATE: 2002-10-25  
NUMBER OF SEQ ID NOS: 674  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 181  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial Sequence

FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense  
US-10-205-309-181

Query Match 100.0%; Score 9; DB 13; Length 19;  
Best Local Similarity 77.8%; Pred.No 1.7e+04;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTATGAG 9  
|||:|  
Db 9 GAGUAGAG 17

Search completed: January 1, 2004, 01:10:34  
Job time : 105.924 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 11:36:21 ; Search time 828.57 Seconds  
(without alignments)  
444.364 Million cell updates/sec

Title: US-09-540-843-2  
Perfect score: 9  
Sequence: 1 taggagat 9

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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	9	100.0	17	6	AX673343	AX673343 Sequence
C 4	9	100.0	17	6	AX727498	AX727498 Sequence
C 5	9	100.0	17	6	AX730036	AX730036 Sequence
C 6	9	100.0	17	6	AX731799	AX731799 Sequence
C 7	9	100.0	17	6	AX732235	AX732235 Sequence
C 8	9	100.0	17	6	AX734589	AX734589 Sequence
C 9	9	100.0	17	6	AX738033	AX738033 Sequence
C 10	9	100.0	20	6	AX9511	AX9511 Sequence 6
C 11	9	100.0	20	6	AR166936	AR166936 Sequence
C 12	9	100.0	20	6	AR294569	AR294569 Sequence
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C 17	9	100.0	22	6	E55148	E55148 Method for
C 18	9	100.0	23	6	E36547	E36547 Method of g
C 19	9	100.0	23	6	E40169	E40169 Genetic dia
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C 21	9	100.0	24	6	AR135197	AR135197 Sequence
C 22	9	100.0	24	6	AR146693	AR146693 Sequence
C 23	9	100.0	24	6	AR152264	AR152264 Sequence
C 24	9	100.0	24	6	AR157802	AR157802 Sequence
C 25	9	100.0	26	6	AX477111	AX477111 Sequence
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C 30	9	100.0	27	6	AX555063	AX555063 Sequence
C 31	9	100.0	27	6	AX718093	AX718093 Sequence
C 32	9	100.0	28	6	AR143009	AR143009 Sequence
C 33	9	100.0	29	6	AX556783	AX556783 Sequence
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C 39	8	88.9	11	6	AX631396	AX631396 Sequence
C 40	8	88.9	12	6	AR105116	AR105116 Sequence
C 41	8	88.9	15	6	AR033402	AR033402 Sequence
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AX268754.1	VERSION	AX268754.1	GI:16541826			
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AX268754.1	SOURCE	synthetic construct				
AX268754.1	ORGANISM	artificial sequences.				
AX268754.1	REFERENCE	1				
AX268754.1	AUTHORS	Gilchrest, B.A., Yaar, M. and Eller, M.				
AX268754.1	TITLE	Use of locally applied dna fragments				
AX268754.1	JOURNAL	Patent: WO 0174342-A 2 11-OCT-2001;				
AX268754.1		TRUSTEES OF BOSTON UNIVERSITY (US)				

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ACCESSION AX419832  
VERSION AX419832.1 GI:21524199  
KEYWORDS synthetic construct  
synthetic construct  
artificial sequences.  
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REFERENCE Lyamichev,V., Allawi,H., Dong,F., Neri,B.P. and Vener,I.T.  
AUTHORS Nucleic acid accessible hybridization sites  
TITLE Patent: WO 0198537-A 169 27-DEC-2001;  
JOURNAL THIRD WAVE TECHNOLOGIES, INC. (US)  
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ACCESSION AX673343  
VERSION AX673343.1 GI:29331691  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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REFERENCE Telerman,A., Amson,R. and Tuijinder,M.  
AUTHORS Sequences involved in phenomena of tumour suppression, tumour  
TITLE reversion, apoptosis and/or resistance to viruses and their use as  
medicines  
JOURNAL Patent: WO 03004526-A 1788 16-JAN-2003;  
FEATURES Molecular Engines Laboratories (FR)  
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ACCESSION AX727498  
VERSION AX727498.1 GI:30506841  
KEYWORDS Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
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REFERENCE Telerman,A., Amson,R. and Tuijinder,M.  
AUTHORS Sequences involved in phenomena of tumour suppression, tumour  
TITLE reversion, apoptosis and/or virus resistance and their use as  
medicines  
JOURNAL Patent: WO 03025176-A 5185 27-MAR-2003;  
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VERSION AX730036.1 GI:30509379  
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ORGANISM Homo sapiens  
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REFERENCE Telerman,A., Amson,R. and Tuijinder,M.  
AUTHORS Sequences involved in phenomena of tumour suppression, tumour  
TITLE reversion, apoptosis and/or virus resistance and their use as  
medicines  
JOURNAL Patent: WO 03025175-A 1670 27-MAR-2003;  
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VERSION     AX731799.1 GI:30511142
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SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL     Telerman, A., Anson, R. and Tuijinder, M.
FEATURES    Sequences involved in phenomena of tumour suppression, tumour
SOURCE      reversion, apoptosis and/or virus resistance and their use as
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Patent: WO 03025175-A 3433 27-MAR-2003;
Molecular   Engines Laboratories (FR)
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ACCESSION  AX732235
VERSION     AX732235.1 GI:30511578
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SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL     Telerman, A., Anson, R. and Tuijinder, M.
FEATURES    Sequences involved in phenomena of tumour suppression, tumour
SOURCE      reversion, apoptosis and/or virus resistance and their use as
Molecular   medicines
Patent: WO 03025175-A 3869 27-MAR-2003;
Molecular   Engines Laboratories (FR)
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ACCESSION  AX734589
VERSION     AX734589.1 GI:30513866
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL     Telerman, A., Anson, R. and Tuijinder, M.
FEATURES    Sequences involved in phenomena of tumour suppression, tumour
SOURCE      reversion, apoptosis and/or resistance to viruses and the use
Molecular   thereof as medicaments
Patent: WO 03025177-A 179 27-MAR-2003;
Molecular   Engines Laboratories (FR)
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ACCESSION  AX738033
VERSION     AX738033.1 GI:30517321
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SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL     Telerman, A., Anson, R. and Tuijinder, M.
FEATURES    Sequences involved in phenomena of tumour suppression, tumour
SOURCE      reversion, apoptosis and/or resistance to viruses and the use
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VERSION  A39511.1 GI:2295829
KEYWORDS
ORGANISM unidentified
SOURCE   unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS  Mehtali,M. and Sorg,T.
TITLE    TAT transdominant variants from human Immunodeficiency virus
JOURNAL  TRANSGENE SA (FR)
COMMENT  Patent: EP 0614980-A 6 14-SEP-1994;
        Other publication CA 2112652 940705
        Other publication JP 6234791 940823
        Other publication AU 5280393 940714
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        Other publication FR 2700169 940708.
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ACCESSION AR166936
VERSION  AR166936.1 GI:16243331
KEYWORDS
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS  Mehtali,M. and Sorg,T.
TITLE    Transdominant TAT variants of the human immunodeficiency virus
JOURNAL  Patent: US 6284252-A 6 04-SEP-2001;
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ACCESSION AR294569
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KEYWORDS
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS  Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE    Biallelic markers for use in constructing a high density
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JOURNAL  Patent: US 6537751-A 6304 25-MAR-2003;
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ACCESSION AX298850
VERSION  AX298850.1 GI:17128840
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ORGANISM Mus sp.
REFERENCE 1
AUTHORS  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE    Bachmanov,A.A., Beauchamp,G.K., Chatterjee,A., de Jong,P.J., Li,S.,
        Li,X., Ohmen,J.D., Reed,D.R., Ross,D. and Tordoff,M.G.
        Gene and sequence variation associated with sensing carbohydrate
        compounds and other sweeteners
JOURNAL  Patent: WO 0183749-A 484 08-NOV-2001;
        WARNER-LAMBERT COMPANY (US) ; The Monell Chemical Senses Center
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ACCESSION AX327004
VERSION  AX327004.1 GI:18097715
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SOURCE   synthetic construct
ORGANISM synthetic construct
REFERENCE 1

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AUTHORS Keith, T.  
 TITLE Novel human gene relating to respiratory diseases, obesity, and  
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 JOURNAL Patent: WO 0178894-A 200 25-OCT-2001;  
 Genome Therapeutics Corp. (US)

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 ACCESSION AB069488  
 VERSION AB069488.1 GI:15130292  
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 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 artificial sequences.

REFERENCE 1  
 CHEN, Y. Z., HAYASHI, Y., WU, J. G., TAKAKA, E., MAEKAWA, K.,  
 WATANABE, N., INAZAWA, J., HOSODA, F., ARAI, Y., MIZUSHIMA, H.,  
 MOROHASHI, A., OHIRA, M., NAKAGAWARA, A., LIU, S., HOSHI, M., HORII, A.  
 and Soeda, E.  
 A BAC-based STS-content map spanning a 35-Mb region of human  
 chromosome 1p35-p36

JOURNAL Chromosomes 74 (1), 55-70 (2001)  
 MEDLINE 21269192  
 PUBMED 11374902  
 REFERENCE 2 (bases 1 to 20)  
 AUTHORS Horii, A.  
 TITLE Direct Submission  
 JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of  
 Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,  
 Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,  
 Tel: 81-22-717-8042, Fax: 81-22-717-8047)

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 11:36:21 ; Search time 260.089 Seconds  
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93.410 Million cell updates/sec

Title: US-09-540-843-2

Perfect score: 9

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- 4: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.\*
- 5: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.\*
- 6: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.\*
- 7: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.\*
- 8: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.\*
- 9: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.\*
- 10: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.\*
- 11: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.\*
- 12: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.\*
- 13: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.\*
- 14: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.\*
- 15: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.\*
- 16: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.\*
- 17: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.\*
- 18: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.\*
- 19: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.\*
- 20: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.\*
- 21: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.\*
- 22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.\*
- 23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*
- 24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*
- 25: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	100.0	9	20	AAZ10693
2	9	100.0	9	23	AAZ14906
3	9	100.0	10	25	ACC41655
4	9	100.0	12	23	ABH73149
5	9	100.0	12	23	ABH79033
6	9	100.0	12	23	ABH83668
7	9	100.0	12	23	ABH86802
8	9	100.0	12	23	ABH95571

C	9	9	100.0	12	23	ABH99034	Oligonucleotide pr
	10	9	100.0	12	23	ABI06447	Oligonucleotide pr
	11	9	100.0	12	23	ABI14652	Oligonucleotide pr
	12	9	100.0	12	23	ABI16049	Oligonucleotide pr
C	13	9	100.0	12	23	ABI138611	Oligonucleotide pr
	14	9	100.0	12	23	ABI39203	Oligonucleotide pr
	15	9	100.0	12	23	ABI40401	Oligonucleotide pr
C	16	9	100.0	12	23	ABI75163	Oligonucleotide pr
C	17	9	100.0	12	23	ABI76166	Oligonucleotide pr
	18	9	100.0	12	23	ABI78087	Oligonucleotide pr
C	19	9	100.0	12	23	ABI80232	Oligonucleotide pr
	20	9	100.0	13	23	ABC06168	Oligonucleotide SE
C	21	9	100.0	13	23	ABC06169	Oligonucleotide SE
	22	9	100.0	13	23	ABC20906	Oligonucleotide SE
C	23	9	100.0	13	23	ABC20907	Oligonucleotide SE
	24	9	100.0	13	23	ABC40316	Oligonucleotide SE
C	25	9	100.0	13	23	ABC40317	Oligonucleotide SE
	26	9	100.0	13	23	ABC54924	Oligonucleotide SE
C	27	9	100.0	13	23	ABC54925	Oligonucleotide SE
	28	9	100.0	13	23	ABC72172	Oligonucleotide SE
C	29	9	100.0	13	23	ABC72173	Oligonucleotide SE
	30	9	100.0	13	23	ABC84890	Oligonucleotide SE
C	31	9	100.0	13	23	ABC84891	Oligonucleotide SE
	32	9	100.0	13	23	ABF18052	Oligonucleotide SE
C	33	9	100.0	13	23	ABF18053	Oligonucleotide SE
	34	9	100.0	13	23	ABF28786	Oligonucleotide SE
C	35	9	100.0	13	23	ABF28787	Oligonucleotide SE
	36	9	100.0	13	23	ABF66366	Oligonucleotide SE
C	37	9	100.0	13	23	ABF66367	Oligonucleotide SE
	38	9	100.0	13	23	ABF92852	Oligonucleotide SE
C	39	9	100.0	13	23	ABF92853	Oligonucleotide SE
	40	9	100.0	13	23	ABH01812	Oligonucleotide SE
C	41	9	100.0	13	23	ABH01813	Oligonucleotide SE
	42	9	100.0	13	23	ABH16364	Oligonucleotide SE
C	43	9	100.0	13	23	ABH16365	Oligonucleotide SE
	44	9	100.0	13	23	ABH32012	Oligonucleotide SE
C	45	9	100.0	13	23	ABH32013	Oligonucleotide SE

ALIGNMENTS

RESULT 1  
AAZ10693  
ID AAZ10693 standard; DNA; 9 BP.  
XX  
AC AAZ10693;  
XX  
23-NOV-1999 (first entry)  
DE Oligonucleotide sequence that increases p53 activity in a cell.  
XX p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;  
KW UV-induced hyperproliferative disease; psoriasis; vitiligo;  
KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;  
KW skin cancer; ss.  
XX  
OS Synthetic.  
XX  
PN GB2336157-A.  
XX  
PD 13-OCT-1999.  
XX  
PF 24-MAR-1999; 99GB-0006758.  
XX  
PR 26-MAR-1998; 98US-0048927.  
PA (UYBO-) UNIV BOSTON.  
XX  
PI Gilchrest BA, Yaar M, Eller M;  
XX  
DR WPI; 1999-543520/46.  
XX

PT DNA fragments useful for increasing p53 activity in a cell and reducing  
 PT susceptibility to UV-induced hyperproliferative diseases -  
 XX Claim 11; Page 29; 44pp; English.

XX AA210692-97 represent DNA fragments that are used for increasing p53  
 CC activity in a cell. The oligonucleotides are UV mimetics and  
 CC protect cells against subsequent exposure to UV-irradiation or  
 CC chemicals. The oligonucleotides are useful for increasing p53 activity  
 CC in a cell, reducing the susceptibility to UV-induced hyperproliferative  
 CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic  
 CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging  
 CC and reducing susceptibility to skin cancer.

XX Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;

Query Match 100.0%; Score 9; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+08;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TAGGAGGAT 9  
 |||||  
 1 TAGGAGGAT 9

RESULT 2  
 AAS14906  
 AAS14906 standard; DNA; 9 BP.

AAS14906;

14-FEB-2002 (first entry)

Melanogenesis associated oligonucleotide #2.

Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;  
 anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;  
 immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;  
 tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;  
 carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;  
 conjunctivitis; allergic rhinitis; vitiligo; ss.

Synthetic.

WO200174342-A2.

11-OCT-2001.

30-MAR-2001; 2001WO-US10162.

31-MAR-2000; 2000US-0540843.

(UYBO-) UNIV BOSTON.

Gilchrest BA, Yaar M, Eller M;

WPI; 2001-626338/72.

Inhibiting proliferation of epithelial cells, useful e.g. for treating  
 carcinoma, using specific oligonucleotides that mimic the effects of  
 ultra-violet light -

Claim 1; Page 36; 74pp; English.

The invention describes inhibition of mammalian epithelial cell  
 proliferation by treating cells with at least one oligonucleotide, or  
 its fragment. The compounds, which have cytostatic, anti-allergic,  
 anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and  
 immunosuppressive activities, function as 'ultra-violet mimics' to induce  
 DNA repair processes (or a protective response to later exposure to  
 radiation or chemicals), as a proliferation inhibitor, apoptosis inducer  
 or a tumour necrosis factor inhibitor. Probably they mimic products of  
 DNA damage, or processed DNA-damage intermediates, by inducing the p53

CC pathway, resulting in transient arrest of cell growth, allowing more time  
 CC for DNA repair to occur before cell division takes place. The method is  
 CC especially used to treat carcinoma but may also be used to: treat other  
 CC hyperproliferative states (e.g. psoriasis or precancerous conditions);  
 CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat  
 CC allergically mediated inflammation (atopic or contact dermatitis,  
 CC allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in  
 CC cells caused by radiation or chemicals; increase melanin production  
 CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to  
 CC promote apoptosis in epithelial cells that contain damaged DNA. Also  
 CC oligonucleotides that contain non-hydrolyzable backbones are used to  
 CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This  
 CC sequence is melanogenesis associated oligonucleotide #2, a scrambled  
 CC version of the oligonucleotide shown in AAS14905, one of the  
 CC oligonucleotides used to inhibit mammalian epithelial cell proliferation,  
 CC described in the method of the invention.

XX Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;

Query Match 100.0%; Score 9; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+08;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAGGAGGAT 9  
 |||||  
 Db 1 TAGGAGGAT 9

RESULT 3  
 ACC41655  
 ID ACC41655 standard; DNA; 10 BP.

AC ACC41655;

DT 21-MAY-2003 (first entry)

Zinc finger protein DNA-binding domain target sequence SEQ ID NO:202.

Zinc finger domain; zinc finger; zinc finger binding domain; probe;  
 chimeric nucleic acid; library; PCR primer; ss.

Synthetic.

WO2003016571-A1.

27-FEB-2003.

17-AUG-2002; 2002WO-KR01560.

17-AUG-2001; 2001US-313402P.

22-APR-2002; 2002US-374355P.

(TOOL-) TOOLGEN INC.

Kim J, Bae K, Park K, Kwon Y, Ryu E, Hwang M;

WPI; 2003-268344/26.

New library comprising polypeptides having zinc finger domains, useful  
 for producing chimeric nucleic acids -

Claim 40; Page 101; 234pp; English.

The present invention describes a library comprising polypeptides. Each  
 polypeptide comprises a first or second zinc finger domain. The domains  
 of each polypeptide are identical to a zinc finger domain from a  
 naturally occurring protein and either do not occur in the same naturally  
 occurring protein or occur in the same naturally occurring protein in a  
 different configuration than in the polypeptide. The domains vary among  
 polypeptides. Also described: (1) producing chimeric nucleic acids;  
 (2) generating an artificial zinc finger polypeptide that specifically  
 binds to a target DNA site; and (3) identifying a nucleic acid encoding  
 a zinc finger polypeptide that specifically recognises a target DNA site.

CC The library can be used for producing chimeric nucleic acids. ACC41551  
 CC to ACC41758 and ABR40919 to ABR41015 represent nucleotide and amino acid  
 CC sequences given in the exemplification of the present invention.  
 XX  
 SQ Sequence 10 BP; 3 A; 0 C; 5 G; 2 T; 0 other;

Query Match 100.0%; Score 9; DB 25; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+04;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAGGAGGAT 9  
 DB 2 TAGGAGGAT 10

## RESULT 4

ABH73149  
 ID ABH73149 standard; DNA; 12 BP.

XX AC ABH73149;  
 XX XX

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 273134 for detecting SNP TSC0003058.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB00713.

XX 07-APR-2000; 2000DE-1019173.

XX (EPIC-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 XX designed to detect single nucleotide polymorphisms and cytosine  
 XX methylation status -

XX Claim 1; SEQ ID 273134; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 XX and cytosine methylation status in chemically pretreated genomic DNA. The  
 XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 XX range of diseases including immune system, gastrointestinal, respiratory,  
 XX central nervous system, cardiovascular and metabolic disorders. The  
 XX oligomers are also used for detecting cell type differentiation.  
 XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and  
 XX ABH00010-ABH82073 represent the oligomers described in the invention.  
 XX NOTE: The sequence data for this patent did not form part of the printed  
 XX specification, but was obtained in electronic format from WIPO at  
 XX ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 12 BP; 4 A; 0 C; 6 G; 2 T; 0 other;

Query Match 100.0%; Score 9; DB 23; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+04;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAGGAGGAT 9  
 DB 3 TAGGAGGAT 11

## RESULT 5

ABH79033/c  
 ID ABH79033 standard; DNA; 12 BP.

XX AC ABH79033;  
 XX XX

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 279026 for detecting SNP TSC0006799.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB00713.

XX 07-APR-2000; 2000DE-1019173.

XX (EPIC-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 XX designed to detect single nucleotide polymorphisms and cytosine  
 XX methylation status -

XX Claim 1; SEQ ID 279026; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 XX and cytosine methylation status in chemically pretreated genomic DNA. The  
 XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 XX range of diseases including immune system, gastrointestinal, respiratory,  
 XX central nervous system, cardiovascular and metabolic disorders. The  
 XX oligomers are also used for detecting cell type differentiation.  
 XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and  
 XX ABH00010-ABH82073 represent the oligomers described in the invention.  
 XX NOTE: The sequence data for this patent did not form part of the printed  
 XX specification, but was obtained in electronic format from WIPO at  
 XX ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 other;

Query Match 100.0%; Score 9; DB 23; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+04;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAGGAGGAT 9  
 DB 12 TAGGAGGAT 4

## RESULT 6

ABH83668  
 ID ABH83668 standard; DNA; 12 BP.

XX AC ABH83668;  
 XX XX

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 283661 for detecting SNP TSC0011446.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB00713.

07-APR-2000; 2000DE-1019173.

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Berlin K;

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is  
designed to detect single nucleotide polymorphisms and cytosine  
methylation status -

Claim 1; SEQ ID 283661; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic  
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
and cytosine methylation status in chemically pretreated genomic DNA. The  
oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
range of diseases including immune system, gastrointestinal, respiratory,  
central nervous system, cardiovascular and metabolic disorders. The  
oligonucleotides are also used for detecting cell type differentiation.

AB000010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

ABT00010-ABT82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed  
specification, but was obtained in electronic format from WIPO at  
ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 12 BP; 4 A; 0 C; 6 G; 2 T; 0 other;

Query Match 100.0%; Score 9; DB 23; Length 12;

Best Local Similarity 100.0%; Pred. No. 2.9e+04;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TAGGAGGAT 9

|||||||

3 TAGGAGGAT 11

RESULT 7

ABH86802/c

ABH86802 standard; DNA; 12 BP.

ABH86802;

22-FEB-2002 (first entry)

Oligonucleotide primer SEQ ID NO 286795 for detecting SNP TSC0012825.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB00713.

07-APR-2000; 2000DE-1019173.

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Berlin K;

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is  
designed to detect single nucleotide polymorphisms and cytosine  
methylation status -

Claim 1; SEQ ID 286795; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic  
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
and cytosine methylation status in chemically pretreated genomic DNA. The  
oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
range of diseases including immune system, gastrointestinal, respiratory,  
central nervous system, cardiovascular and metabolic disorders. The  
oligonucleotides are also used for detecting cell type differentiation.

AB000010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

ABT00010-ABT82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed  
specification, but was obtained in electronic format from WIPO at  
ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 other;

Query Match 100.0%; Score 9; DB 23; Length 12;

Best Local Similarity 100.0%; Pred. No. 2.9e+04;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TAGGAGGAT 9

|||||||

9 TAGGAGGAT 1

RESULT 8

ABH95571

ID ABH95571 standard; DNA; 12 BP.

ABH95571;

22-FEB-2002 (first entry)

Oligonucleotide primer SEQ ID NO 295564 for detecting SNP TSC0016640.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB00713.

07-APR-2000; 2000DE-1019173.

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Berlin K;

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is  
designed to detect single nucleotide polymorphisms and cytosine  
methylation status -

Claim 1; SEQ ID 295564; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation.  
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and  
 CC ABH00010-ABH82073 represent the oligomers described in the invention.  
 CC NOTE: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 SQ Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 other;

Query Match 100.0%; Score 9; DB 23; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+04;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TAGGAGGAT 9  
 DB 4 TAGGAGGAT 12  
 |||||

RESULT 9  
 ID ABH99034/C  
 AC ABH99034 standard; DNA; 12 BP.  
 AC ABH99034;  
 DT 22-FEB-2002 (first entry)

Oligonucleotide primer SEQ ID NO 299027 for detecting SNP TSC0018404.  
 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 Homo sapiens.

WO200177384-A2.  
 18-OCT-2001.  
 06-APR-2001; 2001WO-IB00713.  
 07-APR-2000; 2000DE-1019173.  
 (EPIG-) EPIGENOMICS AG.  
 Olek A, Piepenbrock C, Berlin K;  
 WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is  
 designed to detect single nucleotide polymorphisms and cytosine  
 methylation status -  
 Claim 1; SEQ ID 299027; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic  
 acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 and cytosine methylation status in chemically pretreated genomic DNA. The  
 oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 range of diseases including immune system, gastrointestinal, respiratory,  
 central nervous system, cardiovascular and metabolic disorders. The  
 oligomers are also used for detecting cell type differentiation.  
 ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and  
 ABH00010-ABH82073 represent the oligomers described in the invention.  
 NOTE: The sequence data for this patent did not form part of the printed  
 specification, but was obtained in electronic format from WIPO at  
 ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 12 BP; 3 A; 5 C; 0 G; 4 T; 0 other;

Query Match 100.0%; Score 9; DB 23; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+04;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TAGGAGGAT 9  
 DB 12 TAGGAGGAT 4  
 |||||

RESULT 10  
 ID ABI06447  
 AC ABI06447 standard; DNA; 12 BP.  
 AC ABI06447;  
 DT 22-FEB-2002 (first entry)

Oligonucleotide primer SEQ ID NO 306420 for detecting SNP TSC0022000.  
 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 Homo sapiens.

WO200177384-A2.  
 18-OCT-2001.  
 06-APR-2001; 2001WO-IB00713.  
 07-APR-2000; 2000DE-1019173.  
 (EPIG-) EPIGENOMICS AG.  
 Olek A, Piepenbrock C, Berlin K;  
 WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is  
 designed to detect single nucleotide polymorphisms and cytosine  
 methylation status -  
 Claim 1; SEQ ID 306420; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic  
 acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 and cytosine methylation status in chemically pretreated genomic DNA. The  
 oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 range of diseases including immune system, gastrointestinal, respiratory,  
 central nervous system, cardiovascular and metabolic disorders. The  
 oligomers are also used for detecting cell type differentiation.  
 ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and  
 ABH00010-ABH82073 represent the oligomers described in the invention.  
 NOTE: The sequence data for this patent did not form part of the printed  
 specification, but was obtained in electronic format from WIPO at  
 ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 12 BP; 4 A; 0 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 9; DB 23; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+04;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TAGGAGGAT 9  
 DB 1 TAGGAGGAT 9  
 |||||

RESULT 11  
 ID AB114652  
 AB114652 standard; DNA; 12 BP.

XX AC AB114652;  
 XX DT 22-FEB-2002 (first entry)  
 XX DE Oligonucleotide primer SEQ ID NO 314625 for detecting SNP TSC0026468.  
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX OS Homo sapiens.  
 XX PN WO200177384-A2.  
 XX PD 18-OCT-2001.  
 XX PR 06-APR-2001; 2001WO-IB00713.  
 XX PR 07-APR-2000; 2000DE-1019173.  
 XX PR (EPIG-) EPIGENOMICS AG.  
 XX PI Olek A, Piepenbrock C, Berlin K;  
 XX PI WPI; 2001-657177/75.  
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 XX PT designed to detect single nucleotide polymorphisms and cytosine  
 XX PT methylation status -  
 XX PS Claim 1; SEQ ID 314625; 29pp + Sequence Listing; German.  
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
 XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 XX CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 XX CC range of diseases including immune system, gastrointestinal, respiratory,  
 XX CC central nervous system, cardiovascular and metabolic disorders. The  
 XX CC oligomers are also used for detecting cell type differentiation.  
 XX CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and  
 XX CC ABT00010-ABT99989 represent the oligomers described in the invention.  
 XX CC NOTE: The sequence data for this patent did not form part of the printed  
 XX CC specification, but was obtained in electronic format from WIPO at  
 XX CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX SQ Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 other;  
 XX  
 XX Query Match 100.0%; Score 9; DB 23; Length 12;  
 XX Best Local Similarity 100.0%; Pred. No. 2.9e+04;  
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX Qy 1 TAGGAGGAT 9  
 XX Db |||||  
 XX 4 TAGGAGGAT 12  
 XX  
 XX RESULT 12  
 XX AB116049  
 XX ID AB116049 standard; DNA; 12 BP.  
 XX AC AB116049;  
 XX DT 22-FEB-2002 (first entry)  
 XX DE Oligonucleotide primer SEQ ID NO 316022 for detecting SNP TSC0027234.  
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX OS Homo sapiens.

PN WO200177384-A2.  
 XX PD 18-OCT-2001.  
 XX PR 06-APR-2001; 2001WO-IB00713.  
 XX PR 07-APR-2000; 2000DE-1019173.  
 XX PR (EPIG-) EPIGENOMICS AG.  
 XX PI Olek A, Piepenbrock C, Berlin K;  
 XX PI WPI; 2001-657177/75.  
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 XX PT designed to detect single nucleotide polymorphisms and cytosine  
 XX PT methylation status -  
 XX PS Claim 1; SEQ ID 316022; 29pp + Sequence Listing; German.  
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic  
 XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 XX CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 XX CC range of diseases including immune system, gastrointestinal, respiratory,  
 XX CC central nervous system, cardiovascular and metabolic disorders. The  
 XX CC oligomers are also used for detecting cell type differentiation.  
 XX CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and  
 XX CC ABT00010-ABT99989 represent the oligomers described in the invention.  
 XX CC NOTE: The sequence data for this patent did not form part of the printed  
 XX CC specification, but was obtained in electronic format from WIPO at  
 XX CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX SQ Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 other;  
 XX  
 XX Query Match 100.0%; Score 9; DB 23; Length 12;  
 XX Best Local Similarity 100.0%; Pred. No. 2.9e+04;  
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX Qy 1 TAGGAGGAT 9  
 XX Db |||||  
 XX 2 TAGGAGGAT 10  
 XX  
 XX RESULT 13  
 XX AB138611/C  
 XX ID AB138611 standard; DNA; 12 BP.  
 XX AC AB138611;  
 XX DT 22-FEB-2002 (first entry)  
 XX DE Oligonucleotide primer SEQ ID NO 338584 for detecting SNP TSC0040564.  
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX OS Homo sapiens.  
 XX PN WO200177384-A2.  
 XX PD 18-OCT-2001.  
 XX PR 06-APR-2001; 2001WO-IB00713.  
 XX PR 07-APR-2000; 2000DE-1019173.  
 XX PR (EPIG-) EPIGENOMICS AG.  
 XX PI Olek A, Piepenbrock C, Berlin K;  
 XX PI WPI; 2001-657177/75.  
 XX DR



09980559 ၀၈/၀၅/၁၉/၂၀၀၈

Qv 1 TAGGAGGAT 9  
| | | | |  
Db 1 TAGGAGGAT 9

Search completed: December 31, 2003, 15:08:13  
Job time : 261.089 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 13:58:09 ; Search time 1034.09 Seconds  
(without alignments)  
211.530 Million cell updates/sec

Title: US-09-540-843-2  
Perfect score: 9  
Sequence: 1 tagaggat 9

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 33330

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_man:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	88.9	19	28	AZ500675 1M0339J10
2	8	88.9	20	28	AZ393773 1M0157B04
3	8	88.9	21	28	AZ387199 1M0146P20
4	8	88.9	21	28	AZ645664 1M0511C13

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5	8	88.9	22	9	AI631347
6	8	88.9	23	28	AZ411934
7	8	88.9	24	28	AZ822831
8	8	88.9	24	12	BG925475
9	8	88.9	24	28	AZ503909
10	8	88.9	24	28	BH789331
11	8	88.9	25	28	AZ491057
12	8	88.9	25	28	AZ496986
13	8	88.9	27	13	B0592300
14	8	88.9	27	28	BH903668
15	8	88.9	28	28	AZ480483
16	8	88.9	28	28	AZ799431
17	8	88.9	29	14	N22525
18	8	88.9	29	28	AZ759923
19	8	88.9	29	28	BH904824
20	8	88.9	29	29	TA6H120
21	8	88.9	30	28	AZ312621
22	8	88.9	30	28	AZ658025
23	8	88.9	30	28	AZ817062
24	7.4	82.2	19	28	AZ375581
25	7.4	82.2	19	28	AZ481449
26	7.4	82.2	20	28	AZ592780
27	7.4	82.2	21	28	AZ316626
28	7.4	82.2	21	29	TA27H100
29	7.4	82.2	22	9	AA912639
30	7.4	82.2	22	9	AW246467
31	7.4	82.2	23	28	AZ345904
32	7.4	82.2	23	28	AZ346779
33	7.4	82.2	23	29	TA12H100
34	7.4	82.2	23	29	TA264E04Q
35	7.4	82.2	24	28	AZ488765
36	7.4	82.2	24	28	AZ805942
37	7.4	82.2	25	14	L32051
38	7.4	82.2	25	28	AZ483180
39	7.4	82.2	25	29	BZ596812
40	7.4	82.2	26	28	AG263801
41	7.4	82.2	26	28	AZ307304
42	7.4	82.2	26	29	CC458487
43	7.4	82.2	27	28	AZ345588
44	7.4	82.2	27	28	AZ827243
45	7.4	82.2	28	28	AZ463404

ALIGNMENTS

RESULT 1	AZ500675	19 bp	DNA	linear	GSS 05-OCT-2000
LOCUS	1M0339J10F	Mouse 10kb plasmid	UUGC1M	library	Mus musculus genomic
DEFINITION	clone UUGC1M0339J10 F,	genomic survey	sequence.		
ACCESSION	AZ500675	GI:10680728			
VERSION	GSS.				
KEYWORDS	Mus musculus				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Eukaryota; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 19)				
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177				

Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0339 row: J column: 10  
 Seq primer: CGTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers

## FEATURES

source

1. 19  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0339J10"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT  
 ORIGIN

Query Match 88.9%; Score 8; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TAGGAGGA 8  
 |||||  
 11 TAGGAGGA 18

## RESULT 2

AZ393773/c

LOCUS AZ393773 20 bp DNA linear GSS 03-OCT-2000  
 DEFINITION IM0157B04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0157B04 F, genomic survey sequence.

ACCESSION

AZ393773

VERSION

GSS.

KEYWORDS

Mus musculus (house mouse)

SOURCE

Mus musculus

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah

University of Utah

Rm. 308, Biomedical

84112, USA

Tel: 801 585 5606

20 S. 2030 E., SLC, UT

Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0157 row: B column: 04  
 Seq primer: CGTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 20.  
 Location/Qualifiers

## FEATURES

source

1. 20  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0157B04"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 11 c 1 g 6 t

## ORIGIN

Query Match 88.9%; Score 8; DB 28; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 AGGAGGAT 9  
 |||||  
 Db 20 AGGAGGAT 13

## RESULT 3

AZ387199/c

LOCUS

DEFINITION

ACCESSION

AZ387199

VERSION

GSS.

KEYWORDS

Mus musculus (house mouse)

SOURCE

Mus musculus

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah

University of Utah

Rm. 308, Biomedical

84112, USA

20 S. 2030 E., SLC, UT

84112, USA

```

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0146 row: P column: 20
Seq primer: CACACAGGAACACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. 21
/organism="Mus musculus"
/mol_type="genomic DNA"
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/db_xref="taxon:10090"
/clone="UUGC1M0146P20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
3 a 13 c 0 g 5 t
BASE COUNT
ORIGIN
Query Match 88.9%; Score 8; DB 28; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 TAGGAGGA 8
|||||||
15 TAGGAGGA 8
Db

RESULT 4
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
AZ645664 21 bp DNA linear GSS 14-DEC-2000
1M0511C13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0511C13 F, genomic survey sequence.
AZ645664
AZ645664.1 GI:11775376
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
1 (bases 1 to 21)
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0511 row: C column: 13
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
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/mol_type="genomic DNA"
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/db_xref="taxon:10090"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
2 a 9 c 0 g 10 t
BASE COUNT
ORIGIN
Query Match 88.9%; Score 8; DB 28; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 TAGGAGGA 8
|||||||
8 TAGGAGGA 1
Db

RESULT 5
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
AI631347 22 bp mRNA linear EST 16-DEC-1999
tz83c04.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2295174 3'
similar to SW:PRP2_HUMAN P02812 SALIVARY PROLINE-RICH PROTEIN
PRECURSOR ; contains element MER22 repetitive element ;, mRNA
sequence.
AI631347
AI631347.1 GI:4682677
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 22)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center

```

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
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High quality sequence stop: 1.  
Location/Qualifiers

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/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: Salt; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"

BASE COUNT 6 a 9 c 5 g 2 t

#### ORIGIN

Query Match 88.9%; Score 8; DB 9; Length 22;  
Best Local Similarity 100.0%; Pred. No. 6.2e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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12 TAGGAGGA 19

#### RESULT 6

AZ411934/c  
LOCUS  
DEFINITION  
1M0185M09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0185M09 F, genomic survey sequence.

ACCESSION  
AZ411934  
VERSION  
GSS.  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00  
Plate: 0185 row: M column: 09  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers

#### FEATURES

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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD22nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD22 (G14732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 8 c 5 g 7 t

#### ORIGIN

Query Match 88.9%; Score 8; DB 28; Length 22;  
Best Local Similarity 100.0%; Pred. No. 6.2e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGGAGGAT 9  
|||||||  
Db 9 AGGAGGAT 2

#### RESULT 7

AZ822831/c  
LOCUS  
DEFINITION  
2M0096J21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0096J21 F, genomic survey sequence.

ACCESSION  
AZ822831  
VERSION  
GSS.  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00  
Plate: 0096 row: J column: 21  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 23.  
Location/Qualifiers

#### JOURNAL COMMENT

1..23  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"

#### FEATURES

1..23  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"

Copied from 0998055 on 05/19/2004

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 4 a 3 c 9 g 8 t

ORIGIN

Query Match 88.9%; Score 8; DB 28; Length 24;  
Best Local Similarity 100.0%; Pred. No. 6.3e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAGGAGGA 8  
| | | | | | | |  
Db 7 TAGGAGGA 14

RESULT 10  
BH789331/c

LOCUS 24 bp DNA linear GSS 02-APR-2002

DEFINITION SALK\_019058.23.05.x Arabidopsis thaliana TDNA insertion lines

DESCRIPTION Arabidopsis thaliana genomic clone SALK\_019058.23.05.x, genomic survey sequence.

ACCESSION BH789331

VERSION BH789331.1 GI:19882429

KEYWORDS GSS.

ORGANISM Arabidopsis thaliana (thale cress)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1 (bases 1 to 24)

AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J., and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL Unpublished

COMMENT Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of TDNA.

FEATURES

Location/Qualifiers

1..24

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SALK\_019058.23.05.x"

/clone\_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

BASE COUNT 2 a 14 c 0 g 8 t

ORIGIN

Query Match 88.9%; Score 8; DB 28; Length 24;  
Best Local Similarity 100.0%; Pred. No. 6.3e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGGAGGAT 9  
| | | | | | | |  
Db 8 AGGAGGAT 1

RESULT 11

AZ491057

LOCUS 25 bp DNA linear GSS 05-OCT-2000

DEFINITION M0324124F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0324124 F, genomic survey sequence.

ACCESSION AZ491057

VERSION AZ491057.1 GI:10662392

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 25)

AUTHORS Dunn,D., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,Islam,H., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A., and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0324 row: I column: 24  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 25.

FEATURES

Location/Qualifiers

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/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0324124"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 7 a 4 c 12 g 2 t

ORIGIN

Query Match 88.9%; Score 8; DB 28; Length 25;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGGAGGAT 9  
| | | | | | | |  
Db 9 AGGAGGAT 16



RESULT 12  
A2496986 25 bp DNA linear GSS 05-OCT-2000  
LOCUS 1M0333H09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION Clone UUGC1M0333H09 R, genomic survey sequence.  
ACCESSION A2496986  
VERSION A2496986.1 GI:10673556  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 25)  
REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
TITLE Unpublished  
JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0333 row: H column: 09  
Seq primer: CACACAGGAACACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 25.  
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source Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0333H09"  
/sex="Male"  
/lab\_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWB42 (gil4732114[gb]|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 12 a 1 c 10 g 2 t  
ORIGIN  
Query Match 88.9%; Score 8; DB 28; Length 25;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TAGGAGCA 8  
|||||  
Db 17 TAGGAGCA 24

RESULT 13  
BQ592300/c 27 bp mRNA linear EST 06-DEC-2002  
LOCUS BQ592300  
DEFINITION BQ592300 27 bp mRNA linear EST 06-DEC-2002  
CDNA clone 024-021-P06 5-PRIME, mRNA sequence.  
ACCESSION BQ592300  
VERSION BQ592300.1 GI:26121873  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Anaranthaceae; Beta.  
1 (bases 1 to 27)  
REFERENCE Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radloff,U.  
AUTHORS Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
Contact: Weishaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weishaar@mpiz-koeln.mpg.de  
Insert Length: 27 Std Error: 0.00  
Plate: 21 row: P column: 06  
Seq primer: SP6; CATACGATTAGTGACACTATAG.  
FEATURES  
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/cultivar="KWS320 (double haploid, monogerm breeding line  
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/db\_xref="taxon:161934"  
/clone="024-021-P06"  
/tissue\_type="developing root"  
/lab\_host="EMDH10B"  
/clone\_lib="MPIZ-ADIS-024-developing root"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet project  
, local PI: Dr. Katharina Schneider, coordinator: Prof.  
Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

BASE COUNT 8 a 5 c 5 g 9 t  
ORIGIN  
Query Match 88.9%; Score 8; DB 13; Length 27;  
Best Local Similarity 100.0%; Pred. No. 6.6e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 AGGAGGAT 9  
|||||  
Db 18 AGGAGGAT 11

RESULT 14  
BH903668 27 bp DNA linear GSS 04-SEP-2002  
LOCUS BH903668  
DEFINITION SALK\_103141.14.55.x Arabidopsis thaliana TDNA insertion lines  
Arabidopsis thaliana genomic clone SALK\_103141.14.55.x, genomic  
survey sequence.  
ACCESSION BH903668  
VERSION BH903668.1 GI:22714878  
KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
 ; eurosid II; Brassicales; Brassicaceae; Arabidopsi.  
 1 (bases 1 to 27)  
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab  
 ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,  
 Zimmerman,J. and Ecker,J.R.  
 A Sequence-Indexed Library of Insertion Mutations in the  
 Arabidopsis genome  
 JOURNAL Unpublished  
 COMMENT Contact: Joseph R. Ecker  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: ecker@salk.edu  
 This is single pass sequence recovered from the left border of  
 TDNA. This sequence lies within an annotated exon of Atgll1590.  
 Class: TDNA tagged.  
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 /organism="Arabidopsis thaliana"  
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 /note="PCR was performed on Arabidopsis thaliana lines  
 each of which contains one or more TDNA insertion  
 elements. The resultant fragment for each line was  
 directly sequenced to determine the genomic sequence at  
 the site of insertion. Details of the protocols used can  
 be found at http://signal.salk.edu/tdna\_protocols.html"  
 BASE COUNT 8 a 2 c 11 g 6 t  
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 Query Match 88.9%; Score 8; DB 28; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 6.6e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 TAGGAGGA 8  
 |||||  
 15 TAGGAGGA 22  
 RESULT 15  
 LOCUS AZ480483/c  
 DEFINITION 1M0302J04F Mouse 10kb plasmid UUGClM library Mus musculus genomic  
 clone UUGClM0302J04 F, genomic survey sequence.  
 ACCESSION AZ480483  
 VERSION AZ480483.1 GI:10641548  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 28)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
 ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.  
 and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0302 row: J column: 04  
 Seq primer: CGTGTAAACGACGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 28.  
 Location/Qualifiers  
 1..28  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGClM0302J04"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGClM library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."  
 BASE COUNT 4 a 11 c 6 g 7 t  
 ORIGIN  
 Query Match 88.9%; Score 8; DB 28; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 6.6e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TAGGAGGA 8  
 |||||  
 Db 13 TAGGAGGA 6  
 Search completed: December 31, 2003, 19:41:13  
 Job time : 1038.09 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 17:10:00 ; Search time 104.924 Seconds  
(without alignments)  
296.896 Million cell updates/sec

Title: US-09-540-843-2  
Perfect score: 9  
Sequence: 1 taggaggat 9

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2263443 seqs, 1730637950 residues

Total number of hits satisfying chosen parameters: 998502

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:  
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8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:  
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12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:  
13: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:  
14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	100.0	9	15	US-10-122-630-2
2	9	100.0	9	15	US-10-122-633-2
3	9	100.0	10	13	US-10-223-765-202
C 4	9	100.0	16	13	US-09-882-945A-169
C 5	9	100.0	17	13	US-10-340-192-22
C 6	9	100.0	17	13	US-10-339-793-97
7	9	100.0	20	9	US-09-766-154-19
8	9	100.0	20	11	US-09-828-344-162
9	9	100.0	20	11	US-09-828-344-163
10	9	100.0	20	11	US-09-828-344-164
11	9	100.0	20	13	US-10-006-191-104
C 12	9	100.0	21	11	US-09-816-814-13
13	9	100.0	21	13	US-10-160-764-17
C 14	9	100.0	21	13	US-10-165-099-341
C 15	9	100.0	23	13	US-10-027-632-68219

16	9	100.0	23	13	US-10-379-836-12	Sequence 12, Appl
C 17	9	100.0	23	13	US-10-379-836-13	Sequence 13, Appl
C 18	9	100.0	23	14	US-10-027-632-68219	Sequence 68219, A
19	9	100.0	25	15	US-10-098-263B-7075	Sequence 7075, Ap
20	9	100.0	25	15	US-10-098-263B-9560	Sequence 9560, Ap
C 21	9	100.0	25	15	US-10-098-263B-17185	Sequence 17185, A
C 22	9	100.0	25	15	US-10-098-263B-23551	Sequence 23551, A
C 23	9	100.0	25	15	US-10-098-263B-23552	Sequence 23552, A
C 24	9	100.0	25	15	US-10-098-263B-72304	Sequence 72304, A
C 25	9	100.0	25	15	US-10-098-263B-86788	Sequence 86788, A
C 26	9	100.0	25	15	US-10-098-263B-97448	Sequence 97448, A
C 27	9	100.0	25	15	US-10-098-263B-97906	Sequence 97906, A
28	9	100.0	25	15	US-10-098-263B-99873	Sequence 99873, A
29	9	100.0	25	15	US-10-098-263B-99874	Sequence 99874, A
C 30	9	100.0	25	15	US-10-098-263B-112143	Sequence 112143, A
C 31	9	100.0	25	15	US-10-098-263B-125474	Sequence 125474, A
C 32	9	100.0	26	11	US-09-949-427-202	Sequence 202, App
C 33	9	100.0	27	15	US-10-008-140B-15	Sequence 15, Appl
C 34	9	100.0	27	15	US-10-008-140B-26	Sequence 26, Appl
C 35	9	100.0	28	9	US-09-764-246-33	Sequence 33, Appl
C 36	9	100.0	30	13	US-10-104-019-105	Sequence 105, App
C 37	9	100.0	30	13	US-10-428-826-43	Sequence 43, Appl
C 38	9	100.0	30	14	US-10-104-019-105	Sequence 105, App
C 39	9	100.0	30	15	US-10-263-872-28	Sequence 28, Appl
40	8	88.9	10	9	US-09-989-789-1611	Sequence 1611, Ap
41	8	88.9	10	11	US-09-990-186-1611	Sequence 1611, Ap
42	8	88.9	10	11	US-09-989-994-1611	Sequence 1611, Ap
43	8	88.9	10	12	US-10-418-552-53	Sequence 53, Appl
44	8	88.9	10	15	US-10-055-713-67	Sequence 67, Appl
45	8	88.9	10	15	US-10-055-711-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1  
US-10-122-630-2  
; Sequence 2, Application US/10122630  
; Publication No. US20030032610A1  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrist, Barbara A.  
; APPLICANT: Eller, Mark S.  
; APPLICANT: Yaar, Mina  
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
; TITLE OF INVENTION: Oligonucleotides  
; FILE REFERENCE: 0054.1088-018  
; CURRENT APPLICATION NUMBER: US/10/122,630  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US 08/467,012  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: PCT/US96/08386  
; PRIOR FILING DATE: 1996-06-03  
; PRIOR APPLICATION NUMBER: US 09/048,927  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: US 09/540,843  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: PCT/US01/10162  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 9  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA Fragment  
US-10-122-630-2

Query Match 100.0%; Score 9; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.8e+08;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAGGAGGAT 9

Db 1 TAGGAGGAT 9  
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## RESULT 2

US-10-122-633-2  
; Sequence 2, Application US/10122633  
; Publication No. US20030032611A1  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrest, Barbara A.  
; APPLICANT: Eller, Mark S.  
; APPLICANT: Yaar, Mina  
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
; TITLE OF INVENTION: Oligonucleotides  
; FILE REFERENCE: 0054.1088-019  
; CURRENT APPLICATION NUMBER: US/10/122,633  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: US 09/540,843  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: PCT/US01/10162  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 9  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA Fragment  
US-10-122-633-2

Query Match 100.0%; Score 9; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.8e+08; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

1 TAGGAGGAT 9  
|||||

## RESULT 3

US-10-223-765-202  
; Sequence 202, Application US/10223765  
; Publication No. US20030165997A1  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Jin-Soo  
; APPLICANT: Bae, Kwang-Hee  
; APPLICANT: Park, Kyung-Soon  
; APPLICANT: Kwon, Young Do  
; APPLICANT: Ryu, Eun-Hyun  
; APPLICANT: Hwang, Moon-Sun  
; TITLE OF INVENTION: ZINC FINGER DOMAIN LIBRARIES  
; FILE REFERENCE: 12279-005001  
; CURRENT APPLICATION NUMBER: US/10/223,765  
; CURRENT FILING DATE: 2002-08-19  
; PRIOR APPLICATION NUMBER: 60/374,355  
; PRIOR FILING DATE: 2002-04-22  
; PRIOR APPLICATION NUMBER: 60/313,402  
; PRIOR FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 305  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 202  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetically generated oligonucleotide  
US-10-223-765-202

Query Match 100.0%; Score 9; DB 13; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.9e+04; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

Qy 1 TAGGAGGAT 9  
|||||

Db 2 TAGGAGGAT 10  
|||||

## RESULT 4

US-09-882-945A-169/c  
; Sequence 169, Application US/09882945A  
; Publication No. US20030143535A1  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Allawi, Hatim  
; APPLICANT: Dong, Fang  
; APPLICANT: Neri, Bruce  
; APPLICANT: Vener, Tatiana  
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
; FILE REFERENCE: FORS-04586  
; CURRENT APPLICATION NUMBER: US/09/882,945A  
; CURRENT FILING DATE: 2001-06-15  
; NUMBER OF SEQ ID NOS: 334  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 169  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-882-945A-169

Query Match 100.0%; Score 9; DB 13; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.7e+04; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

Qy 1 TAGGAGGAT 9  
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Db 12 TAGGAGGAT 4  
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## RESULT 5

US-10-340-192-22/c  
; Sequence 22, Application US/10340192  
; Publication No. US20030170700A1  
; GENERAL INFORMATION:  
; APPLICANT: Lynx Therapeutics, Inc.  
; APPLICANT: Shang, Jin  
; APPLICANT: Bowen, Benjamin A  
; TITLE OF INVENTION: SECRETED AND CELL SURFACE POLYPEPTIDES AFFECTED BY CHOLESTEROL ANT  
; FILE REFERENCE: 37-000610US  
; CURRENT APPLICATION NUMBER: US/10/340,192  
; CURRENT FILING DATE: 2003-01-08  
; NUMBER OF SEQ ID NOS: 88  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 22  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-340-192-22

Query Match 100.0%; Score 9; DB 13; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.7e+04; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

Qy 1 TAGGAGGAT 9  
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Db 10 TAGGAGGAT 2  
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## RESULT 6

US-10-339-793-97/c  
; Sequence 97, Application US/10339793  
; Publication No. US20030180764A1  
; GENERAL INFORMATION:

; APPLICANT: Lynx Therapeutics, Inc.  
 ; APPLICANT: Shang, Jin  
 ; APPLICANT: Bowen, Benjamin  
 ; TITLE OF INVENTION: GENES AFFECTED BY CHOLESTEROL TREATMENT AND DURING ADIPOGENESIS  
 ; FILE REFERENCE: 37-000310US  
 ; CURRENT APPLICATION NUMBER: US/10/339,793  
 ; CURRENT FILING DATE: 2003-01-08  
 ; NUMBER OF SEQ ID NOS: 443  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 97  
 ; LENGTH: 17  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-339-793-97  
  
 Query Match 100.0%; Score 9; DB 13; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+04;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 TAGGAGGAT 9  
 Db 10 TAGGAGGAT 2  
  
 RESULT 7  
 US-09-766-154-19  
 ; Sequence 19, Application US/09766154  
 ; Patent No. US20020010948A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Patience, Clive  
 ; TITLE OF INVENTION: Swine Defective for Transmission of Porcine Endogenous  
 ; FILE REFERENCE: 61750-311  
 ; CURRENT APPLICATION NUMBER: US/09/766,154  
 ; PRIOR FILING DATE: 2001-01-19  
 ; PRIOR APPLICATION NUMBER: U.S. 60/243695  
 ; PRIOR FILING DATE: 2000-10-27  
 ; PRIOR APPLICATION NUMBER: U.S. 60/182965  
 ; PRIOR FILING DATE: 2000-02-16  
 ; PRIOR APPLICATION NUMBER: U.S. 60/177003  
 ; PRIOR FILING DATE: 2000-01-19  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: Patent in Ver. 2.1  
 ; SEQ ID NO 19  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Primer  
 ; OTHER INFORMATION: sequence used in amplification of PERV-sequences.  
 ; US-09-766-154-19  
  
 Query Match 100.0%; Score 9; DB 9; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+04;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 TAGGAGGAT 9  
 Db 2 TAGGAGGAT 10  
  
 RESULT 8  
 US-09-828-344-162  
 ; Sequence 162, Application US/09828344  
 ; Publication No. US20030044979A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: C. Frank Bennett  
 ; APPLICANT: Jacqueline Wyatt  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPID SCRAMBLASE I EXPRESSION  
 ; FILE REFERENCE: RTS-0147  
 ; CURRENT APPLICATION NUMBER: US/09/828,344  
 ; CURRENT FILING DATE: 2001-04-06  
 ; NUMBER OF SEQ ID NOS: 176  
 ; SOFTWARE: Patent in Ver. 2.1  
 ; SEQ ID NO 19  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 ; US-09-828-344-162

; SEQ ID NO 162  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 ; US-09-828-344-162  
  
 Query Match 100.0%; Score 9; DB 11; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+04;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 TAGGAGGAT 9  
 Db 1 TAGGAGGAT 9  
  
 RESULT 9  
 US-09-828-344-163  
 ; Sequence 163, Application US/09828344  
 ; Publication No. US20030044979A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: C. Frank Bennett  
 ; APPLICANT: Jacqueline Wyatt  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPID SCRAMBLASE I EXPRESSION  
 ; FILE REFERENCE: RTS-0147  
 ; CURRENT APPLICATION NUMBER: US/09/828,344  
 ; CURRENT FILING DATE: 2001-04-06  
 ; NUMBER OF SEQ ID NOS: 176  
 ; SEQ ID NO 163  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 ; US-09-828-344-163  
  
 Query Match 100.0%; Score 9; DB 11; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+04;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 TAGGAGGAT 9  
 Db 3 TAGGAGGAT 11  
  
 RESULT 10  
 US-09-828-344-164  
 ; Sequence 164, Application US/09828344  
 ; Publication No. US20030044979A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: C. Frank Bennett  
 ; APPLICANT: Jacqueline Wyatt  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPID SCRAMBLASE I EXPRESSION  
 ; FILE REFERENCE: RTS-0147  
 ; CURRENT APPLICATION NUMBER: US/09/828,344  
 ; CURRENT FILING DATE: 2001-04-06  
 ; NUMBER OF SEQ ID NOS: 176  
 ; SEQ ID NO 164  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 ; US-09-828-344-164  
  
 Query Match 100.0%; Score 9; DB 11; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+04;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 TAGGAGGAT 9  
 Db 4 TAGGAGGAT 12

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RESULT 11
US-10-006-191-104
; Sequence 104, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 104
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-104
Query Match 100.0%; Score 9; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.6e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAGGAGGAT 9
Db 7 TAGGAGGAT 15

RESULT 12
US-09-816-814-13/c
; Sequence 13, Application US/09816814
; Publication No. US20030027136A1
; GENERAL INFORMATION:
; APPLICANT: Goronzy, Jorg J.
; APPLICANT: Weyand, Cornelia M.
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS MARKERS
; FILE REFERENCE: 07039-251001
; CURRENT APPLICATION NUMBER: US/09/816,814
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for PCR
US-09-816-814-13
Query Match 100.0%; Score 9; DB 11; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAGGAGGAT 9
Db 15 TAGGAGGAT 7

RESULT 13
US-10-160-764-17
; Sequence 17, Application US/10160764
; Publication No. US20030167535A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Yafan
; APPLICANT: Chalifoux, Maryse
; APPLICANT: Wang, Yang
; APPLICANT: Kuzma, Monika Maria
; APPLICANT: Gilley, Angela Patricia
; TITLE OF INVENTION: Compositions and Methods of Increasing Stress Tolerance
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/219,006
; PRIOR FILING DATE: 2000-07-12
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FILE REFERENCE: 22542-008
; CURRENT APPLICATION NUMBER: US/10/160,764
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/294,766
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/348,909
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
US-10-160-764-17
Query Match 100.0%; Score 9; DB 13; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAGGAGGAT 9
Db 8 TAGGAGGAT 16

RESULT 14
US-10-165-099-341/c
; Sequence 341, Application US/10165099
; Publication No. US20030189326A1
; GENERAL INFORMATION:
; APPLICANT: D'Andrea, Alan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS OF CANCER SUSCEPTIBILITY
; FILE REFERENCE: 7032/2055
; CURRENT APPLICATION NUMBER: US/10/165,099
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 09/998,027
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US 60/245,756
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 352
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 341
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-165-099-341
Query Match 100.0%; Score 9; DB 13; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAGGAGGAT 9
Db 17 TAGGAGGAT 9

RESULT 15
US-10-027-632-68219/c
; Sequence 68219, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/219,006
; PRIOR FILING DATE: 2000-07-12
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; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 68219
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-68219
Query Match      100.0%; Score 9; DB 13; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.6e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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          |||||
          18 TAGGAGGAT 10

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Job time : 105.924 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Title: us-09-540-843-3  
Perfect score: 7  
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Scoring table: IDENTITY NUC  
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Searched: 288711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 1010434

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.mu.\*
- 20: em.om.\*
- 21: em.or.\*
- 22: em.ov.\*
- 23: em.pat.\*
- 24: em.ph.\*
- 25: em.pl.\*
- 26: em.ro.\*
- 27: em.sts.\*
- 28: em.un.\*
- 29: em.vi.\*
- 30: em.htg.hum.\*
- 31: em.htg.inv.\*
- 32: em.htg.other.\*
- 33: em.htg.mus.\*
- 34: em.htg.pin.\*
- 35: em.htg.rod.\*
- 36: em.htg.mam.\*
- 37: em.htg.vrt.\*
- 38: em.sy.\*
- 39: em.htgo.hum.\*
- 40: em.htgo.mus.\*
- 41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	7	100.0	7	6	AX268755	AX268755 Sequence
2	7	100.0	7	6	AX268759	AX268759 Sequence
3	7	100.0	9	6	AX268753	AX268753 Sequence
4	7	100.0	10	6	AX377258	AX377258 Sequence
5	7	100.0	10	6	AX573597	AX573597 Sequence
6	7	100.0	10	6	AX573610	AX573610 Sequence
7	7	100.0	10	6	BD007857	BD007857 LPS activ
8	7	100.0	10	6	BD083254	BD083254 Human mat
9	7	100.0	11	6	AX470905	AX470905 Sequence
10	7	100.0	11	6	AX624159	AX624159 Sequence
11	7	100.0	11	6	AX624334	AX624334 Sequence
12	7	100.0	11	6	AX625574	AX625574 Sequence
13	7	100.0	11	6	AX626182	AX626182 Sequence
14	7	100.0	11	6	AX626780	AX626780 Sequence
15	7	100.0	11	6	AX629189	AX629189 Sequence
16	7	100.0	11	6	AX631580	AX631580 Sequence
17	7	100.0	11	6	AX631755	AX631755 Sequence
18	7	100.0	12	6	AX1497	AX1497 Sequence 24
19	7	100.0	12	6	AX573600	AX573600 Sequence
20	7	100.0	12	6	AX573602	AX573602 Sequence
21	7	100.0	12	6	BD023279	BD023279 Method fo
22	7	100.0	13	6	AR285089	AR285089 Sequence
23	7	100.0	13	6	AR285099	AR285099 Sequence
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25	7	100.0	13	6	AX523264	AX523264 Sequence
26	7	100.0	14	6	AX3152	AX3152 Synthetic H
27	7	100.0	14	6	AR082813	AR082813 Sequence
28	7	100.0	14	6	AR088823	AR088823 Sequence
29	7	100.0	14	6	AX018748	AX018748 Sequence
30	7	100.0	14	6	AX343036	AX343036 Sequence
31	7	100.0	15	6	AX3153	AX3153 Synthetic H
32	7	100.0	15	6	AR041154	AR041154 Sequence
33	7	100.0	15	6	AR082814	AR082814 Sequence
34	7	100.0	15	6	AR130719	AR130719 Sequence
35	7	100.0	15	6	AR130720	AR130720 Sequence
36	7	100.0	15	6	AR131705	AR131705 Sequence
37	7	100.0	15	6	AR132890	AR132890 Sequence
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41	7	100.0	15	6	AX637888	AX637888 Sequence
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43	7	100.0	15	6	I77317	I77317 Sequence 24
44	7	100.0	15	6	I77620	I77620 Sequence 32
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ALIGNMENTS

RESULT 1	AX268755	AX268755	Sequence 3 from Patent WO0174342.	7 bp	DNA	linear	PAT 29-OCT-2001
LOCUS	AX268755						
DEFINITION	AX268755						
ACCESSION	AX268755						
VERSION	AX268755.1	GI:16541827					
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							

Gilchrest, B.A., Yaar, M. and Eller, M.  
Use of locally applied dna fragments  
Patent: WO 0174342-A 3 11-OCT-2001;  
TRUSTEES OF BOSTON UNIVERSITY (US)



```

Db          8 AGTATGA 2
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/db_xref="taxon:9606"
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RESULT 6
AX573610/c
LOCUS       AX573610               10 bp    DNA    linear    PAT 07-JAN-2003
DEFINITION   Sequence 20 from Patent WO02079467.
ACCESSION    AX573610
VERSION      AX573610.1 GI:27551280
KEYWORDS     synthetic construct
SOURCE       synthetic construct
ORGANISM     artificial sequences.
1
REFERENCE    1
AUTHORS      Nielsen,P.E. and Good,L.
TITLE        Antibiotic-free bacterial strain selection with antisense molecules
JOURNAL      Patent: WO 02079467-A 20 10-OCT-2002;
              Koebenhavns Univesitet (DK)
FEATURES     Location/Qualifiers
              1..10
               /organism="synthetic construct"
               /mol_type="genomic DNA"
               /db_xref="taxon:32630"
               /note="Peptide nucleic acid SP4"
misc_feature 1
              /note="The polypeptide KFFKFFKFFK (SEQ ID NO:1) is linked
              to N-terminal of the PNA sequence via the ethylene glycol
              linker called 'egl'"
              4 c      4 c      0 g      4 t
BASE COUNT   2 a      4 c      0 g      4 t
ORIGIN
Query Match 100.0%; Score 7; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7
|||||
8 AGTATGA 2

RESULT 7
AX573610/c
LOCUS       AX573610               10 bp    DNA    linear    PAT 31-JAN-2002
DEFINITION   LPS activated human monocyte expressing genes.
ACCESSION    BD007857
VERSION      BD007857.1 GI:18636230
KEYWORDS     JP 2001069993-A/133.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
REFERENCE    1
AUTHORS      Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE        LPS activated human monocyte expressing genes
JOURNAL      Patent: JP 2001069993-A 133 21-MAR-2001;
              JAPAN SCIENCE AND TECHNOLOGY CORP
OS          Homo sapiens (human)
PN          JP 2001069993-A/133
PD          21-MAR-2001
PF          28-APR-2000 JP 2000131079
PR          KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
              C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53/A61K45/00, PC
              A61P29/00,
PC          A61P31/00,C12P21/08,C12N15/00
CC          Homo sapiens (human)
FH          Key
              Location/Qualifiers
              1..10
               /organism="Homo sapiens (human)"
              /db_xref="taxon:9606"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
              2 t

BASE COUNT   4 a      0 c      4 g      2 t
ORIGIN
Query Match 100.0%; Score 7; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7
|||||
8 AGTATGA 2

FEATURES     source
              1..10
               /organism="Homo sapiens"
               /mol_type="genomic DNA"
               /db_xref="taxon:9606"
               /mol_type="genomic DNA"
               /db_xref="taxon:9606"
               2 t

BASE COUNT   4 a      0 c      4 g      2 t
ORIGIN
Query Match 100.0%; Score 7; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7
|||||
1 AGTATGA 7

RESULT 9
AX470905
LOCUS       AX470905               11 bp    DNA    linear    PAT 09-AUG-2002
DEFINITION   Sequence 482 from Patent WO02053773.
ACCESSION    AX470905
VERSION      AX470905.1 GI:22206030
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE    1
AUTHORS      Hofmann,K., Conradt,M. and Petersohn,D.
TITLE        Method for determining skin stress or skin ageing in vitro
JOURNAL      Patent: WO 02053773-A 482 11-JUL-2002;
              HENKEL KGAA (DE)
FEATURES     Location/Qualifiers
              1..10
               /organism="Homo sapiens"

```



```

RESULT 14
AX626780
LOCUS AX626780 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3821 from Patent WO02053774.
ACCESSION AX626780
VERSION AX626780.1 GI:28454818
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3821 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 5 a 0 c 3 g 3 t
ORIGIN
Query Match 100.0%; Score 7; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. NO. 9.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 AGTATGA 7
|||||
4 AGTATGA 10

RESULT 15
AX629189/c
LOCUS AX629189 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6230 from Patent WO02053774.
ACCESSION AX629189
VERSION AX629189.1 GI:28457227
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6230 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 4 a 3 c 1 g 3 t
ORIGIN
Query Match 100.0%; Score 7; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. NO. 9.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 AGTATGA 7
|||||
10 AGTATGA 4

```

Search completed: December 31, 2003, 17:09:43  
 Job time : 646.443 secs



Result No.	Query	Score	Match	Length	DB	ID	Description
1	7	100.0	7	20	AAZ10694		Oligonucleotide se
2	7	100.0	7	23	AAS14907		Melanogenesis asso
3	7	100.0	7	23	AAS14911		Melanogenesis asso
4	7	100.0	9	20	AAZ10692		Oligonucleotide se
5	7	100.0	9	23	AAS14905		Melanogenesis asso
6	7	100.0	10	21	AAZ78995		Human dendritic ce
7	7	100.0	10	21	AAZ86425		Metastatic breast
8	7	100.0	10	22	AAH32760		LPS activated huma

DNA fragments useful for increasing p53 activity in a cell and reducing susceptibility to UV-induced hyperproliferative diseases -  
 Claim 11; Page 30; 44pp; English.  
 AA210592-97 represent DNA fragments that are used for increasing p53 activity in a cell. The oligonucleotides are UV mimetics and protect cells against subsequent exposure to UV-irradiation or chemicals. The oligonucleotides are useful for increasing p53 activity in a cell, reducing the susceptibility to UV-induced hyperproliferative diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging and reducing susceptibility to skin cancer.  
 Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;  
 Query Match 100.0%; Score 7; DB 20; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+08;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 AGTATGA 7  
 1 AGTATGA 7  
 RESULT 2  
 AAS14907  
 AAS14907 standard; DNA; 7 BP.  
 AAS14907;  
 14-FEB-2002 (first entry)  
 Melanogenesis associated oligonucleotide #3.  
 Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53; anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; immunosuppressive; DNA repair; proliferation inhibitor; apoptosis; tumour necrosis factor inhibitor; photoaging; hyperproliferative disease; carcinoma; oxidative stress; skin cancer; allergy mediated inflammation; conjunctivitis; allergic rhinitis; vitiligo; ss.  
 Synthetic.  
 WO200174342-A2.  
 11-OCT-2001.  
 30-MAR-2001; 2001WO-US10162.  
 31-MAR-2000; 2000US-0540843.  
 (UYBO-) UNIV BOSTON.  
 Gilchrist BA, Yaar M, Eller M;  
 WPI; 2001-626338/72.  
 Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonucleotides that mimic the effects of ultra-violet light -  
 Claim 1; Page 36; 74pp; English.  
 The invention describes inhibition of mammalian epithelial cell proliferation by treating cells with at least one oligonucleotide, or its fragment. The compounds, which have cytostatic, anti-allergic, anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and immunosuppressive activities, function as 'ultra-violet mimics' to induce DNA repair processes (or a protective response to later exposure to radiation or chemicals), as a proliferation inhibitor, apoptosis inducer or a tumour necrosis factor inhibitor. Probably they mimic products of DNA damage, or processed DNA-damage intermediates, by inducing the p53

pathway, resulting in transient arrest of cell growth, allowing more time for DNA repair to occur before cell division takes place. The method is especially used to treat carcinoma but may also be used to: treat other hyperproliferative states (e.g. psoriasis or precancerous conditions); reduce photoaging, oxidative stress or damage; prevent skin cancer; treat allergic rhinitis and conjunctivitis; prevent or reduce DNA damage in cells caused by radiation or chemicals; increase melanin production (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to promote apoptosis in epithelial cells that contain damaged DNA. Also oligonucleotides that contain non-hydrolyzable backbones are used to inhibit apoptosis, in response to DNA damage, in epithelial cell. This sequence is melanogenesis associated oligonucleotide #3, a truncated version of the oligonucleotide shown in AAS14906, one of the oligonucleotides used to inhibit mammalian epithelial cell proliferation, described in the method of the invention.  
 Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;  
 Query Match 100.0%; Score 7; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+08;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 AGTATGA 7  
 1 AGTATGA 7  
 RESULT 3  
 AAS14911  
 ID AAS14911 standard; DNA; 7 BP.  
 AC AAS14911;  
 DT 14-FEB-2002 (first entry)  
 DE Melanogenesis associated oligonucleotide #7.  
 DE Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53; anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; immunosuppressive; DNA repair; proliferation inhibitor; apoptosis; tumour necrosis factor inhibitor; photoaging; hyperproliferative disease; carcinoma; oxidative stress; skin cancer; allergy mediated inflammation; conjunctivitis; allergic rhinitis; vitiligo; ss.  
 Synthetic.  
 Key Location/Qualifiers  
 modified\_base 1  
 /\*tag= a  
 /mod\_base= a  
 /note= "Phosphorylated"  
 WO200174342-A2.  
 11-OCT-2001.  
 30-MAR-2001; 2001WO-US10162.  
 31-MAR-2000; 2000US-0540843.  
 (UYBO-) UNIV BOSTON.  
 Gilchrist BA, Yaar M, Eller M;  
 WPI; 2001-626338/72.  
 Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonucleotides that mimic the effects of ultra-violet light -  
 Claim 1; Page 38; 74pp; English.



CC The invention describes inhibition of mammalian epithelial cell  
 CC proliferation by treating cells with at least one oligonucleotide, or  
 CC its fragment. The compounds, which have cytostatic, anti-allergic,  
 CC anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and  
 CC immunosuppressive activities, function as 'ultra-violet mimics' to induce  
 CC DNA repair processes (or a protective response to later exposure to  
 CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer  
 CC or a tumour necrosis factor inhibitor. Probably they mimic products of  
 CC DNA damage, or processed DNA-damage intermediates, by inducing the p53  
 CC pathway, resulting in transient arrest of cell growth, allowing more time  
 CC for DNA repair to occur before cell division takes place. The method is  
 CC especially used to treat carcinoma but may also be used to treat other  
 CC hyperproliferative states (e.g. psoriasis or precancerous conditions);  
 CC reduce photoaging, oxidative stress or damage; prevent skin cancer; treat  
 CC allergic rhinitis and conjunctivitis; prevent skin dermatitis;  
 CC allergic rhinitis and conjunctivitis; prevent or reduce DNA damage in  
 CC cells caused by radiation or chemicals; increase melanin production  
 CC (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to  
 CC promote apoptosis in epithelial cells that contain damaged DNA. Also  
 CC oligonucleotides that contain non-hydrolyzable backbones are used to  
 CC inhibit apoptosis, in response to DNA damage, in epithelial cell. This  
 CC sequence is melanogenesis associated oligonucleotide #7, one of the  
 CC oligonucleotides used to inhibit mammalian epithelial cell  
 CC proliferation, described in the method of the invention.

XX Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 7; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+08;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGCA 7  
 |||||  
 1 AGTATGCA 7

## RESULT 4

AAZ10692  
 AAZ10692 standard; DNA; 9 BP.

AAZ10692;

23-NOV-1999 (first entry)

Oligonucleotide sequence that increases p53 activity in a cell.

p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;  
 UV-induced hyperproliferative disease; psoriasis; vitiligo;  
 atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;  
 skin cancer; ss.

Synthetic.

GB2336157-A.

13-OCT-1999.

24-MAR-1999; 99GB-0006758.

26-MAR-1998; 98US-0048927.

(UYBO-) UNIV BOSTON.

Gilchrest BA, Yaar M, Eller M;

WPI; 1999-543520/46.

DNA fragments useful for increasing p53 activity in a cell and reducing  
 susceptibility to UV-induced hyperproliferative diseases -

Claim 11; Page 29; 44pp; English.

AAZ10692-97 represent DNA fragments that are used for increasing p53

CC activity in a cell. The oligonucleotides are UV mimetics and  
 CC protect cells against subsequent exposure to UV-irradiation or  
 CC chemicals. The oligonucleotides are useful for increasing p53 activity  
 CC in a cell, reducing the susceptibility to UV-induced hyperproliferative  
 CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic  
 CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging  
 CC and reducing susceptibility to skin cancer.

XX Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;

Query Match 100.0%; Score 7; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+08;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGCA 7  
 |||||  
 2 AGTATGCA 8

## RESULT 5

AAS14905  
 AAS14905 standard; DNA; 9 BP.

AAS14905;

14-FEB-2002 (first entry)

Melanogenesis associated oligonucleotide #1.

Melanin; melanogenic; oligomer; cytostatic; anti-allergic; p53;  
 anti-inflammatory; dermatological; ophthalmological; anti-psoriatic;  
 immunosuppressive; DNA repair; proliferation inhibitor; apoptosis;  
 tumour necrosis factor inhibitor; photoaging; hyperproliferative disease;  
 carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;  
 conjunctivitis; allergic rhinitis; vitiligo; ss.

Synthetic.

Key Location/Qualifiers

modified\_base 1

/tag= a

/mod\_base= g

/note= "Optionally phosphorylated"

WO200174342-A2.

11-OCT-2001.

30-MAR-2001; 2001WO-US10162.

31-MAR-2000; 2000US-0540843.

(UYBO-) UNIV BOSTON.

Gilchrest BA, Yaar M, Eller M;

WPI; 2001-626338/72.

Inhibiting proliferation of epithelial cells, useful e.g. for treating  
 carcinoma, using specific oligonucleotides that mimic the effects of  
 ultra-violet light -

Claim 1; Page 36; 74pp; English.

The invention describes inhibition of mammalian epithelial cell  
 proliferation by treating cells with at least one oligonucleotide, or  
 its fragment. The compounds, which have cytostatic, anti-allergic,  
 CC anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and  
 CC immunosuppressive activities, function as 'ultra-violet mimics' to induce  
 CC DNA repair processes (or a protective response to later exposure to  
 CC radiation or chemicals), as a proliferation inhibitor, apoptosis inducer  
 CC or a tumour necrosis factor inhibitor. Probably they mimic products of  
 CC DNA damage, or processed DNA-damage intermediates, by inducing the p53

pathway, resulting in transient arrest of cell growth, allowing more time for DNA repair to occur before cell division takes place. The method is especially used to treat carcinoma but may also be used to: treat other hyperproliferative states (e.g. psoriasis or precancerous conditions); reduce photodamage, oxidative stress or damage; prevent skin cancer; treat allergic rhinitis and conjunctivitis; prevent or reduce DNA damage in cells caused by radiation or chemicals; increase melanin production (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to promote apoptosis in epithelial cells that contain damaged DNA. Also oligonucleotides that contain non-hydrolyzable backbones are used to inhibit apoptosis, in response to DNA damage, in epithelial cell. This sequence is melanogenesis associated oligonucleotide #1, one of the oligonucleotides used to inhibit mammalian epithelial cell proliferation, described in the method of the invention.

Sequence 9 BP; 3 A; 0 C; 4 G; 2 T; 0 other;  
 Query Match 100.0%; Score 7; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+08;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7  
 |||||  
 2 AGTATGA 8

RESULT 6  
 AAZ78995/c  
 AAZ78995 standard; DNA; 10 BP.  
 AAZ78995;

10-APR-2000 (first entry)

Human dendritic cell SAGE tag, SEQ ID NO:1423.

SAGE tag; serial analysis of gene expression; antigen-presenting cell; APC; monocyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL; cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

Homo sapiens.

WO9565924-A2.

23-DEC-1999.

18-JUN-1999; 99WO-US13800.

19-JUN-1998; 98US-0089833.

19-JUN-1998; 98US-0089844.

19-JUN-1998; 98US-0089853.

19-JUN-1998; 98US-0089878.

19-JUN-1998; 98US-0089991.

19-JUN-1998; 98US-0089992.

19-JUN-1998; 98US-0089993.

19-JUN-1998; 98US-0089994.

19-JUN-1998; 98US-0089997.

19-JUN-1998; 98US-0089999.

19-JUN-1998; 98US-0090000.

19-JUN-1998; 98US-0090035.

19-JUN-1998; 98US-0090036.

19-JUN-1998; 98US-0090039.

19-JUN-1998; 98US-0090040.

19-JUN-1998; 98US-0090041.

19-JUN-1998; 98US-0090042.

19-JUN-1998; 98US-0090043.

19-JUN-1998; 98US-0090044.

19-JUN-1998; 98US-0090045.

19-JUN-1998; 98US-0090047.

19-JUN-1998; 98US-0090076.  
 19-JUN-1998; 98US-0090077.  
 19-JUN-1998; 98US-0090078.  
 19-JUN-1998; 98US-0090079.  
 19-JUN-1998; 98US-0090080.  
 08-DEC-1998; 98US-0111715.

(GENZ ) GENZYME CORP.

(ROBE/) ROBERTS B.L.

(SHAN/) SHANKARA S.

Roberts BL, Shankara S;

WPI; 2000-106077/09.

Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer -

Claim 1; Page 105; 130pp; English.

Sequences AA277573-279709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTs (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while other transcripts correspond to novel genes. Antigen-presenting cell (APC)-associated costimulatory factors play an important role in the activation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in an APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cell differentially expressed genes, or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell-rich sites, secretion of T cell growth factors and secretion of chemokines for recruitment of immune effector cells.

Sequence 10 BP; 4 A; 2 C; 1 G; 3 T; 0 other;

Query Match 100.0%; Score 7; DB 21; Length 10;

Best Local Similarity 100.0%; Pred. No. 5.7e+04;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AGTATGA 7

|||||

7 AGTATGA 1

RESULT 7

AAZ86425

ID AAZ86425 standard; DNA; 10 BP.

XX AAZ86425;

AC AAZ86425;

XX 07-APR-2000 (first entry)

DE Metastatic breast tumour cell downregulated transcript tag #5659.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
 KW antimetastatic; vaccine; diagnosis; ss.  
 XX Homo sapiens.  
 XX WO9965928-A2.  
 XX 23-DEC-1999.  
 XX 18-JUN-1999; 99WO-US13647.  
 XX 19-JUN-1998; 98US-0089853.  
 PR 19-JUN-1998; 98US-0089997.  
 PR 19-JUN-1998; 98US-0090039.  
 PR 19-JUN-1998; 98US-0090040.  
 PR 19-JUN-1998; 98US-0090041.  
 XX (GENZ ) GENZYME CORP.  
 XX (ROBE/) ROBERTS B L.  
 XX (SHAN/) SHANKARA S.  
 XX Roberts BL, Shankara S;  
 WPI; 2000-106079/09.  
 Isolated polynucleotides differentially expressed between metastatic  
 and non-metastatic breast cancer cells, useful for diagnosis,  
 prevention and treatment of cancer -  
 Claim 1; Page 208; 219pp; English.  
 AAZ80767 to AAZ83941 represent tags corresponding to distinct  
 transcripts that are preferentially transcribed in the metastatic breast  
 tumour tissue (i.e. are upregulated in metastatic breast tumour cells).  
 AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts  
 that are preferentially transcribed in the primary or non-metastatic  
 breast tumour tissue (i.e. are downregulated in metastatic breast tumour  
 cells). These transcripts can be used for diagnosis, prognosis,  
 monitoring and treatment of breast cancer, particularly where metastatic.  
 Diagnosis is by standard immunoassays or hybridisation/amplification  
 reactions. Compounds that modulate expression of the transcripts are  
 potentially useful for treatment of (metastatic) breast cancer, while  
 promoters from the transcripts are used to direct expression, in selected  
 cell types, of e.g. therapeutic genes (also ribozymes or antisense  
 sequences), particularly an antigen-encoding sequence for use in gene or  
 cell-based vaccines. Polypeptides encoded by the transcripts are also  
 useful in vaccines; for diagnosing breast cancer and for raising  
 specific antibodies (Ab). Ab are used to detect the polypeptides or as  
 therapeutic agents. Host cells that produce the polypeptides can be used  
 to expand and isolate populations of educated, antigen-specific immune  
 effector cells, e.g. cytotoxic T lymphocytes, and these used for  
 adoptive immunotherapy.  
 XX  
 SQ Sequence 10 BP; 5 A; 0 C; 3 G; 2 T; 0 other;  
 Query Match 100.0%; Score 7; DB 21; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+04;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGTATGCA 7  
 Db 4 AGTATGCA 10  
 RESULT 8  
 AAH32760  
 ID AAH32760 standard; cDNA; 10 BP.  
 XX  
 AC AAH32760;  
 XX  
 DT 13-AUG-2001 (first entry)

XX LPS activated human monocyte expression gene cDNA tag SEQ:133.  
 DE Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;  
 KW expressed sequence tag; diagnosis; human disease; treatment; ss.  
 XX Homo sapiens.  
 OS  
 XX JP2001069993-A.  
 XX 21-MAR-2001.  
 XX 28-APR-2000; 2000JP-0131079.  
 PF 08-JUL-1999; 99JP-0195103.  
 PR  
 XX (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.  
 PA WPI; 2001-304369/32.  
 DR LPS activated human monocyte expression gene group -  
 XX LPS activated human monocyte expression gene group -  
 PT Claim 10; Page 28; 52pp; Japanese.  
 XX  
 PS The present invention describes an lipopolysaccharide (LPS) activated  
 CC human monocyte expression gene group consisting of the high-ranking 50  
 CC genes of the highest expression among the genes expressed by human  
 CC monocyte stimulated by LPS in which the cDNA of each gene has the 'base  
 CC sequence of (AAH32628 to AAH32677) continuous to the base sequence  
 CC 5'-CATG-3' nearest to the polyA region. The gene group is useful for the  
 CC development of new means for the diagnosis and the treatment of various  
 CC human diseases in which human monocyte plays an important role.  
 CC AAH32628 to AAH32943 represent specifically claimed LPS activated human  
 CC monocyte expression gene cDNA tags from the present invention. AAH32944  
 CC represents an LPS activated human monocyte expression gene cDNA sequence  
 CC encoding AAB98009, which are given in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 10 BP; 4 A; 0 C; 4 G; 2 T; 0 other;  
 Query Match 100.0%; Score 7; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+04;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGTATGCA 7  
 Db 1 AGTATGCA 7  
 RESULT 9  
 AAF38936  
 ID AAF38936 standard; DNA; 10 BP.  
 XX  
 AC AAF38936;  
 XX  
 DT 23-MAR-2001 (first entry)  
 XX  
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5675.  
 XX  
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 KW serial analysis of gene expression; antifungal; tag; identification;  
 KW linker; PCR primer; ds.  
 XX  
 OS Saccharomyces cerevisiae.  
 OS  
 XX WO200077214-A2.  
 PN  
 XX 21-DEC-2000.  
 PD  
 XX 14-JUN-2000; 2000WO-US16223.  
 PF  
 XX 16-JUN-1999; 99US-0335032.  
 PR

XX PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX PI Velculescu V, Vogelstein B, Kinzler K;  
 XX DR WPI; 2001-061874/07.  
 XX PT Yeast gene coding sequences comprising NORF genes with serial analysis  
 XX PT of gene expression (SAGE) tags, useful for studying, monitoring and  
 XX PT affecting phases of the cell cycle -  
 XX PS Example; Page 202; 419pp; English.  
 XX CC The present invention describes an isolated DNA molecule comprising a  
 XX CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 XX CC previously assigned open reading frame; or nonannotated ORF) genes  
 XX CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 XX CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 XX CC cycle comprising administering a NORF gene whose expression varies by at  
 XX CC least 10% between any two phases of the cell cycle selected from log  
 XX CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 XX CC antifungal drugs comprising: (a) contacting a test substance with a  
 XX CC yeast cell; and (b) monitoring expression of a NORF gene whose  
 XX CC expression varies as in M1, where a test substance which modifies the  
 XX CC expression of the yeast gene is a candidate antifungal drug; (3) a method  
 XX CC (M3) for identifying human genes which are involved in cell cycle  
 XX CC progression comprising contacting human DNA with a probe which comprises  
 XX CC at least 10 contiguous nucleotides of a NORF gene whose expression varies  
 XX CC as in M1; and (4) a method (M4) for identifying a candidate drug as a  
 XX CC member of a class of drugs having a characteristic effect on gene  
 XX CC expression in a yeast cell comprising contacting a yeast cell with a  
 XX CC candidate drug and monitoring expression in the yeast cell of at least 1  
 XX CC NORF gene whose expression is affected by the class of drugs. The NORF  
 XX CC genes may be used to study, monitor and affect phases of the cell cycle,  
 XX CC the differentially expressed genes may be used as markers of phases of  
 XX CC the cell cycle. The methods may be used to identify candidate drugs which  
 XX CC affect the cell cycle and for identification of antifungal drugs.  
 XX CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of  
 XX CC the present invention. AAF33262 to AAF33267 represent linkers and PCR  
 XX CC primers used in the SAGE method, in the exemplification of the present  
 XX CC invention.  
 XX SQ Sequence 10 BP; 4 A; 1 C; 3 G; 2 T; 0 other;  
 Query Match 100.0%; Score 7; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+04;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 AGTATGA 7  
 |||||  
 2 AGTATGA 8  
 RESULT 10  
 AAF39793  
 ID AAF39793 standard; DNA; 10 BP.  
 XX AC AAF39793;  
 XX DT 23-MAR-2001 (first entry)  
 XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6532.  
 XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 XX KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 XX KW serial analysis of gene expression; antifungal; tag; identification;  
 XX KW linker; PCR primer; ds.  
 XX OS Saccharomyces cerevisiae.  
 XX PN WO200077214-A2.  
 XX PD 21-DEC-2000.

XX PF 14-JUN-2000; 2000WO-US16223.  
 XX PR 16-JUN-1999; 99US-0335032.  
 XX PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX PI Velculescu V, Vogelstein B, Kinzler K;  
 XX DR WPI; 2001-061874/07.  
 XX PT Yeast gene coding sequences comprising NORF genes with serial analysis  
 XX PT of gene expression (SAGE) tags, useful for studying, monitoring and  
 XX PT affecting phases of the cell cycle -  
 XX PS Example; Page 233; 419pp; English.  
 XX CC The present invention describes an isolated DNA molecule comprising a  
 XX CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
 XX CC previously assigned open reading frame; or nonannotated ORF) genes  
 XX CC comprising a SAGE (serial analysis of gene expression) tag. Also  
 XX CC described are: (1) a method (M1) of using NORF genes to affect the cell  
 XX CC cycle comprising administering a NORF gene whose expression varies by at  
 XX CC least 10% between any two phases of the cell cycle selected from log  
 XX CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
 XX CC antifungal drugs comprising: (a) contacting a test substance with a  
 XX CC yeast cell; and (b) monitoring expression of a NORF gene whose  
 XX CC expression varies as in M1, where a test substance which modifies the  
 XX CC expression of the yeast gene is a candidate antifungal drug; (3) a method  
 XX CC (M3) for identifying human genes which are involved in cell cycle  
 XX CC progression comprising contacting human DNA with a probe which comprises  
 XX CC at least 10 contiguous nucleotides of a NORF gene whose expression varies  
 XX CC as in M1; and (4) a method (M4) for identifying a candidate drug as a  
 XX CC member of a class of drugs having a characteristic effect on gene  
 XX CC expression in a yeast cell comprising contacting a yeast cell with a  
 XX CC candidate drug and monitoring expression in the yeast cell of at least 1  
 XX CC NORF gene whose expression is affected by the class of drugs. The NORF  
 XX CC genes may be used to study, monitor and affect phases of the cell cycle,  
 XX CC the differentially expressed genes may be used as markers of phases of  
 XX CC the cell cycle. The methods may be used to identify candidate drugs which  
 XX CC affect the cell cycle and for identification of antifungal drugs.  
 XX CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of  
 XX CC the present invention. AAF33262 to AAF33267 represent linkers and PCR  
 XX CC primers used in the SAGE method, in the exemplification of the present  
 XX CC invention.  
 XX SQ Sequence 10 BP; 4 A; 1 C; 2 G; 3 T; 0 other;  
 Query Match 100.0%; Score 7; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+04;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 AGTATGA 7  
 |||||  
 1 AGTATGA 7  
 RESULT 11  
 AAF40876  
 ID AAF40876 standard; DNA; 10 BP.  
 XX AC AAF40876;  
 XX DT 23-MAR-2001 (first entry)  
 XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7615.  
 XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
 XX KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
 XX KW serial analysis of gene expression; antifungal; tag; identification;  
 XX KW linker; PCR primer; ds.  
 XX OS Saccharomyces cerevisiae.

XX WO200077214-A2.  
XX 21-DEC-2000.  
XX 14-JUN-2000; 2000WO-US16223.  
XX 16-JUN-1999; 99US-0335032.  
XX (UYJO ) UNIV JOHNS HOPKINS.  
XX Velulescu V, Vogelstein B, Kinzler K;  
XX WPI; 2001-061874/07.  
XX Yeast gene coding sequences comprising NORF genes with serial analysis  
XX of gene expression (SAGE) tags, useful for studying, monitoring and  
XX affecting phases of the cell cycle -  
XX Example; Page 272; 419pp; English.  
XX The present invention describes an isolated DNA molecule comprising a  
XX coding sequence of a yeast gene selected from a group of 745 NORF (not  
XX previously assigned open reading frame; or nonannotated ORF) genes  
XX comprising a SAGE (serial analysis of gene expression) tag. Also  
XX described are: (1) a method (M1) of using NORF genes to affect the cell  
XX cycle comprising administering a NORF gene whose expression varies by at  
XX least 10% between any two phases of the cell cycle selected from log  
XX phase, S phase and G2/M; (2) a method (M2) for screening candidate  
XX antifungal drugs comprising: (a) contacting a test substance with a  
XX yeast cell; and (b) monitoring expression of a NORF gene whose  
XX expression varies as in M1, where a test substance which modifies the  
XX expression of the yeast gene is a candidate antifungal drug; (3) a method  
XX (M3) for identifying human genes which are involved in cell cycle  
XX progression comprising contacting human DNA with a probe which comprises  
XX at least 10 contiguous nucleotides of a NORF gene whose expression varies  
XX as in M1; and (4) a method (M4) for identifying a candidate drug as a  
XX member of a class of drugs having a characteristic effect on gene  
XX expression in a yeast cell comprising contacting a yeast cell with a  
XX candidate drug and monitoring expression in the yeast cell of at least 1  
XX NORF gene whose expression is affected by the class of drugs. The NORF  
XX genes may be used to study, monitor and affect phases of the cell cycle,  
XX the differentially expressed genes may be used as markers of phases of  
XX the cell cycle. The methods may be used to identify candidate drugs which  
XX affect the cell cycle and for identification of antifungal drugs.  
XX AAF33268 to AAF4064 represent SAGE tags used in the exemplification of  
XX the present invention. AAF33262 to AAF33267 represent linkers and PCR  
XX primers used in the SAGE method, in the exemplification of the present  
XX invention.  
XX Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 other;  
XX Query Match 100.0%; Score 7; DB 22; Length 10;  
XX Best Local Similarity 100.0%; Pred. No. 5.7e+04;  
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX QY 1 AGTATGA 7  
XX Db 3 AGTATGA 9  
XX RESULT 12  
XX AAD44180  
XX ID AAD44180 standard; DNA; 10 BP.  
XX AC AAD44180;  
XX DT 13-DEC-2002 (first entry)  
XX DE Probe #3 used to illustrate the method of the invention.  
XX Target nucleotide; analyte; signal; drug discovery; probe; ss.  
XX

OS Unidentified.  
XX US2002051973-A1.  
XX 02-MAY-2002.  
XX 17-SEP-1999; 99US-0398399.  
XX 17-SEP-1999; 99US-0398399.  
XX (DELE/) DELENSTARR G C.  
XX (LEFK/) LEFKOWITZ S M.  
XX (LUEB/) LUEBKE K J.  
XX (OVER/) OVERMAN L B.  
XX (SAMP/) SAMPSON N M.  
XX (SAMP/) SAMPSON J R.  
XX (WOLB/) WOLBER P K.  
XX Delenstarr GC, Lefkowitz SM, Luebke KJ, Overman LB, Sampras NM;  
XX Sampson JR, Wolber PK;  
XX WPI; 2002-443693/47.  
XX Detecting a target nucleotide sequence in an analyte, for use in e.g.  
XX drug discovery, comprises using a set of features having  
XX oligophosphodiester probes, and subtracting a background signal from an  
XX observed signal -  
XX Claim 7; Page 19; 35pp; English.  
XX The invention relates to a method for detecting the presence and/or  
XX amount of a target nucleotide sequence in an analyte. The method  
XX comprising: contacting an aliquot of an analyte suspected of containing  
XX the target sequence with a set of features comprising oligophosphodiester  
XX probes; and subtracting a background signal from an observed signal to  
XX determine the presence and/or amount of the target sequence in the  
XX analyte. The method is used to detect the presence and/or amount of a  
XX target sequence in an analyte. The method is used for estimating  
XX background noise in a nucleic acid hybridisation assay and for validating  
XX a test-background feature. The method is useful in chemical, biological  
XX medical and diagnostic techniques, and for drug discovery. The present  
XX sequence is a probe used to illustrate the method of the invention.  
XX Sequence 10 BP; 5 A; 1 C; 2 G; 2 T; 0 other;  
XX Query Match 100.0%; Score 7; DB 24; Length 10;  
XX Best Local Similarity 100.0%; Pred. No. 5.7e+04;  
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX QY 1 AGTATGA 7  
XX Db 1 AGTATGA 7  
XX RESULT 13  
XX AAL44343/c  
XX ID AAL44343 standard; DNA; 10 BP.  
XX AC AAL44343;  
XX 24-OCT-2002 (first entry)  
XX Peptide nucleic acid (PNA) oligomer #3.  
XX PNA oligomer; PNA; peptide nucleic acid; polyamide backbone; ss;  
XX aminoethylglycine; aeg; aminoethylprolyl; aep; aminoethylpyrrolidine;  
XX pyr; gene downregulation; bacterial infection; viral infection; cancer;  
XX metabolic disease; immunological disorder; PNA-clamping.  
XX Synthetic.  
XX Key Location/Qualifiers  
XX modified\_base 1..10  
XX

```

FT FT /*tag= a
FT FT /mod base= OTHER
FT FT /note= "This sequence is a peptide nucleic acid, (i.e. it
FT FT contains a polyamide backbone instead of a deoxyribose
FT FT backbone"
FT FT 10
FT FT modified_base
FT FT /mod base= OTHER
FT FT /note= "The base is modified with Lys-NH2"
XX XX
XX XX WO200242316-A2.
XX XX
XX XX 30-MAY-2002.
XX XX
XX XX 23-NOV-2001; 2001WO-DK00779.
XX XX
XX XX 24-NOV-2000; 2000DK-0001776.
XX XX
XX XX 06-MAR-2001; 2001DK-0000371.
XX XX
XX XX 16-JUL-2001; 2001DK-0001117.
XX XX
XX XX (PANT-) PANTHECO AS.
XX XX
XX XX Nielsen PE, Pueschl A;
XX XX
XX XX WPI; 2002-490198/52.
XX XX
XX XX New peptide nucleic acid oligomer, useful as antisense molecules to
XX XX treat bacterial and viral infections, has single units comprising
XX XX different amino acid backbones such as aminoethylglycine -
XX XX
XX XX Example 7; Page 34; 40pp; English.
XX XX
XX XX The invention comprises peptide nucleic acid (PNA) oligomers, where the
XX XX single units of the oligomers comprise different amino acid backbones
XX XX selected from any amino acid, such as: including aminoethylglycine (aeg);
XX XX aminoethylprolyl (aep); and aminoethylpyrrolidine (pyr). The PNA
XX XX oligomers of the invention are useful for the downregulation of specific
XX XX genes by targeting the genes at the mRNA or DNA level. The PNA oligomers
XX XX are useful for treating bacterial and viral infections, cancer, metabolic
XX XX diseases and immunological disorders. The PNA oligomers are also useful
XX XX in PCR monitoring/modulation by PNA-clamping. The present DNA sequence
XX XX represents a PNA oligomer of the invention.
XX XX
XX XX Sequence 10 BP; 2 A; 4 C; 0 G; 4 T; 0 other;
XX XX
XX XX Query Match 100.0%; Score 7; DB 24; Length 10;
XX XX Best Local Similarity 100.0%; Pred. No. 5.7e+04;
XX XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX XX 1 AGTATGA 7
XX XX |||||
XX XX 8 AGTATGA 2
XX XX
XX XX RESULT 14
XX XX ASK99556
XX XX ID ASK99556 standard; DNA; 10 BP.
XX XX
XX XX ASK99556;
XX XX
XX XX 21-OCT-2002 (first entry)
XX XX
XX XX Nucleic acid microarray probe #3.
XX XX
XX XX Nucleic acid microarray; probe; ss.
XX XX
XX XX Synthetic.
XX XX
XX XX US2002068293-A1.
XX XX
XX XX 06-JUN-2002.
XX XX
XX XX 02-JUL-2001; 2001US-0899381.
XX XX

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XX XX 17-SEP-1999; 99US-0398399.
XX XX
XX XX (DELE/) DELENSTARR G C.
XX XX (WOLB/) WOLBER P K.
XX XX (SANA/) SANA T R.
XX XX
XX XX Delenstarr GC, Wolber PK, Sana TR;
XX XX
XX XX WPI; 2002-582474/62.
XX XX
XX XX Nucleic acid arrays for qualitatively or quantitatively determining the
XX XX presence of analyte target nucleic acid in a sample comprises both
XX XX hybridisation features and background features -
XX XX
XX XX Claim 8; Page 17; 38pp; English.
XX XX
XX XX The invention relates to a nucleic acid array (I) comprising at least
XX XX one hybridisation feature and at least one background feature. (I) is
XX XX useful for detecting the presence of an analyte nucleic acid in a sample.
XX XX The detection comprises contacting the nucleic acid array with the sample
XX XX under stringent hybridisation conditions, subtracting the background
XX XX signal from the hybridisation signal to obtain a background corrected
XX XX hybridisation signal and relating the background corrected hybridisation
XX XX signal to the presence of the analyte target nucleic acid in the sample
XX XX The method further comprises a labeling step comprising labeling any
XX XX analyte target nucleic acids present in the sample with a member of a
XX XX signal producing system prior to contacting the array with the sample.
XX XX CC ABK99529-ABK99544 and ABK99549-ABK99578 represent nucleic acid probes
XX XX of the invention.
XX XX
XX XX Sequence 10 BP; 5 A; 1 C; 2 G; 2 T; 0 other;
XX XX
XX XX Query Match 100.0%; Score 7; DB 24; Length 10;
XX XX Best Local Similarity 100.0%; Pred. No. 5.7e+04;
XX XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX XX 1 AGTATGA 7
XX XX |||||
XX XX 1 AGTATGA 7
XX XX
XX XX RESULT 15
XX XX ABK47394/C
XX XX ID ABK47394 standard; DNA; 10 BP.
XX XX
XX XX AC ABK47394;
XX XX
XX XX 18-JUN-2002 (first entry)
XX XX
XX XX Human PLA2G1B ASO primer extension primer 3' end #5.
XX XX
XX XX Human; ss; primer; SNP; single nucleotide polymorphism; pancreatitis;
XX XX pancreatic cancer; Phospholipase A2 group1B; PLA2G1B; gene therapy;
XX XX KW haplotype; genotype; chromosome 12q23-q24.1; transgenic; drug screening;
XX XX KW ASO; allele specific oligonucleotide; primer extension.
XX XX
XX XX OS Homo sapiens.
XX XX
XX XX WO200212562-A2.
XX XX
XX XX 14-FEB-2002.
XX XX
XX XX 06-AUG-2001; 2001WO-US24663.
XX XX
XX XX 04-AUG-2000; 2000US-223179P.
XX XX
XX XX (GENA-) GENAISSANCE PHARM INC.
XX XX
XX XX Kazemi A, Kliehm SE, Koshy B;
XX XX
XX XX WPI; 2002-303982/34.
XX XX

```

PT Novel isolated human Phospholipase A2, Group IB pancreas  
PT polynucleotide, for therapeutic purposes, for studying expression and  
PT function of the polynucleotide and for expressing the phospholipase  
PT protein  
XX  
XX  
PS Claim 19; Page 13; 51pp; English.  
XX  
XX  
CC The invention relates to an isolated human Phospholipase A2, Group IB  
CC (pancreas) (PLA2G1B) polynucleotide comprising a sequence which is a  
CC polymorphic variant for a reference sequence for the PLA2G1B gene or  
CC its fragment, or a polymorphic variant of a reference sequence for a  
CC PLA2G1B cDNA or its fragment. Also included are haplotyping/genotyping  
CC the PLA2G1B gene of an individual, predicting the haplotype pair for the  
CC PLA2G1B gene of an individual, identifying an association between a trait  
CC and at least one haplotype or haplotype pair of the PLA2G1B gene, an  
CC isolated genotyping oligonucleotide for detecting a polymorphism in the  
CC PLA2G1B gene, a recombinant non-human organism transformed or transfected  
CC with the PLA2G1B sequence, where the organism expresses a PLA2G1B  
CC protein encoded by the first nucleotide sequence or by the polymorphic  
CC variant sequence, an isolated polypeptide comprising a sequence which is  
CC a polymorphic variant of a reference sequence for the PLA2G1B protein or  
CC its fragment, an anti-PLA2G1B monoclonal antibody, screening for drugs  
CC targeting PLA2G1B, a computer system for storing and analysing  
CC polymorphism data for the PLA2G1B gene and a genome anthology for PLA2G1B  
CC gene. The PLA2G1B variant is useful in studying the expression and  
CC function of PLA2G1B, and in expressing PLA2G1B protein for use in  
CC screening for candidate drugs to treat diseases related to PLA2G1B  
CC activity (e.g. pancreatitis and pancreatic cancer) and for  
CC therapeutic purposes. The transgenic organism is useful for studying  
CC expression of the PLA2G1B isogenes in vivo, for in vivo screening and  
CC testing of drugs targeted against PLA2G1B protein, and for testing the  
CC efficacy of therapeutic agents and compounds in a biological system.  
CC The antibody is useful for studying the effect of the variation on the  
CC biological activity of PLA2G1B as well as on the binding affinity of  
CC candidate drugs targeting PLA2G1B. The PLA2G1B gene is located on  
CC chromosome 12q23-q24.1. The present sequence is an allele specific  
CC oligonucleotide (ASO) primer extension primer 3' end used to detect the  
CC polymorphisms in PLA2G1B.

Sequence 10 BP; 3 A; 3 C; 0 G; 4 T; 0 other;

Query Match 100.0%; Score 7; DB 24; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.7e+04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7  
|||||||  
9 AGTATGA 3

Search completed: December 31, 2003, 15:08:13  
Job time : 202.291 secs





GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 13:58:09 ; Search time 804.291 Seconds  
(without alignments)  
211.530 Million cell updates/sec

Title: US-09-540-843-3  
Perfect score: 7  
Sequence: 1 agtatga 7

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 33330

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estmu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_htc:\*
- 9: gb\_estl:\*
- 10: gb\_estc2:\*
- 11: gb\_htc:\*
- 12: gb\_estc3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: em\_gss\_hum:\*
- 18: em\_gss\_inv:\*
- 19: em\_gss\_pln:\*
- 20: em\_gss\_vrt:\*
- 21: em\_gss\_fun:\*
- 22: em\_gss\_mam:\*
- 23: em\_gss\_mus:\*
- 24: em\_gss\_pro:\*
- 25: em\_gss\_rod:\*
- 26: em\_gss\_phg:\*
- 27: em\_gss\_vrl:\*
- 28: gb\_gssl:\*
- 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	19	28	AZ817238 2M0086E01
2	7	100.0	19	28	AZ990856 2M0274F14
3	7	100.0	22	28	AZ623945 1M0462J10
4	7	100.0	22	28	AZ658158 1M0534H17

C 5	7	100.0	24	9	AW059679
C 6	7	100.0	24	28	AZ423817
C 7	7	100.0	24	28	AZ478673
C 8	7	100.0	24	28	AZ816657
C 9	7	100.0	25	14	H96935
C 10	7	100.0	25	28	AZ605844
C 11	7	100.0	25	28	AZ802490
C 12	7	100.0	25	28	BH852860
C 13	7	100.0	25	28	BH852866
C 14	7	100.0	25	28	BH857761
C 15	7	100.0	26	28	AZ345685
C 16	7	100.0	26	28	AZ473354
C 17	7	100.0	27	14	D45824
C 18	7	100.0	27	29	AI187C01P
C 19	7	100.0	28	9	AI790546
C 20	7	100.0	28	28	AZ861130
C 21	7	100.0	28	28	BH904074
C 22	7	100.0	29	28	BH856420
C 23	7	100.0	29	29	TA230F03P
C 24	7	100.0	30	14	C21099
C 25	7	100.0	30	29	AL766985
C 26	6	85.7	16	12	BG928185
C 27	6	85.7	17	12	BG929060
C 28	6	85.7	17	14	C21103
C 29	6	85.7	19	9	AI747751
C 30	6	85.7	19	28	AZ406137
C 31	6	85.7	19	28	AZ464990
C 32	6	85.7	19	28	AZ579566
C 33	6	85.7	19	28	AZ647364
C 34	6	85.7	19	28	AZ815067
C 35	6	85.7	20	13	BQ593049
C 36	6	85.7	20	28	AZ336039
C 37	6	85.7	20	28	AZ359199
C 38	6	85.7	20	28	AZ579536
C 39	6	85.7	20	28	AZ615402
C 40	6	85.7	20	28	AZ665083
C 41	6	85.7	20	28	AZ795800
C 42	6	85.7	20	29	TA199G02Q
C 43	6	85.7	21	28	AZ346766
C 44	6	85.7	21	28	AZ383946
C 45	6	85.7	21	28	AZ477879

## ALIGNMENTS

RESULT 1  
AZ817238

LOCUS  
DEFINITION

ACCESSION  
VERSION

KEYWORDS  
SOURCE

ORGANISM  
MUS MUSCULUS

REFERENCE  
AUTHORS

TITLE  
JOURNAL

COMMENT

AZ817238  
2M0086E01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0086E01 R, genomic survey sequence.

AZ817238.1 GI:12987145

GSS.

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

.M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

Contact: Robert B. Weiss

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0086 row: E column: 01  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.

## FEATURES

source

1..19  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
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 /db\_xref="taxon:10090"  
 /clone="UUGC2M0086E01"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

6 a

1 c

6 g

6 t

ORIGIN

Query Match 100.0%; Score 7; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7

10 AGTATGA 16

## RESULT 2

LOCUS

AZ990856 19 bp DNA linear GSS 27-APR-2001  
 2M0274F14R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
 clone UUGC2M0274F14 R, genomic survey sequence.

ACCESSION

AZ990856

VERSION

AZ990856.1

KEYWORDS

GSS.

SOURCE

Mus musculus

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished  
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 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606

Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0274 row: F column: 14  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.

## FEATURES

source

1..19  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
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 /db\_xref="taxon:10090"  
 /clone="UUGC2M0274F14"  
 /sex="Female"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC2M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

8 a

5 c

0 g

6 t

ORIGIN

Query Match 100.0%; Score 7; DB 28; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATGA 7

Db 18 AGTATGA 12

## RESULT 3

AZ623945/c

LOCUS

AZ623945 22 bp DNA linear GSS 13-DEC-2000  
 1M0462J10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0462J10 F, genomic survey sequence.

ACCESSION

AZ623945

VERSION

AZ623945.1

KEYWORDS

GSS.

SOURCE

Mus musculus

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
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 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0462 row: J column: 10  
 Seq primer: CGTTGTAAACGACGCGCCAT  
 Class: plasmid ends  
 High quality sequence stop: 22.

FEATURES

Location/Qualifiers  
 1. 22  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0462J10"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

7 a 5 c 2 g 8 t

Query Match 100.0%; Score 7; DB 28; Length 22;

Best Local Similarity 100.0%; Pred. No. 2.2e+05; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7

11 AGTATGA 5

RESULT 4

LOCUS

AZ658158 22 bp DNA linear GSS 14-DEC-2000  
 1M0534H17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0534H17 R, genomic survey sequence.

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished

Contact: Robert B. Weiss

University of Utah

University of Utah

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84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0534 row: H column: 17  
 Seq primer: CACAGAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 22.

FEATURES

Location/Qualifiers  
 1. 22  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0534H17"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 6 a 0 c 9 g 7 t

Query Match 100.0%; Score 7; DB 28; Length 22;

Best Local Similarity 100.0%; Pred. No. 2.2e+05; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7

4 AGTATGA 10

RESULT 5

LOCUS

AW059679 24 bp mRNA linear EST 23-AUG-2000  
 AHUTH.Best.dnc15.aa.A050g08 Dnc15 Homo sapiens cDNA, mRNA sequence.

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

10677516

Contact: Burcham TS

LYNX Therapeutics, Inc.

25861 Industrial Blvd., Hayward, CA 94545, USA

Tel: 510 670 9338  
 Fax: 510 670 9302  
 Email: tim@lynxgen.com  
 Sequence obtained from LYNX Therapeutics Megasort technology.  
 Collected from the down-regulated gate.  
 High quality sequence stop: 24.  
 Location/Qualifiers  
 1..24  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /cell\_type="monocytic leukemia"  
 /cell\_line="THP-1 (TIB-202)"  
 /clone\_lib="DNC15"  
 /note="Vector: PCR2.1; Cloning of PCR products from micro-beads carrying 3' end of down-regulated cDNA. THP-1 cells non-induced (treated with DMSO only)."  
 9 a 6 c 1 g 8 t  
 BASE COUNT  
 9 a 6 c 1 g 8 t  
 ORIGIN  
 1 AGTATGA 7  
 |||||  
 23 AGTATGA 17

Query Match 100.0%; Score 7; DB 9; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7  
 |||||  
 Db 23 AGTATGA 17

RESULT 6  
 AZ423817/c  
 LOCUS  
 DEFINITION  
 1M0203P19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0203P19 F, genomic survey sequence.  
 AZ423817  
 ACCESSION  
 VERSION  
 GSS.  
 AZ423817.1 GI:10547830  
 SOURCE  
 Mus musculus (house mouse)  
 ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 24)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
 ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
 and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0203 row: P column: 19  
 Seq primer: CGTTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 24.  
 Location/Qualifiers  
 1..24  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0203P19"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWB42 (GII4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 7 a 3 c 2 g 12 t  
 ORIGIN  
 Query Match 100.0%; Score 7; DB 28; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7  
 |||||  
 Db 17 AGTATGA 11

RESULT 7  
 AZ478673/c  
 LOCUS  
 DEFINITION  
 1M0298J20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0298J20 R, genomic survey sequence.  
 AZ478673  
 ACCESSION  
 VERSION  
 GSS.  
 AZ478673.1 GI:10637794  
 SOURCE  
 Mus musculus (house mouse)  
 ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 24)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
 ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
 and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0298 row: J column: 20  
 Seq primer: CACACAGGAACAGCATGACC  
 Class: plasmid ends  
 High quality sequence stop: 24.  
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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0298J20"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 6 a 8 c 3 g 7 t  
ORIGIN  
Query Match 100.0%; Score 7; DB 28; Length 24;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 AGTATGA 7  
|||||||  
8 AGTATGA 2

RESULT 8  
H96935/c  
LOCUS  
DEFINITION  
A2816657 24 bp DNA linear GSS 20-FEB-2001  
clone UUGC2M0085E05 R, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 24)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,  
and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished

TITLE  
JOURNAL  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0085 row: E column: 05  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 24.

FEATURES  
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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0085E05"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 7 a 6 c 3 g 8 t  
ORIGIN  
Query Match 100.0%; Score 7; DB 28; Length 24;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 AGTATGA 7  
|||||||  
19 AGTATGA 13

RESULT 9  
H96935/c  
LOCUS  
DEFINITION  
H96935 25 bp mRNA linear EST 11-DEC-1995  
yuo1d01.r1 Soares\_pineal\_gland\_N3HPG Homo sapiens cDNA clone  
IMAGE:232513 5' similar to SP:S36112 S36112 RETINOBLASTOMA-BINDING  
PROTEIN - ; mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
H96935.1 GI:1113978  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 25)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman,  
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,  
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston,  
R., Williamson, A., Wohldmann, P. and Wilson, R.  
The WashU-Merck EST Project  
Unpublished

TITLE  
JOURNAL  
COMMENT  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estewatson.wustl.edu  
High quality sequence starts: 1  
High quality sequence stops: 1  
Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Insert Length: 1325 Std Error: 0.00  
Seq primer: M13RP1  
High quality sequence stop: 1.

FEATURES  
source  
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Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="GDB:3862504"

/db\_xref="taxon:9606"  
 /clone="IMAGE:232513"  
 /lab\_host="DHI10B (ampicillin resistant)"  
 /clone\_lib="Soares\_pineal\_gland\_N3HPG"  
 /note="Organ: pineal gland; Vector: pT7J3D (Pharmacia)  
 with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;  
 let strand cDNA was primed with a Not I - oligo(dT) primer  
 [5' TGTTACCAATCTGAAGTGGAGCGCGCGTGTGTTTTTTTTTTT 3']  
 double-stranded cDNA was size selected, ligated to Eco  
 RI adapters (Pharmacia), digested with Not I and cloned  
 into the Not I and Eco RI sites of a modified pT7J3 vector  
 (Pharmacia). Library constructed by Bento Soares and  
 M.Fatima Bonaudo."

BASE COUNT 6 a 5 c 6 g 8 t

## ORIGIN

Query Match 100.0%; Score 7; DB 14; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7

|||||

19 AGTATGA 13

## RESULT 10

AZ605844/c

LOCUS

IM0427J22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0427J22 F, genomic survey sequence.

AZ605844

ACCESSION

AZ605844.1 GI:11728034

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 25)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
 ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.  
 and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

JOURNAL

COMMENT

Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0427 row: J column: 22

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 25.

## FEATURES

source

1. .25

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0427J22"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (GI14732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT 7 a 6 c 5 g 7 t

## ORIGIN

Query Match 100.0%; Score 7; DB 28; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7

|||||

17 AGTATGA 11

## RESULT 11

AZ802490/c

LOCUS

2M0061122F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0061122 F, genomic survey sequence.

AZ802490

ACCESSION

AZ802490.1 GI:12954813

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 25)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
 ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.  
 and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

JOURNAL

COMMENT

Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0061 row: I column: 22

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 25.

## FEATURES

source

1. .25

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/clone="UUGC2M0061122"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GII4732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 5 a 6 c 5 g

ORIGIN

Query Match 100.0%; Score 7; DB 28; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7

|||||  
22 AGTATGA 16

RESULT 12

BH852860

LOCUS

DEFINITION SALK\_075689.48.55.x Arabidopsis thaliana TDNA insertion lines  
Arabidopsis thaliana genomic clone SALK\_075689.48.55.x, genomic survey sequence.

ACCESSION BH852860

VERSION 1 GI:21423731

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE

AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab  
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.  
, Zimmermann,J. and Ecker,J.R.

TITLE

A Sequence-Indexed Library of Insertion Mutations in the

JOURNAL

COMMENT

Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of  
TDNA. This sequence lies within an annotated exon of At3g41627.  
Class: TDNA tagged.

FEATURES

source

1..25  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
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/clone="SALK\_075689.48.55.x"  
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/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

BASE COUNT 9 a 2 c 6 g 8 t

ORIGIN

Query Match 100.0%; Score 7; DB 28; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATGA 7

|||||  
12 AGTATGA 18

RESULT 13

BH852866

LOCUS

DEFINITION BH852866 25 bp DNA linear GSS 13-JUN-2002  
SALK\_075697.38.25.x Arabidopsis thaliana TDNA insertion lines  
Arabidopsis thaliana genomic clone SALK\_075697.38.25.x, genomic  
survey sequence.

ACCESSION BH852866

VERSION BH852866.1 GI:21423737

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE

AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab  
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.  
, Zimmermann,J. and Ecker,J.R.

TITLE

A Sequence-Indexed Library of Insertion Mutations in the

JOURNAL

COMMENT

Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of  
TDNA. This sequence lies within an annotated exon of At3g41627.  
Class: TDNA tagged.

FEATURES

source

1..25  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"

/clone="SALK\_075697.38.25.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

BASE COUNT 9 a 2 c 6 g 8 t

ORIGIN

Query Match 100.0%; Score 7; DB 28; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATGA 7

|||||  
12 AGTATGA 18

RESULT 14

BH857761

LOCUS

DEFINITION BH857761 25 bp DNA linear GSS 08-JUL-2002  
SALK\_015664.41.95.x Arabidopsis thaliana TDNA insertion lines  
Arabidopsis thaliana genomic clone SALK\_015664.41.95.x, genomic

BASE COUNT 9 a 2 c 6 g 8 t

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survey sequence.
ACCESSION BH857761
VERSION BH857761.1 GI:21708582
KEYWORDS GSS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 25)
AUTHORS Alonso,J.M., Leisbe,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
, C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
, Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated intron of At3g22930.
Class: TDNA tagged.
FEATURES             source
    Location/Qualifiers
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            /clone_lib="Arabidopsis thaliana TDNA insertion lines"
            /note="PCR was performed on Arabidopsis thaliana lines
            each of which contains one or more TDNA insertion
            elements. The resultant fragment for each line was
            directly sequenced to determine the genomic sequence at
            the site of insertion. Details of the protocols used can
            be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT          9 a      5 c      0 g      11 t
ORIGIN
Query Match          100.0%; Score 7; DB 28; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7
|||||||
8 AGTATGA 2

RESULT 15
ACCESSION AZ345685/1
LOCUS AZ345685.1 26 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0080C06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0080C06 R, genomic survey sequence.
ACCESSION AZ345685
VERSION AZ345685.1 GI:10424922
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 26)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss

```

```

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: C column: 06
Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
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        /sex="Male"
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        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /note="Vector: PWD42nv; Purified genomic DNA from M.
        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA
        was blunt end-repaired with T4 DNA polymerase and T4
        polynucleotide kinase. Adaptor oligonucleotides were
        ligated to the blunt ends in high molar excess. The
        adaptored DNA was purified and size-selected for a 9.5 to
        10.5 kb range using preparative agarose gel
        electrophoresis. Vector DNA was prepared from a derivative
        of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
        inducible derivative of plasmid R1. The vector was ligated
        with adaptors complementary to the insert adaptors and
        purified. The sheared, adaptored mouse DNA was annealed to
        adaptored vector DNA, and transformed into
        chemically-competent E. coli XL10-Gold (Stratagene) cells
        and selected for ampicillin resistance."
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGTATGA 7
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9 AGTATGA 3

Search completed: December 31, 2003, 19:41:16
Job time : 807.291 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 11:36:21 ; Search time 460.316 Seconds  
(without alignments)  
444.364 Million cell updates/sec

Title: US-09-540-843-4  
Perfect score: 5  
Sequence: 1 gtagt 5

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 1010434

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:

1: gb\_ba:  
2: gb\_htg:  
3: gb\_in:  
4: gb\_om:  
5: gb\_ov:  
6: gb\_pat:  
7: gb\_ph:  
8: gb\_pl:  
9: gb\_pr:  
10: gb\_ro:  
11: gb\_sts:  
12: gb\_sy:  
13: gb\_un:  
14: gb\_vi:  
15: em\_ba:  
16: em\_or:  
17: em\_fun:  
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19: em\_mu:  
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26: em\_ro:  
27: em\_sts:  
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30: em\_htg\_hum:  
31: em\_htg\_inv:  
32: em\_htg\_other:  
33: em\_htg\_mus:  
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35: em\_htg\_rnd:  
36: em\_htg\_mam:  
37: em\_htg\_vrt:  
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40: em\_htgo\_mus:  
41: em\_htgo\_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5	100.0	5	6	AX268756 Sequence
2	5	100.0	5	6	AX268758 Sequence
3	5	100.0	7	6	AX268755 Sequence
4	5	100.0	7	6	AX268759 Sequence
5	5	100.0	8	6	AX047565 Sequence
6	5	100.0	8	6	AX104946 Sequence
7	5	100.0	8	6	AX119567 Sequence
8	5	100.0	8	6	BD085298 DNA-based
9	5	100.0	9	6	AX268753 Sequence
10	5	100.0	9	6	AX268754 Sequence
11	5	100.0	9	6	AX667174 Sequence
12	5	100.0	9	6	AX668771 Sequence
13	5	100.0	9	6	AX668807 Sequence
14	5	100.0	9	9	S50583 type I proc
15	5	100.0	9	9	S50585
16	5	100.0	10	6	A18263 oligonucleo
17	5	100.0	10	6	AR065157 Sequence
18	5	100.0	10	6	AR079101 Sequence
19	5	100.0	10	6	AR079103 Sequence
20	5	100.0	10	6	AR098909 Sequence
21	5	100.0	10	6	AR107335 Sequence
22	5	100.0	10	6	AR107344 Sequence
23	5	100.0	10	6	AR123039 Sequence
24	5	100.0	10	6	AR136787 Sequence
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26	5	100.0	10	6	AR202278 Sequence
27	5	100.0	10	6	AR217382 Sequence
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33	5	100.0	10	6	AR303540 Sequence
34	5	100.0	10	6	AR303548 Sequence
35	5	100.0	10	6	AR303553 Sequence
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ALIGNMENTS

RESULT 1	AX268756	AX268756	5 bp	DNA	linear	PAT 29-OCT-2001
LOCUS	Sequence	4	from Patent	WO0174342.		
DEFINITION	AX268756					
ACCESSION	AX268756.1	GI:16541828				
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE	1					
AUTHORS	Gilchrest,B.A., Yaar,M. and Eller,M.					
TITLE	Use of locally applied dna fragments					
JOURNAL	Patent: WO 0174342-A 4 11-OCT-2001;					
	TRUSTEES OF BOSTON UNIVERSITY (US)					



```

; APPLICANT: German, Thomas L.
; TITLE OF INVENTION: ASSAY FOR VERTICILLIUM DAHLIAE
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles and Brady
; STREET: 1 South Plinckney St., PO BOX 2113
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,565A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 960296.93065
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-335-565A-27

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Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.6e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GTATG 5
Db 6 GTATG 10

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RESULT 14
US-08-250-951-1/c
; Sequence 1, Application US/08250951
; Patent No. 5532129
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J
; TITLE OF INVENTION: SELF-ORGANIZING MOLECULAR PHOTONIC
; STRUCTURES BASED ON CHROMOPHORE- AND FLUOROPHORE-CONTAINING
; TITLE OF INVENTION: POLYNUCLEOTIDES AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bingham & Fitting
; STREET: 12526 High Bluff Drive, Suite 300
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92130
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,951
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/790,262
; FILING DATE: 07-NOV-1991

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: HEL0002P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-792-3680
; TELEFAX: 619-792-8477
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc_feature
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; US-08-250-951-1

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Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.6e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15
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; Sequence 1, Application US/08232233
; Patent No. 5565322
; GENERAL INFORMATION:
; APPLICANT: Michael J. Heller
; TITLE OF INVENTION: SELF-ORGANIZING MOLECULAR PHOTONIC
; STRUCTURES BASED ON CHROMOPHORE- AND FLUOROPHORE-
; CONTAINING POLYNUCLEOTIDES AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,233
; FILING DATE: May 4, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/790,262
; FILING DATE: NO. 5565322,ember 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, David B.
; REGISTRATION NUMBER: 31,125
; REFERENCE/DOCKET NUMBER: 207/170
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid

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```

; Sequence 80, Application US/08646789A
; Patent No. 6022863
; GENERAL INFORMATION:
; APPLICANT: Peyman, John A.
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,789A
; FILING DATE: May 21, 1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6523-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; US-08-646-789A-80

Query Match          100.0%; Score 5; DB 3; Length 9;
Best Local Similarity 60.0%; Pred. No. 4.5e+07;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTATG 5
Db      1 GUATG 5

RESULT 11
US-09-048-927-1
; Sequence 1, Application US/09048927
; Patent No. 6147056
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Yaer, Mina
; TITLE OF INVENTION: Use of Locally Applied DNA Fragments
; FILE REFERENCE: BU94-68A2
; CURRENT APPLICATION NUMBER: US/09/048,927
; EARLIER APPLICATION NUMBER: 08/952,697
; EARLIER FILING DATE: 1996-06-03
; EARLIER APPLICATION NUMBER: 08/467,012
; EARLIER FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA Fragment
US-09-048-927-1

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Query Match          100.0%; Score 5; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTATG 5
Db      3 GTATG 7

RESULT 12
US-09-319-648-68/C
; Sequence 68, Application US/09319648
; Patent No. 6451530
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Mary
; TITLE OF INVENTION: Fluorescent Nucleotide Analog Hairpin
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/319,648
; FILING DATE: 30-Jul-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,844
; FILING DATE: 13-DEC-1996
; APPLICATION NUMBER: WO PCT/US97/22448
; FILING DATE: 10-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Pang, Carol
; REGISTRATION NUMBER: 48,631
; REFERENCE/DOCKET NUMBER: 015280-288100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-09-319-648-68

Query Match          100.0%; Score 5; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.5e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTATG 5
Db      7 GTATG 3

RESULT 13
US-08-335-565A-27
; Sequence 27, Application US/08335565A
; Patent No. 5527671
; GENERAL INFORMATION:
; APPLICANT: Li, Kenning
; APPLICANT: Rouse, Douglas I.
US-08-335-565A-27

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CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/142,593  
 FILING DATE: 10-SEP-1998  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/040,664  
 FILING DATE: 11-MAR-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/053,868  
 FILING DATE: 28-JUL-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/065,303  
 FILING DATE: 13-NOV-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US98/04687  
 FILING DATE: 11-MAR-1998  
 ATTORNEY/AGENT INFORMATION:  
 NAME: SANDBERG, VICTORIA A.  
 REGISTRATION NUMBER: 41,287  
 REFERENCE/DOCKET NUMBER: 110.00450101  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 612-305-1226  
 TELEFAX: 612-305-1228  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-09-142-593-11

Query Match 100.0%; Score 5; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5  
 Db 6 GTATG 2

RESULT 8  
 US-08-583-276-1  
 Sequence 1, Application US/08583276  
 Patent No. 5837536  
 GENERAL INFORMATION:  
 APPLICANT: MCDONAGH, Kevin T.  
 APPLICANT: NIENHUIS, Arthur  
 APPLICANT: TOLSTOSHEV, Paul  
 TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN  
 TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED  
 TITLE OF INVENTION: SELECTION OF CELLS TRANSFECTED WITH SUCH GENES  
 NUMBER OF SEQUENCES: 19  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Carelli, Byrne, Bain, Giffillan,  
 ADDRESSEE: Cecchi & Stewart  
 STREET: 6 Becker Farm Road  
 CITY: Roseland  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07068  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch diskette  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: PC-DOS  
 SOFTWARE: DM4.V2  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/583,276  
 FILING DATE: 05-JAN-1996  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/332,444  
 FILING DATE: 31-OCT-1994

APPLICATION NUMBER: 07/887,712  
 FILING DATE: 22-MAY-1992  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 bases  
 TYPE: nucleic acid  
 STRANDEDNESS: singular  
 TOPOLOGY: linear  
 MOLECULE TYPE:  
 DESCRIPTION: Genomic DNA  
 US-08-583-276-1

Query Match 100.0%; Score 5; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5  
 Db 4 GTATG 8

RESULT 9  
 US-08-646-789A-8  
 Sequence 8, Application US/08646789A  
 Patent No. 6022863  
 GENERAL INFORMATION:  
 APPLICANT: PEYMAN, John A.  
 TITLE OF INVENTION: REGULATION OF GENE EXPRESSION  
 NUMBER OF SEQUENCES: 101  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: PENNIE & EDMONDS  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036-2711  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/646,789A  
 FILING DATE: May 21, 1996  
 CLASSIFICATION: 800  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MISTOCK, S. Leslie  
 REGISTRATION NUMBER: 18,872  
 REFERENCE/DOCKET NUMBER: 6523-006  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-9741/8864  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 US-08-646-789A-8

Query Match 100.0%; Score 5; DB 3; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATG 5  
 Db 1 GTATG 5

RESULT 10  
 US-08-646-789A-80

SEQUENCE CHARACTERISTICS:  
LENGTH: 7 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1..7  
OTHER INFORMATION: /standard name= "Sph-II binding  
US-08-615-170-10  
OTHER INFORMATION: site in SV40"  
Query Match 100.0%; Score 5; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 5.8e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTATG 5  
Db 5 GTATG 1  
RESULT 5  
US-08-615-170-12/C  
Sequence 12, Application US/08615170  
Patent No. 5776776  
GENERAL INFORMATION:  
APPLICANT: ORDAHL, Charles P.  
APPLICANT: AZAKIE, Anthony  
APPLICANT: MAR, Janet H.  
APPLICANT: FARRANCE, Iain K.G.  
APPLICANT: HALL, Deborah E.  
APPLICANT: STEWART, Alexandre F.R.  
APPLICANT: LARKIN, Sarah B.  
TITLE OF INVENTION: DREF-1 ISOFORMS AND USES THEREOF  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: Steuart Street Tower, One Market Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105-1493  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/615,170  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/01526  
FILING DATE: 06-FEB-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/191,493  
FILING DATE: 04-FEB-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Healin, James M.  
REGISTRATION NUMBER: 29,541  
REFERENCE/DOCKET NUMBER: 2307U-053120  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1..7  
OTHER INFORMATION: /standard name= "Rat beta-Myosin  
US-08-615-170-12  
OTHER INFORMATION: Heavy Chain M-CAT binding element"  
Query Match 100.0%; Score 5; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 5.8e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTATG 5  
Db 5 GTATG 1  
RESULT 6  
US-09-048-927-3  
Sequence 3, Application US/09048927  
Patent No. 6147056  
GENERAL INFORMATION:  
APPLICANT: Gilchrist, Barbara A.  
APPLICANT: Yaer, Mina  
APPLICANT: Eller, Mark  
TITLE OF INVENTION: Use of Locally Applied DNA Fragments  
FILE REFERENCE: BU94-68A2  
CURRENT APPLICATION NUMBER: US/09/048,927  
CURRENT FILING DATE: 1998-03-26  
EARLIER APPLICATION NUMBER: 08/952,697  
EARLIER FILING DATE: 1996-06-03  
EARLIER APPLICATION NUMBER: 08/467,012  
EARLIER FILING DATE: 1995-06-06  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PasteSeq for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 7  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: DNA Fragment  
US-09-048-927-3  
Query Match 100.0%; Score 5; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 5.8e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTATG 5  
Db 2 GTATG 6  
RESULT 7  
US-09-142-593-11/C  
Sequence 11, Application US/09142593  
Patent No. 6489458  
GENERAL INFORMATION:  
APPLICANT: HACKETT ET AL.  
TITLE OF INVENTION: DNA-BASED TRANSPOSON SYSTEM FOR THE  
INTRODUCTION OF NUCLEIC ACID INTO DNA OF A CELL  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MUETING, RASCH & GEBHARDT, P.A.  
STREET: 119 NORTH FOURTH STREET, SUITE 203  
CITY: MINNEAPOLIS  
STATE: MINNESOTA  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

QY 1 GTATG 5  
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 Db 1 GTATG 5

RESULT 2  
 US-09-048-927-4  
 ; Sequence 4, Application US/09048927  
 ; Patent No. 6147056  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gilchrist, Barbara A.  
 ; APPLICANT: Yaar, Mina  
 ; APPLICANT: Eller, Mark  
 ; TITLE OF INVENTION: Use of Locally Applied DNA Fragments  
 ; FILE REFERENCE: 8094-6842  
 ; CURRENT APPLICATION NUMBER: US/09/048,927  
 ; CURRENT FILING DATE: 1998-03-26  
 ; EARLIER APPLICATION NUMBER: 08/952,697  
 ; EARLIER FILING DATE: 1996-06-03  
 ; EARLIER APPLICATION NUMBER: 08/467,012  
 ; EARLIER FILING DATE: 1995-06-06  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO: 4  
 ; LENGTH: 5  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: DNA Fragment  
 ; US-09-048-927-4

Query Match 100.0%; Score 5; DB 3; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 8.2e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTATG 5  
 |||||  
 Db 1 GTATG 5

RESULT 3  
 US-09-498-851-20  
 ; Sequence 20, Application US/09498851  
 ; Patent No. 6440671  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mirzabekov, Andrei D  
 ; APPLICANT: Parinov, Sergei V  
 ; APPLICANT: Barsky, Victor E  
 ; APPLICANT: Kirillov, Eugene V  
 ; APPLICANT: Dubiley, Svetlana A  
 ; TITLE OF INVENTION: Use of Continuous/Continuous  
 ; TITLE OF INVENTION: Stacking Hybridization as a Diagnostic Tool.  
 ; NUMBER OF SEQUENCES: 88  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSEE: CHERSKOV & FLAVNIK  
 ; STREET: 20 N. Wacker Drive  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: United States  
 ; ZIP: 60606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.50 inch, 1.4 MB storage  
 ; COMPUTER: PC  
 ; OPERATING SYSTEM: Microsoft Windows 98  
 ; SOFTWARE: Wordperfect  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/498,851  
 ; FILING DATE:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/855,372  
 ; FILING DATE: 13-MAY-97  
 ; APPLICATION NUMBER: U.S. 08/587,332

FILING DATE: 16-JAN-96  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Cherskov, Michael J.  
 REGISTRATION NUMBER: 33,664  
 REFERENCE/DOCKET NUMBER: ANL-IN-95-027  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (312) 621-1330  
 TELEFAX: (312) 621-0088  
 INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5 bases  
 TYPE: nucleic acid  
 STRANDEDNESS: No. 6440671 Applicable  
 TOPOLOGY: linear  
 MOLECULE TYPE: Genomic DNA  
 ; HYPOTHETICAL: yes  
 ; US-09-498-851-20

Query Match 100.0%; Score 5; DB 4; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 8.2e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTATG 5  
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 Db 1 GTATG 5

RESULT 4  
 US-08-615-170-10/c  
 ; Sequence 10, Application US/08615170  
 ; Patent No. 5776776  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ORDASH, Charles P.  
 ; APPLICANT: AZAKIE, Anthony  
 ; APPLICANT: MAR, Janet H.  
 ; APPLICANT: FARRANCE, Iain K.G.  
 ; APPLICANT: HALL, Deborah E.  
 ; APPLICANT: STEWART, Alexandre F.R.  
 ; APPLICANT: LARKIN, Sarah B.  
 ; TITLE OF INVENTION: DTEF-1 ISOFORMS AND USES THEREOF  
 ; NUMBER OF SEQUENCES: 32  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSEE: Townsend and Townsend Kourie and Crew  
 ; STREET: Stewart Street Tower, One Market Plaza  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: US  
 ; ZIP: 94105-1493  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/615,170  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/01526  
 ; FILING DATE: 06-FEB-1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/191,493  
 ; FILING DATE: 04-FEB-1994  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Heslin, James M.  
 ; REGISTRATION NUMBER: 29,541  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 326-2400  
 ; TELEFAX: (415) 326-2422  
 ; INFORMATION FOR SEQ ID NO: 10:

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 14:40:05 ; Search time 19.4304 Seconds  
(without alignments)  
113.581 Million cell updates/sec

Title: US-09-540-843-4  
Perfect score: 5  
Sequence: 1 gtagc 5

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 547746

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
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3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5	100.0	5	3	US-08-855-372B-20
2	5	100.0	5	3	US-08-048-927-4
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4	5	100.0	7	1	US-08-615-170-10
5	5	100.0	7	1	US-08-615-170-12
6	5	100.0	7	3	US-09-048-927-3
7	5	100.0	8	4	US-09-142-593-11
8	5	100.0	9	2	US-08-583-276-1
9	5	100.0	9	3	US-08-646-789A-8
10	5	100.0	9	3	US-08-646-789A-80
11	5	100.0	9	3	US-09-048-927-1
12	5	100.0	9	4	US-09-319-648-68
13	5	100.0	10	1	US-08-335-565A-27
14	5	100.0	10	1	US-08-250-951-1
15	5	100.0	10	1	US-08-232-233-1
16	5	100.0	10	1	US-08-222-177A-422
17	5	100.0	10	1	US-08-351-748-23
18	5	100.0	10	1	US-08-351-748-25
19	5	100.0	10	1	US-08-202-927-25
20	5	100.0	10	1	US-08-430-536A-23
21	5	100.0	10	1	US-08-430-536A-25
22	5	100.0	10	1	US-08-171-718-45
23	5	100.0	10	2	US-08-703-601-1
24	5	100.0	10	2	US-08-684-547-23
25	5	100.0	10	2	US-08-684-547-25
26	5	100.0	10	3	US-08-469-318-174
27	5	100.0	10	3	US-08-468-609A-174

28	5	100.0	10	3	US-08-478-087-45	Sequence 45, Appl
29	5	100.0	10	3	US-09-063-450-24	Sequence 24, Appl
30	5	100.0	10	3	US-09-063-450-23	Sequence 23, Appl
31	5	100.0	10	3	US-09-123-638-1	Sequence 1, Appl
32	5	100.0	10	3	US-08-646-695-30	Sequence 30, Appl
33	5	100.0	10	3	US-08-875-533-31	Sequence 31, Appl
34	5	100.0	10	4	US-08-446-872A-174	Sequence 174, App
35	5	100.0	10	4	US-09-724-753-1	Sequence 174, App
36	5	100.0	10	4	US-08-762-227A-174	Sequence 174, App
37	5	100.0	10	4	US-09-475-947A-23	Sequence 23, Appl
38	5	100.0	10	4	US-09-427-834A-34	Sequence 34, Appl
39	5	100.0	10	4	US-09-445-388A-7	Sequence 7, Appl
40	5	100.0	10	4	US-09-508-753B-252	Sequence 252, App
41	5	100.0	10	4	US-09-508-753B-265	Sequence 265, App
42	5	100.0	10	4	US-09-508-753B-273	Sequence 273, App
43	5	100.0	10	4	US-09-508-753B-278	Sequence 278, App
44	5	100.0	10	4	US-09-508-753B-294	Sequence 294, App
45	5	100.0	10	4	US-09-508-753B-303	Sequence 303, App

ALIGNMENTS

RESULT 1  
US-08-855-372B-20  
Sequence 20, Application US/08855372B  
Patent No. 6090549  
GENERAL INFORMATION:  
APPLICANT: Mirzabekov, Andrei D  
APPLICANT: Parinov, Sergei V  
APPLICANT: Barsky, Victor E  
APPLICANT: Kirillov, Eugene V  
APPLICANT: Dubiley, Svetlana A  
TITLE OF INVENTION: Use of Continuous/Contiguous Stacking Hybridization as a  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHERSKOV & FLAYNIK  
STREET: 20 N. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.50 inch, 1.4 MB storage  
COMPUTER: PC  
OPERATING SYSTEM: Microsoft Windows 98  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/855,372B  
FILING DATE: 13-MAY-97  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/587,332  
FILING DATE: 16-JAN-96  
ATTORNEY/AGENT INFORMATION:  
NAME: Cherskov, Michael J.  
REGISTRATION NUMBER: 33,664  
REFERENCE/DOCKET NUMBER: ANL-IN-95-027  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 621-1330  
TELEFAX: (312) 621-0088  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 bases  
TYPE: nucleic acid  
STRANDEDNESS: No. 6090549 Applicable  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOTHETICAL: Yes  
US-08-855-372B-20  
Query Match 100.0%; Score 5; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 8.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;





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; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MEBH00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 4624
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-4624

```

```

Query Match          100.0%; Score 7; DB 13; Length 13;
Best Local Similarity 71.4%; Pred. No. 1.1e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      1 AGTATGA 7
        ||:||
Db       6 AGUAGA 12

```

```

RESULT 15
US-09-875-440-22/c
; Sequence 22, Application US/09875440
; Patent No. US20020156035A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Winter, Jill A.
; APPLICANT: Randazzo, Filippo
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; FILE REFERENCE: PP-01/01.002/200130.522
; CURRENT APPLICATION NUMBER: US/09/875,440
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 22
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide NET-4 oligo 868 used for in-situ
; OTHER INFORMATION: hybridization
US-09-875-440-22

```

```

Query Match          100.0%; Score 7; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      1 AGTATGA 7
        |||||
Db       13 AGTATGA 7

```

```

Search completed: January 1, 2004, 01:10:36
Job time : 82.6076 secs

```

QY 1 AGTATGA 7  
 |||||  
 Db 10 AGTATGA 4

## RESULT 10

US-10-033-145-1423/c  
 ; Sequence 1423, Application US/10033145  
 ; Publication No. US2002015155A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GENZYME CORPORATION  
 ; APPLICANT: ROBERTS, BRUCE  
 ; APPLICANT: SHANKARA, SRINIVAS  
 ; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES  
 ; FILE REFERENCE: GA0201C  
 ; CURRENT APPLICATION NUMBER: US/10/033,145  
 ; CURRENT FILING DATE: 2001-11-05  
 ; PRIOR APPLICATION NUMBER: PCT/US99/13800  
 ; PRIOR FILING DATE: 1999-06-18  
 ; NUMBER OF SEQ ID NOS: 2137  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 1423  
 ; LENGTH: 10  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-033-145-1423

Query Match 100.0%; Score 7; DB 14; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATGA 7  
 |||||  
 Db 7 AGTATGA 1

## RESULT 11

US-10-150-779A-15/c  
 ; Sequence 15, Application US/10150779A  
 ; Publication No. US20030125241A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WISENBACH, MARGIT  
 ; APPLICANT: KOCH, TROELS  
 ; APPLICANT: ORUM, HENRIK  
 ; APPLICANT: HANSEN, BO  
 ; TITLE OF INVENTION: THERAPEUTIC USES OF LNA-MODIFIED OLIGONUCLEOTIDES IN  
 ; FILE REFERENCE: 55704 (45120)  
 ; CURRENT APPLICATION NUMBER: US/10/150,779A  
 ; CURRENT FILING DATE: 2003-02-07  
 ; PRIOR APPLICATION NUMBER: 60/291,830  
 ; PRIOR FILING DATE: 2001-05-18  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 15  
 ; LENGTH: 12  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: oligonucleotide  
 US-10-150-779A-15

Query Match 100.0%; Score 7; DB 15; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATGA 7  
 |||||  
 Db 11 AGTATGA 5

## RESULT 12

US-10-150-779A-16/c  
 ; Sequence 16, Application US/10150779A  
 ; Publication No. US20030125241A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WISENBACH, MARGIT  
 ; APPLICANT: KOCH, TROELS  
 ; APPLICANT: ORUM, HENRIK  
 ; APPLICANT: HANSEN, BO  
 ; TITLE OF INVENTION: THERAPEUTIC USES OF LNA-MODIFIED OLIGONUCLEOTIDES IN  
 ; FILE REFERENCE: 55704 (45120)  
 ; CURRENT APPLICATION NUMBER: US/10/150,779A  
 ; CURRENT FILING DATE: 2003-02-07  
 ; PRIOR APPLICATION NUMBER: 60/291,830  
 ; PRIOR FILING DATE: 2001-05-18  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 16  
 ; LENGTH: 12  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: DNA oligonucleotide with phosphorothioate backbone  
 US-10-150-779A-16

Query Match 100.0%; Score 7; DB 15; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATGA 7  
 |||||  
 Db 11 AGTATGA 5

## RESULT 13

US-09-740-332-4624  
 ; Sequence 4624, Application US/09740332  
 ; Publication No. US20030125270A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceuticals Inc.  
 ; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
 ; FILE REFERENCE: RPI 400/003  
 ; CURRENT APPLICATION NUMBER: US/09/740,332  
 ; CURRENT FILING DATE: 2001-03-26  
 ; NUMBER OF SEQ ID NOS: 9704  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 4624  
 ; LENGTH: 13  
 ; TYPE: RNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION:  
 ; OTHER INFORMATION: oligonucleotide substrate  
 US-09-740-332-4624

Query Match 100.0%; Score 7; DB 11; Length 13;  
 Best Local Similarity 71.4%; Pred. No. 1.1e+05;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATGA 7  
 |||||  
 Db 6 AGTATGA 12

## RESULT 14

US-09-817-879-4624  
 ; Sequence 4624, Application US/09817879  
 ; Publication No. US20030171311A1  
 ; GENERAL INFORMATION:

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-1

```

```

Query Match
Best Local Similarity 100.0%; Score 7; DB 15; Length 9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 AGTATGA 7
Db 2 AGTATGA 8

```

```

RESULT 6
US-10-122-633-1
; Sequence 1, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Eller, Mark S.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE REFERENCE: 0054.1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-1

```

```

Query Match
Best Local Similarity 100.0%; Score 7; DB 15; Length 9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 AGTATGA 7
Db 2 AGTATGA 8

```

```

RESULT 7
US-09-398-399-31
; Sequence 31, Application US/09398399
; Patent No. US20020051973A1
; GENERAL INFORMATION:
; APPLICANT: DELENSTARR, GLENDA C.
; APPLICANT: LEFKOWITZ, STEVEN M.
; APPLICANT: LUEBEKE, KEVIN J.
; APPLICANT: OVERMAN, LESLIE B.
; APPLICANT: SAMPSON, NICHOLAS M.
; APPLICANT: WOLBER, JEFFREY R.
; APPLICANT: WOLBER, PAUL K.
; TITLE OF INVENTION: TECHNIQUES FOR ASSESSING NONSPECIFIC BINDING OF NUCLEIC
; TITLE OF INVENTION: ACIDS TO SURFACES
; FILE REFERENCE: 10981620-1
; CURRENT APPLICATION NUMBER: US/09/398,399
; CURRENT FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence

```

```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-09-398-399-31

```

```

Query Match
Best Local Similarity 100.0%; Score 7; DB 9; Length 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 AGTATGA 7
Db 1 AGTATGA 7

```

```

RESULT 8
US-09-899-381-31
; Sequence 31, Application US/09899381
; Patent No. US20020068293A1
; GENERAL INFORMATION:
; APPLICANT: Delenstarr, Glend C.
; APPLICANT: Wolber, Pual K.
; APPLICANT: Sana, Theodore R.
; TITLE OF INVENTION: Arrays Having Background Features and
; TITLE OF INVENTION: Methods for Using the Same
; FILE REFERENCE: 10010760-1
; CURRENT APPLICATION NUMBER: US/09/899,381
; CURRENT FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 09/398,399
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic probe
US-09-899-381-31

```

```

Query Match
Best Local Similarity 100.0%; Score 7; DB 9; Length 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 AGTATGA 7
Db 1 AGTATGA 7

```

```

RESULT 9
US-10-329-465-30/c
; Sequence 30, Application US/10329465
; Publication No. US20030165949A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: GENES ABNORMALLY EXPRESSED IN MYELOID LEUKEMIA CELLS WITH AN MLL-?
; TITLE OF INVENTION: FUSION
; FILE REFERENCE: 27373/37928A
; CURRENT APPLICATION NUMBER: US/10/329,465
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/343,826
; PRIOR FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-329-465-30

```

```

Query Match
Best Local Similarity 100.0%; Score 7; DB 13; Length 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Db 1 AGTATGA 7

## RESULT 2

US-10-122-630-7  
 ; Sequence 7, Application US/10122630  
 ; Publication No. US20030032610A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gilchrist, Barbara A.  
 ; APPLICANT: Eller, Mark S.  
 ; TITLE OF INVENTION: Method to inhibit Cell Growth Using  
 ; FILE REFERENCE: 0054.1088-019  
 ; CURRENT APPLICATION NUMBER: US/10/122,630  
 ; CURRENT FILING DATE: 2002-04-12  
 ; PRIOR FILING DATE: 1995-06-06  
 ; PRIOR FILING DATE: 1996-06-03  
 ; PRIOR FILING DATE: 1996-06-03  
 ; PRIOR FILING DATE: 1996-06-03  
 ; PRIOR FILING DATE: 1998-03-26  
 ; PRIOR FILING DATE: 1998-03-26  
 ; PRIOR FILING DATE: 2000-03-31  
 ; PRIOR FILING DATE: 2000-03-31  
 ; PRIOR FILING DATE: 2001-03-30  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 7  
 ; LENGTH: 7  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic DNA Fragment  
 ; US-10-122-630-7

Query Match 100.0%; Score 7; DB 15; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+08;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7  
 Db 1 AGTATGA 7

## RESULT 3

US-10-122-633-3  
 ; Sequence 3, Application US/10122633  
 ; Publication No. US20030032611A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gilchrist, Barbara A.  
 ; APPLICANT: Eller, Mark S.  
 ; APPLICANT: Yaar, Mina  
 ; TITLE OF INVENTION: Method to inhibit Cell Growth Using  
 ; FILE REFERENCE: 0054.1088-019  
 ; CURRENT APPLICATION NUMBER: US/10/122,633  
 ; CURRENT FILING DATE: 2002-04-12  
 ; PRIOR FILING DATE: 1995-06-06  
 ; PRIOR FILING DATE: 1996-06-03  
 ; PRIOR FILING DATE: 1996-06-03  
 ; PRIOR FILING DATE: 1998-03-26  
 ; PRIOR FILING DATE: 1998-03-26  
 ; PRIOR FILING DATE: 2000-03-31  
 ; PRIOR FILING DATE: 2000-03-31  
 ; PRIOR FILING DATE: 2001-03-30  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 7  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic DNA Fragment  
 ; US-10-122-633-3

Query Match 100.0%; Score 7; DB 15; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+08;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7  
 Db 1 AGTATGA 7

## RESULT 4

US-10-122-633-7  
 ; Sequence 7, Application US/10122633  
 ; Publication No. US20030032611A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gilchrist, Barbara A.  
 ; APPLICANT: Eller, Mark S.  
 ; APPLICANT: Yaar, Mina  
 ; TITLE OF INVENTION: Method to inhibit Cell Growth Using  
 ; FILE REFERENCE: 0054.1088-019  
 ; CURRENT APPLICATION NUMBER: US/10/122,633  
 ; CURRENT FILING DATE: 2002-04-12  
 ; PRIOR FILING DATE: 1995-06-06  
 ; PRIOR FILING DATE: 1996-06-03  
 ; PRIOR FILING DATE: 1996-06-03  
 ; PRIOR FILING DATE: 1998-03-26  
 ; PRIOR FILING DATE: 1998-03-26  
 ; PRIOR FILING DATE: 2000-03-31  
 ; PRIOR FILING DATE: 2000-03-31  
 ; PRIOR FILING DATE: 2001-03-30  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 7  
 ; LENGTH: 7  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic DNA Fragment  
 ; US-10-122-633-7

Query Match 100.0%; Score 7; DB 15; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+08;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGTATGA 7  
 Db 1 AGTATGA 7

## RESULT 5

US-10-122-630-1  
 ; Sequence 1, Application US/10122630  
 ; Publication No. US20030032610A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gilchrist, Barbara A.  
 ; APPLICANT: Eller, Mark S.  
 ; APPLICANT: Yaar, Mina  
 ; TITLE OF INVENTION: Method to inhibit Cell Growth Using  
 ; FILE REFERENCE: 0054.1088-019  
 ; CURRENT APPLICATION NUMBER: US/10/122,630  
 ; CURRENT FILING DATE: 2002-04-12  
 ; PRIOR FILING DATE: 1995-06-06  
 ; PRIOR FILING DATE: 1995-06-06  
 ; PRIOR FILING DATE: 1996-06-03  
 ; PRIOR FILING DATE: 1996-06-03  
 ; PRIOR FILING DATE: 1998-03-26  
 ; PRIOR FILING DATE: 1998-03-26  
 ; PRIOR FILING DATE: 2000-03-31  
 ; PRIOR FILING DATE: 2000-03-31  
 ; PRIOR FILING DATE: 2001-03-30  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 9  
 ; TYPE: DNA

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 17:10:00 ; Search time 81.6076 Seconds  
(without alignments)  
296.896 Million cell updates/sec

Title: US-09-540-843-3

Perfect score: 1 agtatga 7

Sequence: IDENTITY NUC  
Gapop 10-0, Gapext 1.0

Scoring table: 2263443 seqs, 1730637950 residues

Searched: Total number of hits satisfying chosen parameters: 998502

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	15	US-10-122-630-3
2	7	100.0	7	15	US-10-122-630-7
3	7	100.0	7	15	US-10-122-633-3
4	7	100.0	7	15	US-10-122-633-7
5	7	100.0	9	15	US-10-122-630-1
6	7	100.0	9	15	US-10-122-633-1
7	7	100.0	10	9	US-09-398-399-31
8	7	100.0	10	9	US-09-899-381-31
9	7	100.0	10	13	US-10-329-465-30
10	7	100.0	10	14	US-10-033-145-1423
11	7	100.0	12	15	US-10-150-779A-15
12	7	100.0	12	15	US-10-150-779A-16
13	7	100.0	13	11	US-09-740-332-4624
14	7	100.0	13	13	US-09-817-879-4624
15	7	100.0	14	10	US-09-875-440-22

16	7	100.0	15	9	US-09-504-231A-527	Sequence 527, App
17	7	100.0	15	9	US-09-504-231A-528	Sequence 528, App
18	7	100.0	15	9	US-09-504-231A-529	Sequence 529, App
19	7	100.0	15	9	US-09-504-231A-1527	Sequence 1527, App
20	7	100.0	15	9	US-09-504-231A-1569	Sequence 1569, App
21	7	100.0	15	9	US-09-504-231A-1570	Sequence 1570, App
22	7	100.0	15	9	US-09-398-399-30	Sequence 30, App1
23	7	100.0	15	9	US-09-899-381-30	Sequence 30, App1
24	7	100.0	15	9	US-09-274-553D-527	Sequence 527, App
25	7	100.0	15	9	US-09-274-553D-528	Sequence 528, App
26	7	100.0	15	9	US-09-274-553D-529	Sequence 529, App
27	7	100.0	15	9	US-09-274-553D-1527	Sequence 1527, App
28	7	100.0	15	9	US-09-274-553D-1569	Sequence 1569, App
29	7	100.0	15	9	US-09-274-553D-1570	Sequence 1570, App
30	7	100.0	15	10	US-09-272-343-1	Sequence 1, App1
31	7	100.0	15	10	US-09-272-343-2	Sequence 2, App1
32	7	100.0	15	11	US-09-740-332-4558	Sequence 4558, App
33	7	100.0	15	11	US-09-740-332-4571	Sequence 4571, App
34	7	100.0	15	13	US-09-817-879-4558	Sequence 4558, App
35	7	100.0	15	13	US-09-817-879-4571	Sequence 4571, App
36	7	100.0	15	13	US-10-440-850-88	Sequence 88, App1
37	7	100.0	15	13	US-10-440-850-569	Sequence 569, App
38	7	100.0	17	9	US-09-866-108-2749	Sequence 2749, App
39	7	100.0	17	9	US-09-866-108-2750	Sequence 2750, App
40	7	100.0	17	9	US-09-866-108-2751	Sequence 2751, App
41	7	100.0	17	9	US-09-866-108-2752	Sequence 2752, App
42	7	100.0	17	9	US-09-866-108-2753	Sequence 2753, App
43	7	100.0	17	9	US-09-866-108-2754	Sequence 2754, App
44	7	100.0	17	9	US-09-866-108-2755	Sequence 2755, App
45	7	100.0	17	9	US-09-866-108-2756	Sequence 2756, App

## ALIGNMENTS

RESULT 1  
US-10-122-630-3  
Sequence 3, Application US/10122630  
Publication No. US20030032610A1  
GENERAL INFORMATION:  
APPLICANT: Gilchrist, Barbara A.  
APPLICANT: Eller, Mark S.  
TITLE OF INVENTION: Method to Inhibit Cell Growth Using  
Oligonucleotides  
FILE REFERENCE: 0054.1088-018  
CURRENT APPLICATION NUMBER: US/10/122.630  
CURRENT FILING DATE: 2002-04-12  
PRIOR APPLICATION NUMBER: US 08/467,012  
PRIOR FILING DATE: 1995-06-06  
PRIOR APPLICATION NUMBER: PCT/US96/08386  
PRIOR FILING DATE: 1996-06-03  
PRIOR APPLICATION NUMBER: US 09/048,927  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: US 09/540,843  
PRIOR FILING DATE: 2000-03-31  
PRIOR APPLICATION NUMBER: PCT/US01/10162  
PRIOR FILING DATE: 2001-03-30  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 7  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic DNA Fragment  
US-10-122-630-3

Query Match 100.0%; Score 7; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4,8e+08;  
Matches 7; Conservative 0; Mismatches 0; Gaps 0;  
Indels 0;  
1 AGTATGA 7



LOCATION: (1)..(12)  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Flexible Hinge  
 OTHER INFORMATION: Sequence (Fig. 1)  
 Patent No. 6096505  
 US-09-290-449-15

Query Match 88.9%; Score 8; DB 3; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGGAGGAT 9  
 Db 3 AGGAGGAT 10

RESULT 14  
 US-08-182-968A-168/c  
 Sequence 168, Application US/08182968A  
 Patent No. 5610054  
 GENERAL INFORMATION:  
 APPLICANT: Draper, Kenneth G.  
 TITLE OF INVENTION: METHOD AND REAGENT FOR  
 TITLE OF INVENTION: INHIBITING HEPATITIS C  
 TITLE OF INVENTION: VIRUS REPLICATION  
 NUMBER OF SEQUENCES: 497  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071-2066  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/182,968A  
 FILING DATE: 13-JANUARY-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/882,888  
 FILING DATE: 14-MAY-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Waiburg, Richard J.  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 205/277  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 168:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-182-968A-168

Query Match 88.9%; Score 8; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGGAGGAT 9  
 Db 13 AGGAGGAT 6

RESULT 15  
 US-08-182-968A-169/c

Sequence 169, Application US/08182968A  
 Patent No. 5610054  
 GENERAL INFORMATION:  
 APPLICANT: Draper, Kenneth G.  
 TITLE OF INVENTION: METHOD AND REAGENT FOR  
 TITLE OF INVENTION: INHIBITING HEPATITIS C  
 TITLE OF INVENTION: VIRUS REPLICATION  
 NUMBER OF SEQUENCES: 497  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071-2066  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/182,968A  
 FILING DATE: 13-JANUARY-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/882,888  
 FILING DATE: 14-MAY-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Waiburg, Richard J.  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 205/277  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 169:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-182-968A-169

Query Match 88.9%; Score 8; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGGAGGAT 9  
 Db 10 AGGAGGAT 3

Search completed: January 1, 2004, 00:32:18  
 Job time : 35.0858 secs



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; FILING DATE: APRIL 16, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: NONE
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: ARLES A. TAYLOR, JR.
; REGISTRATION NUMBER: 39,395
; REFERENCE/DOCKET NUMBER: 1242/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 493-8000
; TELEFAX: (919) 419-0383
;
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-061-768A-33

Query Match          100.0%; Score 9; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TAGGAGGAT 9
Db      7 TAGGAGGAT 15

RESULT 11
US-08-310-356-20/c
; Sequence 20, Application US/08310356
; Patent No. 5648243
; GENERAL INFORMATION:
; APPLICANT: Hurwitz, David R
; APPLICANT: Nathan, Margaret
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: Transgenic Protein Production
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Legal Department
; STREET: 500 Arcola Road
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System 7.0
; SOFTWARE: Microsoft Word Version 5.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/310,356
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,853
; FILING DATE: 31-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne
; REGISTRATION NUMBER: 32,534
; REFERENCE/DOCKET NUMBER: A0856
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 454-3817
; TELEFAX: (215) 454-3808
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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US-08-310-356-20

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Query Match          100.0%; Score 9; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TAGGAGGAT 9
Db      23 TAGGAGGAT 15

RESULT 12
US-09-019-793A-105/c
; Sequence 105, Application US/09019793A
; Patent No. 6380376
; GENERAL INFORMATION:
; APPLICANT: PAUL, Prem
; APPLICANT: MENG, Xiang-din
; APPLICANT: MOROZOV, Igor
; APPLICANT: HALBUR, Patrick
; TITLE OF INVENTION: PROTEINS ENCODED BY POLYNUCLEIC ACIDS OF PORCINE
; TITLE OF INVENTION: REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS (PRRSV)
; FILE REFERENCE: 4625-0035-55X CIP
; CURRENT APPLICATION NUMBER: US/09/019,793A
; CURRENT FILING DATE: 1998-02-06
; PRIOR APPLICATION NUMBER: 08/478,316
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/301,435
; PRIOR FILING DATE: 1994-09-01
; PRIOR APPLICATION NUMBER: 08/131,625
; PRIOR FILING DATE: 1993-10-05
; PRIOR APPLICATION NUMBER: 07/969,071
; PRIOR FILING DATE: 1992-10-30
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 105
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic DNA
;
US-09-019-793A-105

Query Match          100.0%; Score 9; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TAGGAGGAT 9
Db      15 TAGGAGGAT 7

RESULT 13
US-09-290-449-15
; Sequence 15, Application US/09290449A
; Patent No. 6096505
; GENERAL INFORMATION:
; APPLICANT: SELBY, Mark
; APPLICANT: THUDUM, Kent
; APPLICANT: DINA, Dino
; TITLE OF INVENTION: NONCLONING TECHNIQUE FOR EXPRESSING A GENE OF INTEREST
; FILE REFERENCE: 1448.002
; CURRENT APPLICATION NUMBER: US/09/290,449A
; CURRENT FILING DATE: 1999-04-13
; EARLIER APPLICATION NUMBER: US 60/081,777
; EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS

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Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TAGGAGGAT 9  
17 TAGGAGGAT 17  
Db

RESULT 6  
US-09-416-050A-15/c  
Sequence 15, Application US/09416050A  
Patent No. 6194559  
GENERAL INFORMATION:  
APPLICANT: KIM, Soo Young  
TITLE OF INVENTION: Abscisic Acid Responsive Element - Binding Transcription Factors  
FILE REFERENCE: 1942/42  
CURRENT APPLICATION NUMBER: US/09/416,050A  
CURRENT FILING DATE: 1999-10-12  
NUMBER OF SEQ ID NOS: 83  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15  
LENGTH: 24  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-416-050A-15

Query Match  
Best Local Similarity 100.0%; Score 9; DB 3; Length 24;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAGGAGGAT 9  
17 TAGGAGGAT 9  
Db

RESULT 7  
US-09-664-800-15/c  
Sequence 15, Application US/09664800  
Patent No. 6218527  
GENERAL INFORMATION:  
APPLICANT: KIM, Soo Young  
TITLE OF INVENTION: Abscisic Acid Responsive Element - Binding Transcription Factor  
FILE REFERENCE: 1942/42  
CURRENT APPLICATION NUMBER: US/09/664,800  
CURRENT FILING DATE: 2000-09-19  
PRIOR APPLICATION NUMBER: 09/416,050  
PRIOR FILING DATE: 1999-10-12  
NUMBER OF SEQ ID NOS: 83  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15  
LENGTH: 24  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-664-800-15

Query Match  
Best Local Similarity 100.0%; Score 9; DB 3; Length 24;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAGGAGGAT 9  
17 TAGGAGGAT 9  
Db

RESULT 8  
US-09-665-309-15/c  
Sequence 15, Application US/09665309  
Patent No. 6232461  
GENERAL INFORMATION:  
APPLICANT: KIM, Soo Young  
TITLE OF INVENTION: Abscisic Acid Responsive Element - Binding Transcription Factor  
FILE REFERENCE: 1942/42  
CURRENT APPLICATION NUMBER: US/09/665,309

CURRENT FILING DATE: 2000-09-19  
PRIOR APPLICATION NUMBER: 09/416,050  
PRIOR FILING DATE: 1999-10-12  
NUMBER OF SEQ ID NOS: 83  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15  
LENGTH: 24  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-665-309-15

Query Match  
Best Local Similarity 100.0%; Score 9; DB 3; Length 24;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAGGAGGAT 9  
17 TAGGAGGAT 9  
Db

RESULT 9  
US-09-661-569-15/c  
Sequence 15, Application US/09661569  
Patent No. 6245905  
GENERAL INFORMATION:  
APPLICANT: KIM, Soo Young  
TITLE OF INVENTION: Abscisic Acid Responsive Element - Binding Transcription Factor  
FILE REFERENCE: 1942/42  
CURRENT APPLICATION NUMBER: US/09/661,569  
CURRENT FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 09/416,050  
PRIOR FILING DATE: 1999-10-12  
NUMBER OF SEQ ID NOS: 83  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15  
LENGTH: 24  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-661-569-15

Query Match  
Best Local Similarity 100.0%; Score 9; DB 3; Length 24;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAGGAGGAT 9  
17 TAGGAGGAT 9  
Db

RESULT 10  
US-09-061-768A-33  
Sequence 33, Application US/09061768A  
Patent No. 6204037  
GENERAL INFORMATION:  
APPLICANT: BRASH, ALAN R.  
APPLICANT: BOEGLIN, WILLIAM E.  
TITLE OF INVENTION: LIPXYGENASE PROTEIN AND NUCLEIC ACIDS  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARLES A. TAYLOR, JR.  
STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD  
CITY: DURHAM  
STATE: NORTH CAROLINA  
COUNTRY: USA  
ZIP: 27707  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage  
COMPUTER: IBM PC/XT/AT compatible  
OPERATING SYSTEM: Windows 3.1  
SOFTWARE: WORD PERFECT 6.1 and ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/061,768A

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COUNTRY: United States
ZIP: 22113-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/096,172
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/177,145
FILING DATE: 04-JAN-1994
APPLICATION NUMBER: PR 93 00004
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 017753-040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: mutagenesis oligonucleotide (TAT
US-09-096-172-6
Query Match
Best Local Similarity 100.0%; Score 9; DB 3; Length 20;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TAGGAGCAT 9
DB 5 TAGGAGCAT 13
RESULT 3
US-09-422-978-6304/C
Sequence 6304, Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET 020CPI
CURRENT APPLICATION NUMBER: US/09/422,978
EARLIER FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 6304
LENGTH: 20
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..20
OTHER INFORMATION: upstream amplification primer 99-10661 for SEQ 2370,

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US-09-422-978-6304
Query Match
Best Local Similarity 100.0%; Score 9; DB 4; Length 20;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TAGGAGCAT 9
DB 18 TAGGAGCAT 10
RESULT 4
US-09-422-978-9775/C
Sequence 9775, Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET 020CPI
CURRENT APPLICATION NUMBER: US/09/422,978
EARLIER FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 9775
LENGTH: 21
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..21
OTHER INFORMATION: downstream amplification primer 99-7276 for SEQ 1910, in comp
US-09-422-978-9775
Query Match
Best Local Similarity 100.0%; Score 9; DB 4; Length 21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TAGGAGCAT 9
DB 11 TAGGAGCAT 3
RESULT 5
US-09-240-918-9
Sequence 9, Application US/09240918
Patent No. 6265165
GENERAL INFORMATION:
APPLICANT: Gruenert, Dieter C.
APPLICANT: Xu, Zhidong
TITLE OF INVENTION: METHODS FOR EST-SPECIFIC FULL LENGTH cDNA CLONING
FILE REFERENCE: 480.85.1(HV)
CURRENT APPLICATION NUMBER: US/09/240,918
EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/108,183
PRIOR FILING DATE: 1998-11-12
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-240-918-9
Query Match
100.0%; Score 9; DB 3; Length 22;

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using SW model

Run on: December 31, 2003, 14:40:05 ; Search time 34.9747 Seconds  
(without alignments)  
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Title: US-09-540-843-2

Perfect score: 9

Sequence: 1 tagagagat 9

Scoring table:

IDENTITY NUC  
Gapop 10-0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 547746

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	9	100.0	20	3	US-09-096-172-6
3	9	100.0	20	4	US-09-422-978-6304
4	9	100.0	21	4	US-09-422-978-9775
5	9	100.0	22	3	US-09-240-918-9
6	9	100.0	24	3	US-09-416-050A-15
7	9	100.0	24	3	US-09-664-800-15
8	9	100.0	24	3	US-09-665-309-15
9	9	100.0	24	3	US-09-661-569-15
10	9	100.0	28	3	US-09-061-768A-33
11	9	100.0	29	1	US-08-310-356-20
12	9	100.0	30	4	US-09-019-793A-105
13	8	88.9	12	3	US-09-220-449-15
14	8	88.9	15	1	US-08-182-968A-168
15	8	88.9	15	1	US-08-182-968A-168
16	8	88.9	15	2	US-08-774-306A-168
17	8	88.9	15	2	US-08-774-306A-168
18	8	88.9	15	3	US-09-105-515-4
19	8	88.9	15	3	US-09-064-156A-168
20	8	88.9	15	3	US-09-064-156A-168
21	8	88.9	15	4	US-09-748-044-4
22	8	88.9	16	1	US-07-664-989B-100
23	8	88.9	16	1	US-07-664-989B-100
24	8	88.9	16	2	US-08-282-197C-20
25	8	88.9	17	1	US-08-184-422-4
26	8	88.9	17	1	US-08-758-306-1307
27	8	88.9	17	1	US-08-758-306-1307

C 28	8	88.9	17	1	US-08-758-306-1311	Sequence 1311, Ap
29	8	88.9	17	3	US-08-589-771B-4	Sequence 4, Appl1
C 30	8	88.9	17	3	US-08-606-505B-45	Sequence 45, Appl1
C 31	8	88.9	17	3	US-09-616-990-45	Sequence 45, Appl1
32	8	88.9	17	4	US-08-584-040-1958	Sequence 1958, Ap
33	8	88.9	17	4	US-09-371-772B-503	Sequence 503, App
C 34	8	88.9	18	1	US-08-135-511-12	Sequence 12, Appl1
C 35	8	88.9	18	1	US-08-319-492B-735	Sequence 735, App
36	8	88.9	18	1	US-08-320-559-9	Sequence 9, Appl1
37	8	88.9	18	1	US-08-327-392-9	Sequence 9, Appl1
C 38	8	88.9	18	1	US-08-187-453-12	Sequence 12, Appl1
C 39	8	88.9	18	1	US-08-758-306-1309	Sequence 1309, Ap
C 40	8	88.9	18	1	US-08-207-412B-7	Sequence 7, Appl1
41	8	88.9	18	3	US-08-545-860B-9	Sequence 9, Appl1
42	8	88.9	18	3	US-08-912-272-87	Sequence 87, Appl1
43	8	88.9	18	3	US-09-050-159-26	Sequence 26, Appl1
C 44	8	88.9	18	3	US-09-071-433-79	Sequence 79, Appl1
C 45	8	88.9	18	3	US-08-487-761-9	Sequence 9, Appl1

#### ALIGNMENTS

```

RESULT 1
US-09-048-927-2
; Sequence 2, Application US/09048927
; Patent No. 6147056
; GENERAL INFORMATION:
; APPLICANT: Glitchrest, Barbara A.
; APPLICANT: Yaer, Mina
; APPLICANT: Eller, Mark
; TITLE OF INVENTION: Use of Locally Applied DNA Fragments
; FILE REFERENCE: B094-68A2
; CURRENT APPLICATION NUMBER: US/09/048,927
; CURRENT FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/952,697
; EARLIER FILING DATE: 1996-06-03
; EARLIER APPLICATION NUMBER: 08/467,012
; EARLIER FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA Fragment
; US-09-048-927-2

Query Match          100.0%; Score 9; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.7e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TAGAGAGAT 9
Db      1 TAGAGAGAT 9

RESULT 2
US-09-096-172-6
; Sequence 6, Application US/09096172
; Patent No. 6284252
; GENERAL INFORMATION:
; APPLICANT: MERTALI, Majid
; APPLICANT: SORG, Tanla
; TITLE OF INVENTION: NEW TRANSDOMINANT TAT VARIANTS OF THE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia

```

SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-10-232-927A-20

Query Match 100.0%; Score 11; DB 13; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTAGGGTTAG 11  
|||  
Db 13 GTTAGGGTTAG 3

Search completed: January 1, 2004, 01:10:37  
Job time : 129.241 secs

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US-10-038-335-1
; Sequence 1, Application US/10038335
; Publication No. US20030096776A1
; GENERAL INFORMATION:
; APPLICANT: Eckert, David J.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Bennett, C. Frank
; APPLICANT: Hanecak, Ronnie
; APPLICANT: Brown-Driver, Vickie
; APPLICANT: Vickers, Timothy
; APPLICANT: Chiang, Ming-Yi
; APPLICANT: Anderson, Kevin
; TITLE OF INVENTION: Modulation Of Telomere Length By Oligonucleotides Having A G-Core
; FILE REFERENCE: ISIS-4976
; CURRENT APPLICATION NUMBER: US/10/038,335
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 09/299,058
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: 08/403,888
; PRIOR FILING DATE: 1995-06-12
; PRIOR APPLICATION NUMBER: PCT/US93/09297
; PRIOR FILING DATE: 1993-09-29
; PRIOR APPLICATION NUMBER: 07/954,185
; PRIOR FILING DATE: 1992-09-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2

Query Match      100.0%; Score 11; DB 15; Length 13;
Best Local Similarity 63.6%; Pred. No. 4.7e+03;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTTAGGCTAG 11
Db      3 GUNAGGCUUAC 13

RESULT 14
; Sequence 2, Application US/10038335
; Publication No. US20030096776A1
; GENERAL INFORMATION:
; APPLICANT: Eckert, David J.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Bennett, C. Frank
; APPLICANT: Hanecak, Ronnie
; APPLICANT: Brown-Driver, Vickie
; APPLICANT: Vickers, Timothy
; APPLICANT: Chiang, Ming-Yi
; APPLICANT: Anderson, Kevin
; TITLE OF INVENTION: Modulation Of Telomere Length By Oligonucleotides Having A G-Core
; FILE REFERENCE: ISIS-4976
; CURRENT APPLICATION NUMBER: US/10/038,335
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 09/299,058
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: 08/403,888
; PRIOR FILING DATE: 1995-06-12
; PRIOR APPLICATION NUMBER: PCT/US93/09297
; PRIOR FILING DATE: 1993-09-29
; PRIOR APPLICATION NUMBER: 07/954,185
; PRIOR FILING DATE: 1992-09-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2

```

```

; LENGTH: 13
; TYPE: DNA
; ORGANISM: No. US20030096776A1 sequence
; FEATURE:
; OTHER INFORMATION: Antisense sequence
US-10-038-335-2

Query Match      100.0%; Score 11; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTTAGGCTAG 11
Db      3 GTTAGGCTAG 13

RESULT 15
; Sequence 20, Application US/10232927A
; Publication No. US20030190638A1
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; Calvin B. Hartley
; Scott U. Weinlich
; Catherine M. Strahl
; Michael J. McEachern
; Jerry Shay
; Woodring E. Wright
; Elizabeth H. Blackburn
; Nam Woo Kim
; Homeyoun Vaziri
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; CONDITIONS RELATED TO
; TELOMERE LENGTH AND/OR
; TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/232,927A
; FILING DATE: 29-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,535
; FILING DATE: 20-Aug-1999
; APPLICATION NUMBER: 08/819,867
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Chambers, Daniel M.
; REGISTRATION NUMBER: 34,561
; REFERENCE/DOCKET NUMBER: 224/232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```

```

; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-5

```

```

Query Match      100.0%; Score 11; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GTTAGGGTTAG 11
        |||||
        1 GTTAGGGTTAG 11

```

```

RESULT 9
US-10-122-633-9/c
; Sequence 9, Application US/10122633
; Publication No. US20030032611A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Elter, Mark S.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: Method to Inhibit Cell Growth Using
; FILE REFERENCE: 0054.1088-019
; CURRENT APPLICATION NUMBER: US/10/122,633
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 09/540,843
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: PCT/US01/10162
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-9

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```

Query Match      100.0%; Score 11; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GTTAGGGTTAG 11
        |||||
        11 GTTAGGGTTAG 11

```

```

RESULT 10
US-09-893-252-4
; Sequence 4, Application US/09893252
; Publication No. US20030012755A1
; GENERAL INFORMATION:
; APPLICANT: Styczynski, Peter
; APPLICANT: Ahluwalia, Gurpreet S.
; TITLE OF INVENTION: REDUCTION OF HAIR GROWTH
; FILE REFERENCE: 00216-552001
; CURRENT APPLICATION NUMBER: US/09/893,252
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 13
; TYPE: RNA

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; ORGANISM: Homo sapiens
US-09-893-252-4

```

```

Query Match      100.0%; Score 11; DB 11; Length 13;
Best Local Similarity 63.6%; Pred. No. 4.7e+03;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GTTAGGGTTAG 11
        |||||
        3 GUNAGGGUAG 13

```

```

RESULT 11
US-10-347-253-1
; Sequence 1, Application US/10347253
; Publication No. US20030175776A1
; GENERAL INFORMATION:
; APPLICANT: Hitachi Software Engineering Co., Ltd.
; TITLE OF INVENTION: Accelerator And Acceleration Method For Hybridization
; FILE REFERENCE: 138051
; CURRENT APPLICATION NUMBER: US/10/347,253
; CURRENT FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-347-253-1

```

```

Query Match      100.0%; Score 11; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GTTAGGGTTAG 11
        |||||
        1 GTTAGGGTTAG 11

```

```

RESULT 12
US-10-368-451-1
; Sequence 1, Application US/10368451
; Publication No. US20030186298A1
; GENERAL INFORMATION:
; APPLICANT: Hitachi Software Engineering Co., Ltd.
; TITLE OF INVENTION: POLYMER CHIP AND METHOD FOR IDENTIFYING AN IONIC POLYMER
; FILE REFERENCE: PH-1700
; CURRENT APPLICATION NUMBER: US/10/368,451
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: JP 2002-090129
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Artificial sequence synthesized by a sequencer by the inventors
US-10-368-451-1

```

```

Query Match      100.0%; Score 11; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GTTAGGGTTAG 11
        |||||
        1 GTTAGGGTTAG 11

```

```

RESULT 13

```

```
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/359,935
FILING DATE: 07-Feb-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/057,351
FILING DATE: 08-APR-1994
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: US 08/472,802
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000821US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-359-935-2
Query Match 100.0%; Score 11; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTAGGGTTAG 11
Db 11 GTTAGGGTTAG 1
RESULT 6
US-10-122-630-5
Sequence 5, Application US/10122630
Publication No. US20030032610A1
GENERAL INFORMATION:
APPLICANT: Gilcrest, Barbara A.
APPLICANT: Eller, Mark S.
TITLE OF INVENTION: Method to inhibit Cell Growth Using
TITLE OF INVENTION: Oligonucleotides
FILE REFERENCE: 0054.1088-018
CURRENT APPLICATION NUMBER: US/10/122,630
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US 08/467,012
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: PCT/US96/08386
PRIOR FILING DATE: 1996-06-03
PRIOR APPLICATION NUMBER: US 09/048,927
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: PCT/US01/10162
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
```

```
LENGTH: 11
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-5
Query Match 100.0%; Score 11; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTAGGGTTAG 11
Db 11 GTTAGGGTTAG 1
RESULT 7
US-10-122-630-9/c
Sequence 9, Application US/10122630
Publication No. US20030032610A1
GENERAL INFORMATION:
APPLICANT: Gilcrest, Barbara A.
APPLICANT: Eller, Mark S.
TITLE OF INVENTION: Method to inhibit Cell Growth Using
TITLE OF INVENTION: Oligonucleotides
FILE REFERENCE: 0054.1088-018
CURRENT APPLICATION NUMBER: US/10/122,630
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US 08/467,012
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: PCT/US96/08386
PRIOR FILING DATE: 1996-06-03
PRIOR APPLICATION NUMBER: US 09/048,927
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: PCT/US01/10162
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 11
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-630-9
Query Match 100.0%; Score 11; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTAGGGTTAG 11
Db 11 GTTAGGGTTAG 1
RESULT 8
US-10-122-633-5
Sequence 5, Application US/10122633
Publication No. US20030032611A1
GENERAL INFORMATION:
APPLICANT: Gilcrest, Barbara A.
APPLICANT: Eller, Mark S.
TITLE OF INVENTION: Method to inhibit Cell Growth Using
TITLE OF INVENTION: Oligonucleotides
FILE REFERENCE: 0054.1088-019
CURRENT APPLICATION NUMBER: US/10/122,633
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR FILING DATE: 2000-03-31
```



REGISTRATION NUMBER: 32,944  
 REFERENCE/DOCKET NUMBER: 015389-000821US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 11 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: RNA  
 US-09-057-351-2

Query Match 100.0%; Score 11; DB 9; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTAGGGTTAG 11  
 |||||  
 Db 11 GTTAGGGTTAG 1

RESULT 2  
 US-09-835-370-63  
 ; Sequence 63, Application US/09835370  
 ; Publication No. US20030022172A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: UHLMANN, EUGEN  
 ; APPLICANT: BREIPOHL, GERHARD  
 ; APPLICANT: WILF, DAVID W  
 ; TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES AND AGENTS AND  
 ; FILE REFERENCE: 02481.1742 SEQUENCE LISTING  
 ; CURRENT APPLICATION NUMBER: US/09/835,370  
 ; NUMBER OF SEQ ID NOS: 64  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 63  
 ; LENGTH: 11  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: nucleotide  
 ; OTHER INFORMATION: base sequence of PNA derivatives that bind to  
 ; OTHER INFORMATION: viral and cellular targets  
 US-09-835-370-63

Query Match 100.0%; Score 11; DB 11; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTAGGGTTAG 11  
 |||||  
 Db 1 GTTAGGGTTAG 11

RESULT 3  
 US-10-255-535-4  
 ; Sequence 4, Application US/10255535  
 ; Publication No. US20030138814A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Geron Corporation  
 ; APPLICANT: Gryaznov, Sergei  
 ; APPLICANT: Pongracz, Kristina  
 ; APPLICANT: Tolman, Richard L.  
 ; APPLICANT: Morin, Gregg B.  
 ; TITLE OF INVENTION: Oligonucleotide Conjugates  
 ; FILE REFERENCE: 072/002P  
 ; CURRENT APPLICATION NUMBER: US/10/255,535  
 ; CURRENT FILING DATE: 2002-09-25  
 ; PRIOR APPLICATION NUMBER: PCT/US02/09138  
 ; PRIOR FILING DATE: 2002-03-21

PRIOR APPLICATION NUMBER: US 60/278,322  
 PRIOR FILING DATE: 2001-03-23  
 NUMBER OF SEQ ID NOS: 19  
 SOFTWARE: Patent In version 3.1  
 SEQ ID NO 4  
 LENGTH: 11  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: oligonucleotide  
 US-10-255-535-4

Query Match 100.0%; Score 11; DB 13; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTAGGGTTAG 11  
 |||||  
 Db 1 GTTAGGGTTAG 11

RESULT 4  
 US-10-255-535-14  
 ; Sequence 14, Application US/10255535  
 ; Publication No. US20030138814A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Geron Corporation  
 ; APPLICANT: Gryaznov, Sergei  
 ; APPLICANT: Pongracz, Kristina  
 ; APPLICANT: Tolman, Richard L.  
 ; APPLICANT: Morin, Gregg B.  
 ; TITLE OF INVENTION: Oligonucleotide Conjugates  
 ; FILE REFERENCE: 072/002P  
 ; CURRENT APPLICATION NUMBER: US/10/255,535  
 ; CURRENT FILING DATE: 2002-09-25  
 ; PRIOR APPLICATION NUMBER: PCT/US02/09138  
 ; PRIOR FILING DATE: 2002-03-21  
 ; PRIOR APPLICATION NUMBER: US 60/278,322  
 ; PRIOR FILING DATE: 2001-03-23  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: Patent In version 3.1  
 ; SEQ ID NO 14  
 ; LENGTH: 11  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: oligonucleotide  
 US-10-255-535-14

Query Match 100.0%; Score 11; DB 13; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTAGGGTTAG 11  
 |||||  
 Db 1 GTTAGGGTTAG 11

RESULT 5  
 US-10-359-935-2/c  
 ; Sequence 2, Application US/10359935  
 ; Publication No. US20030153076A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Villeponteau, Bryant  
 ; APPLICANT: Feng, Junli  
 ; APPLICANT: Funk, Walter  
 ; APPLICANT: Andrews, William H.  
 ; TITLE OF INVENTION: Mammalian Telomerase  
 ; NUMBER OF SEQUENCES: 42  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, Eighth Floor  
 ; CITY: San Francisco

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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 17:10:00 ; Search time 128.241 Seconds  
(without alignments)  
296.896 Million cell updates/sec

Title: US-09-540-843-5  
Perfect score: 11  
Sequence: 1 gtagggctag 11

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 2263443 seqs, 1730637950 residues  
Total number of hits satisfying chosen parameters: 998502

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_NA:\*

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3:	/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4:	/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5:	/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6:	/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7:	/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8:	/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9:	/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10:	/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11:	/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
12:	/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13:	/cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
14:	/cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
15:	/cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
16:	/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
17:	/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
18:	/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	11	100.0	11	9	US-09-057-351-2
C 2	11	100.0	11	11	US-09-835-370-63
C 3	11	100.0	11	13	US-10-255-535-4
C 4	11	100.0	11	13	US-10-255-535-14
C 5	11	100.0	11	13	US-10-359-935-2
C 6	11	100.0	11	13	US-10-122-630-5
C 7	11	100.0	11	15	US-10-122-630-9
C 8	11	100.0	11	15	US-10-122-630-9
C 9	11	100.0	11	15	US-10-122-633-9
C 10	11	100.0	11	11	US-09-893-252-4
C 11	11	100.0	13	13	US-10-347-253-1
C 12	11	100.0	13	13	US-10-368-451-1
C 13	11	100.0	13	15	US-10-038-335-1
C 14	11	100.0	13	15	US-10-038-335-2
C 15	11	100.0	16	13	US-10-232-927A-20

C 16	11	100.0	18	8	US-08-463-404-4	Sequence 4, Appli
C 17	11	100.0	18	8	US-08-463-404-5	Sequence 5, Appli
C 18	11	100.0	18	9	US-09-057-351-26	Sequence 26, Appli
C 19	11	100.0	18	10	US-09-947-659-1	Sequence 1, Appli
C 20	11	100.0	18	10	US-09-947-659-2	Sequence 2, Appli
C 21	11	100.0	18	10	US-09-947-659-7	Sequence 7, Appli
C 22	11	100.0	18	11	US-09-893-252-1	Sequence 11, Appli
C 23	11	100.0	18	13	US-10-336-265-11	Sequence 1, Appli
C 24	11	100.0	18	13	US-10-336-265-15	Sequence 15, Appli
C 25	11	100.0	18	13	US-10-336-265-61	Sequence 61, Appli
C 26	11	100.0	18	13	US-10-359-935-26	Sequence 26, Appli
C 27	11	100.0	18	13	US-10-323-032-4	Sequence 4, Appli
C 28	11	100.0	18	13	US-10-323-032-5	Sequence 5, Appli
C 29	11	100.0	18	13	US-10-330-872-6	Sequence 6, Appli
C 30	11	100.0	18	13	US-10-330-872-7	Sequence 7, Appli
C 31	11	100.0	18	13	US-10-332-927A-3	Sequence 3, Appli
C 32	11	100.0	18	13	US-10-332-927A-4	Sequence 4, Appli
C 33	11	100.0	18	13	US-10-332-927A-8	Sequence 8, Appli
C 34	11	100.0	18	13	US-10-332-927A-21	Sequence 21, Appli
C 35	11	100.0	18	13	US-10-332-927A-24	Sequence 24, Appli
C 36	11	100.0	18	13	US-10-332-927A-62	Sequence 62, Appli
C 37	11	100.0	18	13	US-10-349-507-41	Sequence 41, Appli
C 38	11	100.0	18	15	US-10-132-002-2	Sequence 2, Appli
C 39	11	100.0	18	15	US-10-238-732-2	Sequence 2, Appli
C 40	11	100.0	18	15	US-10-044-692-295	Sequence 295, App
C 41	11	100.0	18	15	US-10-044-692-296	Sequence 296, App
C 42	11	100.0	18	15		
C 43	11	100.0	18	15		
C 44	11	100.0	18	15		
C 45	11	100.0	18	15		

# ALIGNMENTS

RESULT 1  
US-09-057-351-2/c  
; Sequence 2, Application US/09057351  
; Patent No. US20010034439A1  
GENERAL INFORMATION:  
APPLICANT: Villeponteau, Bryant  
APPLICANT: Feng, Junli  
APPLICANT: Funk, Walter  
APPLICANT: Andrews, William H.  
TITLE OR INVENTION: Mammalian Telomerase  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/057,351  
FILING DATE: 08-APR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/472,802  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.